

# Resource Summary Report

Generated by [nidm-terms](#) on Jul 29, 2026

## 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>

**Proper Citation:** OmicCircos (RRID:SCR\_003292)

**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:** 20260725T190538+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 79 mentions in open access literature.

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

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.

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.

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.

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).

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.

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.

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.

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.

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.

Li C, et al. (2022) Comprehensive lncRNA and mRNA profiles in peripheral blood mononuclear cells derived from ankylosing spondylitis patients by RNA-sequencing analysis. *Medicine*, 101(4), e27477.

Gundappa MK, et al. (2022) Genome-Wide Reconstruction of Rediploidization Following Autopolyploidization across One Hundred Million Years of Salmonid Evolution. *Molecular biology and evolution*, 39(1).

Zhang J, et al. (2022) Sequential gene expression analysis of cervical malignant transformation identifies RFC4 as a novel diagnostic and prognostic biomarker. *BMC medicine*, 20(1), 437.

Zhang T, et al. (2021) Identification of key transcriptome biomarkers based on a vital gene module associated with pathological changes in Alzheimer's disease. *Aging*, 13(11), 14940.