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/

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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

Funding:

Availability: GNU General Public License, v2, v3

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: 20250410T064956+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 187 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Liu W, et al. (2025) Identification of macrophage polarisation and mitochondria-related biomarkers in diabetic retinopathy. Journal of translational medicine, 23(1), 23.

Gupta M, et al. (2025) Meta-QTL analysis for mining of candidate genes and constitutive gene network development for viral disease resistance in maize (Zea mays L.). Heliyon, 11(1), e40984.

Liao SX, et al. (2025) Integrating bulk and single-cell RNA sequencing data: unveiling RNA methylation and autophagy-related signatures in chronic obstructive pulmonary disease patients. Scientific reports, 15(1), 4005.

Wu Y, et al. (2025) Identification of cancer-associated fibroblast subtypes and prognostic model development in breast cancer: role of the RUNX1/SDC1 axis in promoting invasion and metastasis. Cell biology and toxicology, 41(1), 21.

Zhou J, et al. (2025) Comprehensive Analysis of Programmed Cell Death-Related Genes in Diagnosis and Synovitis During Osteoarthritis Development: Based on Bulk and Single-Cell RNA Sequencing Data. Journal of inflammation research, 18, 751.

Wen D, et al. (2025) Screening of necroptosis-related genes and evaluating the prognostic capacity, clinical value, and the effect of their copy number variations in acute myeloid leukemia. BMC cancer, 25(1), 71.

Liao W, et al. (2025) Comprehensive analysis of heat shock protein 110, 90, 70, 60 families and tumor immune microenvironment characterization in clear cell renal cell carcinoma. Scientific reports, 15(1), 469.

Jiang Z, et al. (2024) T-cell exhaustion-related genes in Graves' disease: a comprehensive genome mapping analysis. Frontiers in endocrinology, 15, 1364782.

Urbano P, et al. (2024) Transmission ecology of Trypanosoma cruzi by Rhodnius prolixus (Reduviidae: Triatominae) infesting palm-tree species in the Colombian Orinoco, indicates risks to human populations. PLoS neglected tropical diseases, 18(2), e0011981.

Yang H, et al. (2024) Uncovering a novel DNA repair-related radiosensitivity model for evaluation of radiotherapy susceptibility in uterine corpus endometrial cancer. Heliyon, 10(8), e29401.

Chen X, et al. (2024) Identification and validation of Golgi apparatus-related signature for predicting prognosis and immunotherapy response in breast cancer. Journal of cancer research and clinical oncology, 150(2), 61.

Jiang Z, et al. (2024) Assembly and evolutionary analysis of the complete mitochondrial genome of Trichosanthes kirilowii, a traditional Chinese medicinal plant. PeerJ, 12, e17747.

Shen M, et al. (2024) Mitophagy related diagnostic biomarkers for coronary in-stent restenosis identified using machine learning and bioinformatics. Scientific reports, 14(1), 24137.

Mao W, et al. (2024) Integrative Analyses of Mitophagy-Related Genes and Mechanisms Associated with Type 2 Diabetes in Muscle Tissue. Current issues in molecular biology, 46(9), 10411.

Zhang X, et al. (2024) Disulfidptosis and ferroptosis related genes define the immune microenvironment and NUBPL serves as a potential biomarker for predicting prognosis and immunotherapy response in bladder cancer. Heliyon, 10(17), e37638.

Jiang K, et al. (2024) Lactate score classification of hepatocellular carcinoma helps identify patients with tumors that respond to immune checkpoint blockade therapy. Cellular oncology (Dordrecht), 47(1), 175.

Li JJ, et al. (2024) Genome-Wide Identification and Co-Expression Networks of WOX Gene Family in Nelumbo nucifera. Plants (Basel, Switzerland), 13(5).

Cai J, et al. (2024) LncRNA DANA1 promotes drought tolerance and histone deacetylation of drought responsive genes in Arabidopsis. EMBO reports, 25(2), 796.

Wang Y, et al. (2024) Large language models assisted multi-effect variants mining on cerebral cavernous malformation familial whole genome sequencing. Computational and structural biotechnology journal, 23, 843.

Hong Y, et al. (2024) Identification of molecular subtypes and diagnostic model in clear cell

renal cell carcinoma based on collagen-related genes may predict the response of immunotherapy. Frontiers in pharmacology, 15, 1325447.