

Resource Summary Report

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OmicCircos

RRID:SCR_003292

Type: Tool

Proper Citation

OmicCircos (RRID:SCR_003292)

Resource Information

URL: <http://www.bioconductor.org/packages/devel/bioc/html/OmicCircos.html>

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Description: An R software application and package used to generate high-quality circular plots for visualizing genomic variations, including mutation patterns, copy number variations (CNVs), expression patterns, and methylation patterns.

Synonyms: OmicCircos: High-quality circular visualization of omic data

Resource Type: software resource

Defining Citation: [PMID:24526832](#)

Keywords: standalone software, unix/linux, mac os x, windows, r, annotation, statistical method, visualization

Availability: Free, Available for download, Freely available

Resource Name: OmicCircos

Resource ID: SCR_003292

Alternate IDs: OMICS_04659

Alternate URLs:

<http://www.bioconductor.org/packages/release/bioc/html/OmicCircos.html>

Record Creation Time: 20220129T080218+0000

Record Last Update: 20260912T195555+0000

Ratings and Alerts

No rating or validation information has been found for OmicCircos.

No alerts have been found for OmicCircos.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 83 mentions in open access literature.

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

Wang H, et al. (2026) Identification and regulatory mechanism analysis of macrophage-related key genes in diabetic nephropathy. *Diabetology & metabolic syndrome*, 18(1).

Zhang Z, et al. (2026) Analysis of immune and autophagy-related genes and their regulatory mechanisms in osteoporosis patients post-menopause. *Frontiers in endocrinology*, 17, 1783374.

Raude P, et al. (2026) Challenging the control through a single-cell perspective on normal adjacent tissue in colorectal cancer. *iScience*, 29(6), 115671.

Dwivedi S, et al. (2026) Integrated methylome-transcriptome profiling reveals epigenetic regulation of immune activation pathways and CSN3-associated lactation repression in bovine subclinical mastitis. *Journal of animal science and biotechnology*, 17(1).

Fu J, et al. (2025) Exploring the mechanism of metabolic cell death-related genes AKR1C2 and MAP1LC3A as biomarkers in Parkinson's disease. *Scientific reports*, 15(1), 25610.

Fang Q, et al. (2025) Identification of differentially expressed immune-related genes in patients with systemic lupus erythematosus and the development of a hub gene-based diagnostic model. *European journal of medical research*, 30(1), 689.

Wu M, et al. (2025) ACO1 OGDH axis drives mitochondrial immune crosstalk in preeclampsia through systems biology enabling dual target therapy. *Scientific reports*, 15(1), 32034.

Chi Q, et al. (2025) Integrated transcriptome and single-cell RNA sequencing analysis revealed the prognostic significance of GBP4 in pancreatic adenocarcinoma. *Translational oncology*, 61, 102532.

Wang S, et al. (2025) Based exploration of the diagnostic value of oxidative stress-related key genes in chronic obstructive pulmonary disease. *Cell biology and toxicology*, 41(1), 69.

Lin R, et al. (2024) Identification and preliminary validation of biomarkers associated with mitochondrial and programmed cell death in pre-eclampsia. *Frontiers in immunology*, 15,

1453633.

Hai L, et al. (2024) Prognostic modeling of hepatocellular carcinoma based on T-cell proliferation regulators: a bioinformatics approach. *Frontiers in immunology*, 15, 1444091.

Gao X, et al. (2024) Immunotherapy and drug sensitivity predictive roles of a novel prognostic model in hepatocellular carcinoma. *Scientific reports*, 14(1), 9509.

Forest T, et al. (2024) Chromosome-level genome assembly of the European green woodpecker *Picus viridis*. *G3 (Bethesda, Md.)*, 14(5).

Cao Z, et al. (2024) Identification of ibuprofen targeting CXCR family members to alleviate metabolic disturbance in lipodystrophy based on bioinformatics and in vivo experimental verification. *Frontiers in endocrinology*, 15, 1414908.

Fu L, et al. (2023) Negative regulation of angiogenesis and the MAPK pathway may be a shared biological pathway between IS and epilepsy. *PloS one*, 18(10), e0286426.

Beauvais V, et al. (2023) Tho2 is critical for the recruitment of Rrp6 to chromatin in response to perturbed mRNP biogenesis. *RNA (New York, N.Y.)*, 30(1), 89.

Sahm K, et al. (2023) Concurrent gliomas in patients with multiple sclerosis. *Communications medicine*, 3(1), 186.

Campos GR, et al. (2023) Construction and genetic characterization of an interspecific raspberry hybrids panel aiming resistance to late leaf rust and adaptation to tropical regions. *Scientific reports*, 13(1), 15216.

Zhang Y, et al. (2023) Identification of oxidative stress-related genes differentially expressed in Alzheimer's disease and construction of a hub gene-based diagnostic model. *Scientific reports*, 13(1), 6817.

Xiang C, et al. (2023) Genome-wide identification and characterization of SRLK gene family reveal their roles in self-incompatibility of *Erigeron breviscapus*. *BMC genomics*, 24(1), 402.