

Resource Summary Report

Generated by [RRID](#) on Aug 15, 2026

[miloR](#)

RRID:SCR_025630

Type: Tool

Proper Citation

miloR (RRID:SCR_025630)

Resource Information

URL: <https://github.com/MarioniLab/miloR>

Proper Citation: miloR (RRID:SCR_025630)

Description: Software R package implementation of Milo for testing for differential abundance in k-nearest neighbor graphs. Milo can identify perturbations that are obscured by discretizing cells into clusters. Used for differential abundance analysis on KNN graph from single-cell datasets.

Resource Type: software toolkit, source code, software resource

Defining Citation: [PMID:34594043](#)

Keywords: testing for differential abundance, k-nearest neighbor graphs, identify perturbations, differential abundance analysis, KNN graph, single-cell datasets,

Availability: Free, Available for download, Freely available,

Resource Name: miloR

Resource ID: SCR_025630

Alternate URLs: <https://bioconductor.org/packages/miloR/>,
https://github.com/MarioniLab/milo_analysis_2020

License: GNU GPL v3

Record Creation Time: 20240816T053258+0000

Record Last Update: 20260815T042917+0000

Ratings and Alerts

No rating or validation information has been found for miloR.

No alerts have been found for miloR.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 28 mentions in open access literature.

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

Loberg MA, et al. (2026) An integrated single-cell and spatial transcriptomic atlas of thyroid cancer progression identifies prognostic fibroblast subpopulations. JCI insight, 11(1).

Wu M, et al. (2026) Dynamic changes of the immune microenvironment in ovarian cancer following neoadjuvant chemotherapy. Cell death discovery, 12(1).

Bui TM, et al. (2026) Identification of cycling regulatory T cell precursors as conductors of immune escape during breast carcinoma progression. Cancer cell, 44(6), 1179.

Huang Q, et al. (2026) The GFI1-FOXO1 axis regulates NK cell maturation and function. Nature communications, 17(1).

Wang C, et al. (2026) Activated Platelet-Released Heat Shock Protein 90?? Triggers Autophagy-Dependent Neutrophil Extracellular Trap Formation and Amplifies Sepsis. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(25), e15933.

Youngblood MW, et al. (2026) STING activation induces cytotoxic and immune responses in meningiomas via inflammatory cell death pathways. Nature communications, 17(1).

Altendorf L, et al. (2026) Molecular changes during AT/RT progression associated with epithelial-mesenchymal transition and extracellular matrix changes. Acta neuropathologica, 152(1).

Voisin T, et al. (2026) Skin inflammation and itch response are independently regulated by distinct nociceptor subsets. Immunity, 59(5), 1237.

Sandoval TA, et al. (2026) Chemoradiation Reprograms Tumor Cells and the Immune Microenvironment in Cervical Cancer. Cancer research, 86(7), 1639.

Balin S, et al. (2026) Single-cell analysis reveals corticosteroid-associated impairment of tumor-infiltrating NK cells in glioblastoma patients. Scientific reports.

Huangfu N, et al. (2025) METTL3/RBM15 augments the stability of Kdm6b mRNA and promotes STAT1-mediated macrophage activation and atherosclerosis. Experimental & molecular medicine, 57(12), 2916.

Yata T, et al. (2025) Contribution of germline and somatic mutations to risk of neuromyelitis optica spectrum disorder. *Cell genomics*, 5(3), 100776.

Qu X, et al. (2025) Gli1-expressing stromal cells are highly reparative precursors of long-lived chondroprogenitors in the fetal murine limb. *Nature communications*, 16(1), 10107.

Jenkins BH, et al. (2025) Single cell and spatial analysis of immune-hot and immune-cold tumours identifies fibroblast subtypes associated with distinct immunological niches and positive immunotherapy response. *Molecular cancer*, 24(1), 3.

Young J, et al. (2025) CellPhenoX: An Explainable Machine Learning Method for Identifying Cell Phenotypes To Predict Clinical Outcomes from Single-Cell Multi-Omics. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 12(42), e03289.

Wang H, et al. (2025) Phenotypic plasticity and increased infiltration of peripheral blood-derived TREM1+ mono-macrophages following radiotherapy in rectal cancer. *Cell reports. Medicine*, 6(1), 101887.

Azami T, et al. (2025) STAT3 signaling enhances tissue expansion during postimplantation mouse development. *Cell reports*, 44(4), 115506.

Jansma A, et al. (2025) High order expression dependencies finely resolve cryptic states and subtypes in single cell data. *Molecular systems biology*, 21(2), 173.

Young J, et al. (2025) CellPhenoX: An eXplainable Cell-specific machine learning method to predict clinical Phenotypes using single-cell multi-omics. *bioRxiv : the preprint server for biology*.

Ke S, et al. (2025) Single-cell multiomic analysis unveils the immune landscape dynamics of graves' ophthalmopathy. *Communications biology*, 8(1), 732.