

Resource Summary Report

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[pagoda2](#)

RRID:SCR_017094

Type: Tool

Proper Citation

pagoda2 (RRID:SCR_017094)

Resource Information

URL: <https://github.com/hms-dbmi/pagoda2>

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Description: Software R package for analyzing and interactively exploring large single cell RNAseq datasets.

Synonyms: PAGODA, pagoda

Resource Type: software resource, software application, data processing software, data analysis software

Keywords: large, cell, RNAseq, dataset

Availability: Free, Available for download, Freely available

Resource Name: pagoda2

Resource ID: SCR_017094

License: GNU GPL v3

Record Creation Time: 20220129T080333+0000

Record Last Update: 20260817T040621+0000

Ratings and Alerts

No rating or validation information has been found for pagoda2.

No alerts have been found for pagoda2.

Data and Source Information

Usage and Citation Metrics

We found 32 mentions in open access literature.

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

Pang T, et al. (2026) Transcriptomic analysis in autism spectrum disorder suggests three molecular subtypes with distinct phenotypic profiles and functional pathways. Communications biology, 9(1).

Srivastava A, et al. (2025) A single-cell network approach to decode metabolic regulation in gynecologic and breast cancers. NPJ systems biology and applications, 11(1), 26.

Pietilä R, et al. (2025) A comprehensive molecular atlas of the mesenchymal cell types in the mouse liver. EMBO reports, 26(21), 5326.

James J, et al. (2025) Distinct populations of lung capillary endothelial cells and their functional significance. Communications biology, 9(1), 140.

Risley CA, et al. (2025) Transcription factor T-bet regulates the maintenance and differentiation potential of lymph node and lung effector memory B cell subsets. Immunity, 58(7), 1706.

Mei S, et al. (2025) Single-Cell and Spatial Transcriptomics Reveal a Tumor-Associated Macrophage Subpopulation that Mediates Prostate Cancer Progression and Metastasis. Molecular cancer research : MCR, 23(7), 653.

Gisch DL, et al. (2024) The chromatin landscape of healthy and injured cell types in the human kidney. Nature communications, 15(1), 433.

James J, et al. (2023) Novel Populations of Lung Capillary Endothelial Cells and Their Functional Significance. Research square.

Lake BB, et al. (2023) An atlas of healthy and injured cell states and niches in the human kidney. Nature, 619(7970), 585.

Chaudagar K, et al. (2023) Reversal of Lactate and PD-1-mediated Macrophage Immunosuppression Controls Growth of PTEN/p53-deficient Prostate Cancer. Clinical cancer research : an official journal of the American Association for Cancer Research, 29(10), 1952.

Zambrano S, et al. (2022) Molecular insights into the early stage of glomerular injury in IgA nephropathy using single-cell RNA sequencing. Kidney international, 101(4), 752.

Miyao T, et al. (2022) Integrative analysis of scRNA-seq and scATAC-seq revealed transit-amplifying thymic epithelial cells expressing autoimmune regulator. eLife, 11.

Barwinska D, et al. (2021) Molecular characterization of the human kidney interstitium in health and disease. Science advances, 7(7).

Bakken TE, et al. (2021) Comparative cellular analysis of motor cortex in human, marmoset and mouse. *Nature*, 598(7879), 111.

Bost P, et al. (2021) Deciphering the state of immune silence in fatal COVID-19 patients. *Nature communications*, 12(1), 1428.

Kfoury Y, et al. (2021) Human prostate cancer bone metastases have an actionable immunosuppressive microenvironment. *Cancer cell*, 39(11), 1464.

Engelbrecht E, et al. (2020) Sphingosine 1-phosphate-regulated transcriptomes in heterogenous arterial and lymphatic endothelium of the aorta. *eLife*, 9.

Bost P, et al. (2020) Host-Viral Infection Maps Reveal Signatures of Severe COVID-19 Patients. *Cell*, 181(7), 1475.

Krivanek J, et al. (2020) Dental cell type atlas reveals stem and differentiated cell types in mouse and human teeth. *Nature communications*, 11(1), 4816.

Rydbirk R, et al. (2020) Epigenetic modulation of ARL1 and increased HLA expression in brains of multiple system atrophy patients. *Acta neuropathologica communications*, 8(1), 29.