

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: 20260829T182408+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 [NIF](#).

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.

Liu T, et al. (2026) Chromosome-level genome assembly and annotation of the endangered plant *Primula kwangtungensis* (Primulaceae). *Scientific data*, 13(1), 212.

Lee M, et al. (2026) LINE-1 Locus Transcription Nucleates Oncogenic Chromatin Architecture. *Cancer discovery*, 16(4), 800.

van Heule M, et al. (2026) Beyond nocardioform: Transcriptionally active microbes and host responses in equine mucoid placentitis. *Equine veterinary journal*, 58(2), 601.

Han H, et al. (2026) Whole-genome analysis and fermentation-metabolite profiling of a cellulolytic *Arthrobacter* sp. FMD isolated from forest musk-deer faeces. *BMC microbiology*, 26(1), 43.

Shi X, et al. (2026) Diet intervention altered DNA methylation of potassium voltage-gated channel subfamily Q member 1 in metabolic dysfunction-associated steatohepatitis. *Clinical epigenetics*, 18(1).

- Ali F, et al. (2026) Identification and expression profiling of the GRAS gene family reveals candidate genes for enhancing abiotic stress tolerance in lentil. *BMC plant biology*, 26(1), 245.
- 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.
- Nascimento-Vidoti CG, et al. (2026) Overexpression of SOX3 due to an X chromosome inversion leading to ovotesticular difference in sex development. *Biology of sex differences*, 17(1).
- 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).
- Xue L, et al. (2026) Near telomere-to-telomere diploid genome assembly of *Acrossocheilus wenchowensis*. *Scientific data*, 13(1).