

Resource Summary Report

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ShinyCell

RRID:SCR_022756

Type: Tool

Proper Citation

ShinyCell (RRID:SCR_022756)

Resource Information

URL: <https://github.com/SGDDNB/ShinyCell>

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Description: Software R package to create interactive Shiny based web applications to visualise single cell data via visualising cell information and/or gene expression on reduced dimensions e.g. UMAP, visualising coexpression of two genes on reduced dimensions, visualising distribution of continuous cell information e.g. nUMI / module scores using violin plots / box plots, visualising composition of different clusters / groups of cells using proportion plots and visualising expression of multiple genes using bubbleplots / heatmap. Shiny Interactive Web Apps for Single-Cell Data.

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

Keywords: visualise single cell data, visualising cell information, gene expression on reduced dimensions, visualising coexpression of two genes on reduced dimensions, visualising distribution of continuous cell information

Availability: Free, Available for download, Freely available

Resource Name: ShinyCell

Resource ID: SCR_022756

License: GNU GPL v3.0

Record Creation Time: 20220917T050153+0000

Record Last Update: 20260811T043712+0000

Ratings and Alerts

No rating or validation information has been found for ShinyCell.

No alerts have been found for ShinyCell.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 24 mentions in open access literature.

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

Jung W, et al. (2026) Spatial transcriptome mapping identifies Ppara-Anxa2 cross-talk in microplastic-induced hepatotoxicity. *Science advances*, 12(25), eaec8681.

Allen AM, et al. (2026) Differential neuronal survival defines a novel axis of sexual dimorphism in the *Drosophila* brain. *Cell genomics*, 101125.

Wen L, et al. (2026) Stem-like precursors of exhausted Th cells upheld by a Tox-Myb-Eomes transcriptional hierarchy propagate Th cell responses in chronic infection. *Immunity*, 59(7), 1894.

Sharma S, et al. (2025) Taurine from tumour niche drives glycolysis to promote leukaemogenesis. *Nature*, 644(8075), 263.

Ham AS, et al. (2025) Single-nuclei sequencing of skeletal muscle reveals subsynaptic-specific transcripts involved in neuromuscular junction maintenance. *Nature communications*, 16(1), 2220.

Hossain MF, et al. (2025) Neuron-specific Agrin splicing by Nova RNA-binding proteins regulates conserved neuromuscular junction development in chordates. *PLoS biology*, 23(9), e3003392.

Allen AM, et al. (2025) A high-resolution atlas of the brain predicts lineage and birth order underlying neuronal identity. *Cell genomics*, 101103.

Gondal MN, et al. (2025) Integrated cancer cell-specific single-cell RNA-seq datasets of immune checkpoint blockade-treated patients. *Scientific data*, 12(1), 139.

Kondrychyn I, et al. (2025) Combined forces of hydrostatic pressure and actin polymerization drive endothelial tip cell migration and sprouting angiogenesis. *eLife*, 13.

Bozon K, et al. (2025) Impaired yolk sac NAD metabolism disrupts murine embryogenesis with relevance to human birth defects. *eLife*, 13.

Gaertner Z, et al. (2025) Molecular and spatial transcriptomic classification of midbrain dopamine neurons and their alterations in a LRRK2G2019S model of Parkinson's disease. *eLife*, 13.

Sheng J, et al. (2025) A dynamic molecular landscape in colorectal cancer progression at single-cell resolution. *Journal of translational medicine*, 23(1), 723.

Chen C, et al. (2025) Leucine-rich repeat kinase 2 impairs the release sites of Parkinson's disease vulnerable dopamine axons. *bioRxiv : the preprint server for biology*.

Paladini MS, et al. (2025) Fate mapping of peripherally-derived macrophages after traumatic brain injury in mice reveals a long-lasting population with a distinct transcriptomic signature. *Nature communications*, 16(1), 8898.

Devakinandan GVS, et al. (2024) Single-cell transcriptomics of vomeronasal neuroepithelium reveals a differential endoplasmic reticulum environment amongst neuronal subtypes. *eLife*, 13.

Skulimowska I, et al. (2024) Polyclonal regeneration of mouse bone marrow endothelial cells after irradiative conditioning. *Cell reports*, 43(11), 114779.

Wang Z, et al. (2024) Injury distance limits the transcriptional response to spinal injury. *bioRxiv : the preprint server for biology*.

Chen H, et al. (2024) Single-cell landscape of long and short glandular trichomes in *Nicotiana tabacum* leaves. *iScience*, 27(9), 110650.

Frank AK, et al. (2024) Single-Cell Transcriptomic Profiling of Cholangiocyte Organoids Derived from Bile Ducts of Primary Sclerosing Cholangitis Patients. *Digestive diseases and sciences*, 69(10), 3810.

Xie Y, et al. (2024) Single-cell dissection of the human blood-brain barrier and glioma blood-tumor barrier. *Neuron*, 112(18), 3089.