

Resource Summary Report

Generated by [dkNET](#) on Aug 13, 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>

Proper Citation: SingleR (RRID:SCR_023120)

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: 20260810T040831+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 411 mentions in open access literature.

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

Jeong D, et al. (2026) Multidimensional profiling of heterogeneity in supratentorial ependymomas. *Nature*, 652(8111), 1016.

Lian C, et al. (2026) Hexokinase 3 promoted cytokine production of monocytes by targeting metabolic reprogramming and histone lactylation in sepsis. *Clinical epigenetics*, 18(1).

Wang Y, et al. (2026) Integrative transcriptomic profiling reveals NK cell exhaustion-associated prognostic genes and identifies CSF1 as a key immunoregulatory target in hepatocellular carcinoma. *Biology direct*, 21(1).

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

Zhu G, et al. (2026) Deciphering CD4+ Naive T cell-mediated divergent pathogenic links between type 2 diabetes and pathologic scarring via an integrated multi-omics approach. *International journal of surgery (London, England)*, 112(4), 9378.

Chiu YJ, et al. (2026) LIMPACAT: Multi-omics attention transformer for immune prediction in liver cancer using whole-slide imaging. *PloS one*, 21(1), e0339667.

See SB, et al. (2026) Dominant intragraft plasma cells targeting bilirubin implicate local heme catabolism in human cardiac allograft vasculopathy. *The Journal of clinical investigation*, 136(3).

Golec DP, et al. (2026) A PI3K α -Foxo1-FasL signaling amplification loop rewires CD4+ T cell signaling and differentiation. *The Journal of experimental medicine*, 223(4).

- Yin S, et al. (2026) Diethyl Phthalate (DEP) as a potential osteosarcoma risk factor: a multi-omics study integrating network Toxicology, single-cell RNA sequencing, and molecular docking. *Journal of enzyme inhibition and medicinal chemistry*, 41(1), 2611582.
- Peng Y, et al. (2026) Dissecting Heterogeneity Reveals Functional Subpopulation of Stem Cells From Human Exfoliated Deciduous Teeth. *International dental journal*, 76(1), 104014.
- Zhang L, et al. (2026) Deficient extravillous trophoblast invasion caused by impaired sialylation-Siglec-7 interaction contributes to recurrent pregnancy loss. *Cell death & disease*, 17(1).
- Zhang Y, et al. (2026) Integrative bioinformatics, single-cell and experimental evidence for a BPA-m6A-apoptosis axis in granulosa cell dysfunction in polycystic ovary syndrome. *Journal of ovarian research*, 19(1).
- Tian Z, et al. (2026) Construction of a Prognostic Risk Model for *Helicobacter pylori* Infection in Gastric Cancer Patients and Immunological Analysis. *Cancer reports (Hoboken, N.J.)*, 9(4), e70511.
- Zhang J, et al. (2026) Hepatocyte BPGM Induces RET Lactylation and Macrophage Reprogramming to Promote Tumorigenesis in Hepatocellular Carcinoma. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, e18180.
- Zhang H, et al. (2026) Tobacco Smoke Exposure From Prenatal To Adolescent Periods Drives IBD Pathogenesis: Dynamic DNA Methylation Signatures Across Lifespan Stages. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(17), e16704.
- Winkler M, et al. (2026) Consequences of the perivascular niche remodeling for tumoricidal T-cell trafficking into metastasis of ovarian cancer. *ImmunoHorizons*, 10(2).
- Tang S, et al. (2026) SCFAs inhibited NETosis to alleviate lung inflammation in COPD: a potential role for GPR43. *Respiratory research*, 27(1).
- Wu C, et al. (2026) Identification and genetic validation of potential therapeutic targets for pulmonary hypertension through multi-omics causal inference. *Medicine*, 105(6), e47525.
- Cao F, et al. (2026) Integrative multi-omics analysis reveals gut-skin axis mechanisms and novel therapeutic target GALE in atopic dermatitis. *mSystems*, 11(1), e0140325.
- Nie M, et al. (2026) Natural killer cells aggravate neuroinflammation through microglial type I interferon pathway activation after traumatic brain injury. *Journal of neuroinflammation*, 23(1), 52.