

Resource Summary Report

Generated by T1D on Aug 3, 2026

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 [T1D](#).

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.

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.

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.

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.

Zhao K, et al. (2025) Pangenome analysis reveals structural variation associated with seed size and weight traits in peanut. *Nature genetics*, 57(5), 1250.

Wang Y, et al. (2025) Efficient degradation of tylosin by *Kurthia gibsonii* TYL-A1: performance, pathway, and genomics study. *Microbiology spectrum*, 13(6), e0002525.

Zhang LM, et al. (2025) Mendelian randomization combined with single-cell sequencing data analysis of chemokines and chemokine receptors and key genes and molecular mechanisms associated with epilepsy. *Neuroreport*, 36(9), 467.

Zhang Q, et al. (2025) Postoperative continuous saline bladder irrigation reduces active urinary cancer cells: a prospective study in NMIBC. *Cellular oncology (Dordrecht, Netherlands)*, 48(4), 991.

Zeng Y, et al. (2025) Chromosome-level genomes of Arctic and Antarctic mosses: *Aulacomnium turgidum* and *Polytrichastrum alpinum*. *Scientific data*, 12(1), 705.

Pu YL, et al. (2025) The first chromosome-level genome of the lappet moth *Trabala vishnou* (Lepidoptera: Lasiocampidae). *Scientific data*, 12(1), 1154.

Ruiz-Ruano FJ, et al. (2025) Programmed DNA elimination drives rapid genomic innovation in two thirds of all bird species. *bioRxiv : the preprint server for biology*.

Luo S, et al. (2025) Genome assembly at the chromosome level of *Clinopodium barosmum*. *Scientific data*, 12(1), 1406.

Li W, et al. (2025) Exploring ferroptosis-associated immune characteristics in Kawasaki disease through bioinformatics. *Scientific reports*, 15(1), 30261.

Isaza-Correa JM, et al. (2025) Childhood resolution of early abnormal miRNA following neonatal encephalopathy. *Scientific reports*, 15(1), 30489.