

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: 20260815T182433+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 5669 mentions in open access literature.

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

Nawae W, et al. (2026) Genome Assembly of Three Shrub Mangroves in the Genus *Acanthus* Reveals Two Polyploidy Events and Expansion of Genes Linked to Root Adaptation in Coastal Habitats. *GigaScience*, 15.

Fu X, et al. (2026) Genome refinement in Pacific bluefin tuna (*Thunnus orientalis*): chromosome-level assembly using hybrid linkage data. *BMC genomics*, 27(1).

New JS, et al. (2026) Human anti-glycan reactivity emerges from B cells utilizing private gene rearrangements that are affinity matured in germinal centers. *Immunity*, 59(3), 651.

Friske JD, et al. (2026) A Conserved Enhancer Locus in Extrachromosomal DNA and Homogeneously Staining Regions Activates MYC Transcription in Group 3 Medulloblastoma. *Cancer research*, 86(13), 3160.

Mao C, et al. (2026) Chromosome-level genome assembly and transcriptomes of the leaf insect *Cryptophyllum westwoodii* provide insights into the evolution of leaf-like masquerade. *GigaScience*, 15.

Dong YP, et al. (2026) Early replication fragile sites are associated with cancer-related CNVs and SNVs in human embryonic stem cells. *Stem cell reports*, 21(7), 102968.

Ha HT, et al. (2026) Human Atlas of Tooth Decay Progression: Identification of Cellular Mechanisms Driving the Switch from Dental Pulp Repair Toward Irreversible Pulpitis. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(8), e10096.

Hao DL, et al. (2026) Expansion and Functional Divergence of Shaker K⁺ Channels in Bermudagrass Highlight CdKAT1.1 in Salt Tolerance. *International journal of molecular sciences*, 27(7).

Tian Z, et al. (2026) Assembly and comparative analysis of the complete mitochondrial genome of two species of Argentina (*Rosaceae*). *BMC genomics*, 27(1).

Qin Y, et al. (2026) Host genetic regulation of xylem-resident *Pseudomonas* enhances cucumber growth. *Microbiome*, 14(1).

Aoyagi YB, et al. (2026) Chromosome-level genome assembly of the *Gerbera* (*Gerbera hybrida*) using HiFi long-read and Hi-C technologies. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 33(1).

Gaire BP, et al. (2026) Identification of *Chlamydia pneumoniae* and NLRP3 inflammasome activation in Alzheimer's disease retina. *Nature communications*, 17(1), 771.

Tian W, et al. (2026) Genetic alternative splicing regulation mapping of cartilage and synovium reveals tissue-specific mechanisms of joint-related traits. *Nature communications*, 17(1).

Xue T, et al. (2026) Pan-genomic analysis and abiotic stress expression of eight TPS gene families in *Brassica napus*. *BMC plant biology*, 26(1).

Han L, et al. (2026) Genome-Wide Identification and Characterization of Stress-Responsive SNARE Genes in Quinoa (*Chenopodium quinoa* Willd.). *Biology*, 15(5).

Barco-Armengol N, et al. (2026) Identification of autosomal and sex chromosome aneuploidies using next generation sequencing. *Bioinformatics (Oxford, England)*, 42(3).

Pevsner R, et al. (2026) Telomere-to-telomere genome assembly of *Microsporidia* sp. MB, a microsporidian symbiont of *Anopheles coluzzii* isolated from Burkina Faso. *BMC genomics*, 27(1).

Zheng J, et al. (2026) Mitochondrial genome of the invasive weed *Amaranthus palmeri*: structural features, RNA editing, and evolutionary insights. *BMC plant biology*, 26(1).

Ebeed HT, et al. (2026) Integrative gene duplication and genome-wide analysis characterize Peroxin11 gene family in wheat. *BMC genomics*, 27(1).

Jani J, et al. (2026) Atypical El Tor *Vibrio cholerae* from the second major global seventh-pandemic cholera wave is endemic in Sabah, Malaysia. *Microbiology spectrum*, 14(3), e0219125.