

Resource Summary Report

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RCircos

RRID:SCR_003310

Type: Tool

Proper Citation

RCircos (RRID:SCR_003310)

Resource Information

URL: <http://cran.r-project.org/web/packages/RCircos/>

Proper Citation: RCircos (RRID:SCR_003310)

Description: Software package that provides a simple and flexible way to generate Circos 2D track plot images for genomic data visualization. The types of plots include: heatmap, histogram, lines, scatterplot, tiles and plot items for further decorations include connector, link (lines and ribbons), and text (gene) label. All functions require only R graphics package that comes with R base installation.

Synonyms: RCircos: Circos 2D Track Plot

Resource Type: software resource

Defining Citation: [PMID:23937229](#)

Keywords: standalone software, unix/linux, mac os x, windows, r

Availability: Free, Available for download, Freely available

Resource Name: RCircos

Resource ID: SCR_003310

Alternate IDs: OMICS_04661

Alternate URLs: <https://bitbucket.org/henryhzhang/rcircos/>

Record Creation Time: 20220129T080218+0000

Record Last Update: 20260905T132501+0000

Ratings and Alerts

No rating or validation information has been found for RCircos.

No alerts have been found for RCircos.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 285 mentions in open access literature.

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

Liu X, et al. (2026) Cancer-associated fibroblasts and immune escape-related genes serve as biological markers for the prognosis of colorectal cancer. *Hereditas*, 163(1).

Li S, et al. (2026) Utilizing bulk and single-cell RNA sequencing to identify potential biomarkers linked to angiogenesis and integrated stress response in chondrosarcoma. *Scientific reports*, 16(1).

Kou R, et al. (2026) Unveiling prognostic genes and regulatory mechanisms of stress granules in gastric cancers: an integrated analysis of bulk transcriptomics and single-cell RNA sequencing. *Frontiers in oncology*, 16, 1750088.

Zhao X, et al. (2026) Identification and validation of mitochondrial metabolism-related biomarkers in coronary heart disease. *Medicine*, 105(7), e47595.

Ma T, et al. (2026) Identification and validation of biomarkers of Shenggu Zaizao Wan in the treatment of steroid-induced osteonecrosis of the femoral head by integrating network pharmacology and bulk transcriptomic. *Frontiers in medicine*, 13, 1732825.

Wen Y, et al. (2026) Integrative multi-omics reveals that downregulation of HLA-DPA1/DPB1 drives macrophage immune-metabolic dysregulation in pediatric asthma. *Frontiers in immunology*, 17, 1835475.

Pradhan B, et al. (2026) Dynamic and Ongoing De Novo L1 Retrotransposition Contributes to Genome Plasticity and Intrapatient Heterogeneity in Ovarian Cancer. *Cancer research*, 86(4), 1073.

Ling S, et al. (2026) Integrative omics and experimental validation reveal METTL17 and SLC27A1 as biomarkers and potential therapeutic targets in chronic kidney disease. *Frontiers in immunology*, 17, 1724740.

Du Y, et al. (2026) IL6/IL10/TLR4 Govern Immunogenic Cell Death in Aortic Dissection. *Cardiovascular therapeutics*, 2026(1), e4140685.

Xia Y, et al. (2026) Identification of biomarkers associated with endoplasmic reticulum stress-related cell death in osteoporosis based on bulk and single-cell transcriptomic analyses and experimental validation. *Scientific reports*, 16(1).

Jin Y, et al. (2026) m6A target gene signatures reveal immune-related diagnostic biomarkers in systemic sclerosis-associated pulmonary arterial hypertension. *Journal of thoracic disease*, 18(5), 504.

Luo J, et al. (2026) Identification of biomarkers related to γ -aminobutyric acid-associated genes in membranous nephropathy based on transcriptome data and clinical experiments. *Hereditas*, 163(1).

Jiang F, et al. (2026) Machine learning identifies a NETs-related four-gene diagnostic signature for abdominal aortic aneurysm. *Medicine*, 105(21), e48987.

Luo T, et al. (2026) Integrative multi-omics and network analysis identify potential targets of Chaihu Shugan Xiaozheng Formula in breast cancer. *Translational oncology*, 70, 102829.

Weng X, et al. (2026) Identification of COL5A1 and TGFBI as key basement membrane genes and their molecular mechanisms in gestational diabetes mellitus. *Medicine*, 105(18), e48610.

Zhao T, et al. (2026) Identification of key macrophage-related genes in systemic sclerosis-associated interstitial lung disease based on single-cell and bulk transcriptomic data. *PloS one*, 21(3), e0344166.

Peng S, et al. (2026) Discovery of circadian rhythm-related hub genes in acute myocardial infarction: A two-sample Mendelian randomization study. *Medicine*, 105(3), e47228.

Lang Y, et al. (2026) The value of immunogenic cell death-related gene model in the prognosis of gastric cancer. *Discover oncology*, 17(1).

Jiang W, et al. (2026) Identification of core cytotoxic T lymphocyte-related subtypes, establishment of a prognostic model, and analysis tumor microenvironment infiltration in HNSC. *Scientific reports*, 16(1).

Zhang J, et al. (2026) The signature of pyroptosis-related gene diagnosis and immune microenvironment in preeclampsia. *BMC pregnancy and childbirth*, 26(1).