

Resource Summary Report

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Circos

RRID:SCR_011798

Type: Tool

Proper Citation

Circos (RRID:SCR_011798)

Resource Information

URL: <http://circos.ca/>

Proper Citation: Circos (RRID:SCR_011798)

Description: A software package for visualizing data and information. It visualizes data in a circular layout - this makes Circos ideal for exploring relationships between objects or positions.

Abbreviations: Circos

Resource Type: software resource

Defining Citation: [DOI:10.1101/gr.092759.109](https://doi.org/10.1101/gr.092759.109)

Keywords: bio.tools

Resource Name: Circos

Resource ID: SCR_011798

Alternate IDs: biotools:circos, OMICS_00932

Alternate URLs: <https://bio.tools/circos>, <https://sources.debian.org/src/circos/>

Record Creation Time: 20220129T080306+0000

Record Last Update: 20260801T190430+0000

Ratings and Alerts

No rating or validation information has been found for Circos.

No alerts have been found for Circos.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5084 mentions in open access literature.

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

Kirkland C, et al. (2026) Chromosome-Level Genomics and Historical Museum Collections Reveal New Insights Into the Population Structure and Chromosome Evolution of Waterbuck. *Molecular ecology*, 35(1), e70218.

Wang Z, et al. (2026) Multidimensional mapping of stimulation-responsive regulatory elements and candidate causal variants in T cell activation. *Science advances*, 12(1), eady2539.

Risley CA, et al. (2025) Transcription factor T-bet regulates the maintenance and differentiation potential of lymph node and lung effector memory B cell subsets. *Immunity*, 58(7), 1706.

Bian C, et al. (2025) Chromosome-level genome assemblies of five *Sinocyclocheilus* species. *GigaByte (Hong Kong, China)*, 2025, gigabyte155.

Goshayeshi L, et al. (2025) Germline variants in patients from the Iranian hereditary colorectal cancer registry. *Cancer cell international*, 25(1), 140.

Bergsma P, et al. (2025) Integration of Whole-Genome Sequencing Analysis with Unique Patient-Derived Models Reveals Clinically Relevant Drug Targets in TFCP2 Fusion-Defined Rhabdomyosarcoma. *Molecular cancer therapeutics*, 24(12), 1989.

Naktang C, et al. (2025) Chromosome-level assemblies of two hexaploid bamboos, *Thyrsostachys oliveri* and *Thyrsostachys siamensis*, provide a foundation for functional and comparative genomics studies. *GigaScience*, 14.

Zhao YJ, et al. (2025) An endogenous aryl hydrocarbon receptor ligand dysregulates endothelial functions, transcriptome, and phosphoproteome. *American journal of physiology. Cell physiology*, 328(3), C954.

Grimm SL, et al. (2025) CA-125 as a Biomarker in Renal Medullary Carcinoma: Integrated Molecular Profiling, Functional Characterization, and Prospective Clinical Validation. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 31(6), 1057.

Zuccoli E, et al. (2025) Reproducibility of PD patient-specific midbrain organoid data for in vitro disease modeling. *iScience*, 28(10), 113541.

Li X, et al. (2025) Chromosome-level genome assembly for the ecologically and economically important alga *Saccharina japonica*. *Scientific data*, 12(1), 290.

Bibi A, et al. (2025) Behavioral alterations in antibiotic-treated mice associated with gut microbiota dysbiosis: insights from 16S rRNA and metabolomics. *Frontiers in neuroscience*, 19, 1478304.

Galarza Fortuna GM, et al. (2025) Nivolumab adjuvant to chemo-radiation in localized muscle-invasive urothelial cancer: primary analysis of a multicenter, single-arm, phase II, investigator-initiated trial (NEXT). *Journal for immunotherapy of cancer*, 13(3).

Gaikwad AB, et al. (2025) Chromosome-scale genome assembly of *Trigonella corniculata* (L.)L. (Nagauri pan /Kasuri methi), an important spice. *Scientific data*, 12(1), 509.

Wang J, et al. (2025) Multi-omics analysis reveals Jianpi formula-derived bioactive peptide-YG-22 potentially inhibited colorectal cancer via regulating epigenetic reprogram and signal pathway regulation. *Frontiers in genetics*, 16, 1560172.

Feng DD, et al. (2025) Chromosome-level genome assembly of a specialist walnut pest *Atrijuglans aristata*. *Scientific data*, 12(1), 434.

Penaloza JS, et al. (2025) Identification of Long Noncoding RNA Candidate Disease Genes Associated With Clinically Reported Copy Number Variants in Congenital Heart Disease. *Journal of the American Heart Association*, 14(6), e039177.

Muruganantham JK, et al. (2025) Lack of association between the TMPRSS6 gene polymorphism (rs855791) and anemia: a comprehensive meta-analysis. *Hematology, transfusion and cell therapy*, 47(2), 103737.

Xu W, et al. (2025) Plasmodium Infection Modulates Host Inflammatory Response through circRNAs during the Intracellular Stage in Red Blood Cells. *ACS infectious diseases*, 11(4), 1018.

Gao C, et al. (2025) Assembly and comparative analysis of the complete mitochondrial genome of *Echinacanthus longipes* (Acanthaceae), endemic to the Sino-Vietnamese karst flora. *BMC genomics*, 26(1), 251.