

Resource Summary Report

Generated by [PRECISE-TBI](#) on Jul 30, 2026

SingleR

RRID:SCR_023120

Type: Tool

Proper Citation

SingleR (RRID:SCR_023120)

Resource Information

URL: <https://www.bioconductor.org/packages/release/bioc/html/SingleR.html>

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Description: Software R package for unbiased cell type recognition of scRNA-seq data. Performs unbiased cell type recognition from single-cell RNA sequencing data, by leveraging reference transcriptomic datasets of pure cell types to infer cell of origin of each single cell independently.

Synonyms: Single-cell RNA-seq cell types Recognition

Resource Type: software toolkit, software resource

Defining Citation: [PMID:30643263](#)

Keywords: unbiased cell type recognition, scRNA-seq data, reference transcriptomic datasets, pure cell types, infer cell of origin

Funding: UCSF Marcus Award ;
NHLBI HL131560;
UCSF Nina Ireland Program award ;
NHLBI HL139897;
NIAID

Availability: Free, Available for download, Freely available

Resource Name: SingleR

Resource ID: SCR_023120

Alternate URLs: <https://github.com/dviraran/SingleR>, <https://github.com/LTLA/SingleR>

License: GNU GPL v3

Record Creation Time: 20230116T062750+0000

Record Last Update: 20260729T044547+0000

Ratings and Alerts

No rating or validation information has been found for SingleR.

No alerts have been found for SingleR.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 321 mentions in open access literature.

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

Zou Y, et al. (2026) Gut microbiota dysbiosis exacerbates acute pancreatitis via Escherichia coli-driven neutrophil heterogeneity and NETosis. Gut microbes, 18(1), 2606480.

Ran W, et al. (2026) Interferon-stimulated gene GALNT2 restricts respiratory virus infections. Nature microbiology, 11(1), 256.

Kim H, et al. (2026) Myelin antigen capture in the CNS by B cells expressing EBV latent membrane protein 1 leads to demyelinating lesion formation. Cell.

Yao S, et al. (2025) SmartImpute is a targeted imputation framework for single-cell transcriptome data. Cell reports methods, 5(8), 101122.

Li W, et al. (2025) Exploring ferroptosis-associated immune characteristics in Kawasaki disease through bioinformatics. Scientific reports, 15(1), 30261.

Li N, et al. (2025) Single-cell transcriptomic profiling uncovers cellular complexity and microenvironment in gastric tumorigenesis associated with Helicobacter pylori. Journal of advanced research, 74, 471.

Chen J, et al. (2025) The spatiotemporal transcriptional profiling of murine brain during cerebral malaria progression and after artemisinin treatment. Nature communications, 16(1), 1540.

Yijia Z, et al. (2025) Identification of intratumoral microbiome-driven immune modulation and therapeutic implications in diffuse large B-cell lymphoma. Cancer immunology, immunotherapy : CII, 74(4), 131.

Qin D, et al. (2025) Unraveling shared diagnostic genes and cellular microenvironmental changes in endometriosis and recurrent implantation failure through multi-omics analysis.

Scientific reports, 15(1), 9110.

Huang G, et al. (2025) Integrating RNA-seq and scRNA-seq to explore the prognostic features and immune landscape of exosome-related genes in breast cancer metastasis. *Annals of medicine*, 57(1), 2447917.

Qiu Q, et al. (2025) SLC25A39 regulates Hedgehog signaling to promote tumor progression and sorafenib resistance in hepatocellular carcinoma. *Scientific reports*, 15(1), 36061.

Chi F, et al. (2025) Single-cell transcriptomics reveals the interaction between fibroblasts and activated immune cells: an exploratory bioinformatics study of pro-inflammatory mechanisms in slow transit constipation. *International journal of surgery (London, England)*, 111(6), 3767.

Yu J, et al. (2025) Integration of single-cell sequencing and mendelian randomization reveals novel causal pathways between monocytes and hepatocellular carcinoma. *Discover oncology*, 16(1), 604.

Cao Z, et al. (2025) Integrated single-cell and bulk RNA sequencing analysis establishes a cancer associated fibroblast-related signature for predicting prognosis and therapeutic responses in neuroblastoma. *Discover oncology*, 16(1), 1235.

Bai B, et al. (2025) Targeting Hepatic Stellate Cell PD-L1 Alters Liver Inflammation and Fibrosis in CCl4 Liver Injury Mouse Model. *Cellular and molecular gastroenterology and hepatology*, 19(11), 101587.

Ma T, et al. (2025) Pan-Cancer Analyses Refine the Single-Cell Portrait of Tumor-Infiltrating Dendritic Cells. *Cancer research*, 85(19), 3596.

Patai R, et al. (2025) Transcriptomic profiling of senescence effects on blood-brain barrier-related gene expression in brain capillary endothelial cells in a mouse model of paclitaxel-induced chemobrain. *GeroScience*, 47(3), 3677.

Zhang X, et al. (2025) Expression of stearyl coenzyme a desaturase in neuronal cells facilitates pancreatic cancer progression. *Cancer cell international*, 25(1), 57.

Maimaiti Y, et al. (2025) FOXO regulation of TXNIP induces ferroptosis in satellite cells by inhibiting glutathione metabolism, promoting Sarcopenia. *Cellular and molecular life sciences : CMLS*, 82(1), 81.

Zhu J, et al. (2025) Prognostic and immunological characterization of osteosarcoma patients evaluated by liquid-liquid phase separation related genes. *Discover oncology*, 16(1), 958.