

Resource Summary Report

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CytoTRACE

RRID:SCR_022828

Type: Tool

Proper Citation

CytoTRACE (RRID:SCR_022828)

Resource Information

URL: <https://cytotrace.stanford.edu/>

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Description: Software tool that predicts differentiation state of cells from single cell RNA sequencing data. Used for predicting differentiation states from scRNA-seq data.

Synonyms: Cellular (Cyto) Trajectory Reconstruction Analysis using gene Counts and Expression

Resource Type: simulation software, software resource, software application

Defining Citation: [PMID:31974247](#)

Keywords: differentiation state of cells, single cell RNA sequencing data, predicting differentiation states, scRNA-seq data

Funding: NCI R00CA187192;
NCI R01CA100225;
Stinehart Reed foundation ;
Stanford Bio-X Interdisciplinary Initiatives Seed Grants Program ;
Virginia and D.K. Ludwig Fund for Cancer Research ;
U.S. Department of Defense ;
National Science Foundation Graduate Research Fellowship ;
Stanford Bio-X Bowes Graduate Student Fellowship ;
Stanford Medical Science Training Program

Availability: Free, Freely available

Resource Name: CytoTRACE

Resource ID: SCR_022828

Record Creation Time: 20221006T194910+0000

Ratings and Alerts

No rating or validation information has been found for CytoTRACE.

No alerts have been found for CytoTRACE.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 132 mentions in open access literature.

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

Zhao F, et al. (2025) Integration of single-cell and bulk RNA sequencing to identify a distinct tumor stem cells and construct a novel prognostic signature for evaluating prognosis and immunotherapy in LUAD. Journal of translational medicine, 23(1), 222.

Zhang X, et al. (2025) Tumour heterogeneity and personalized treatment screening based on single-cell transcriptomics. Computational and structural biotechnology journal, 27, 307.

Jia H, et al. (2025) The Potential Role of C4 MYH11+ Fibroblasts and the MDK-SDC2 Ligand-Receptor Pair in Lung Adenocarcinoma: Implications for Prognosis and Therapeutic Strategies. Translational oncology, 55, 102364.

Lei T, et al. (2025) Engineering a stem cell-embedded bilayer hydrogel with biomimetic collagen mineralization for tendon-bone interface healing. Bioactive materials, 49, 207.

Huang J, et al. (2025) Single-cell transcriptome analysis reveals the malignant characteristics of tumour cells and the immunosuppressive landscape in HER2-positive inflammatory breast cancer. Journal of experimental & clinical cancer research : CR, 44(1), 196.

Lin S, et al. (2025) Cryoablation-induced modulation of Treg cells and the TGF- β pathway in lung adenocarcinoma: implications for increased antitumor immunity. BMC medicine, 23(1), 89.

Li Y, et al. (2025) Single-cell transcriptomics reveals cellular evolution underlying pleomorphic adenoma recurrence and malignant transformation. Scientific reports, 15(1), 35870.

Zhang H, et al. (2025) CCDC137 knockdown suppresses bladder cancer progression by downregulating SCD. Journal of translational medicine, 23(1), 1013.

Huang Z, et al. (2025) Association of microtubule-based processes gene expression with immune microenvironment and its predictive value for drug response in oestrogen receptor-positive breast cancer. *Frontiers in immunology*, 16, 1608991.

Yu R, et al. (2025) Decoding epithelial-T cell interactions in colorectal cancer through single-cell and spatial transcriptomics. *Discover oncology*, 16(1), 2334.

Li YS, et al. (2025) Cellular dynamics in cerebrospinal fluid unveils the key regulators of intracranial response to immune checkpoint inhibitors in NSCLC brain metastases. *Journal for immunotherapy of cancer*, 13(11).

Li Y, et al. (2025) Integrative analysis identifies radiotherapy resistance-associated CAF subtypes shaping the tumor immune landscape in breast cancer. *BMC cancer*, 25(1), 1603.

Yue L, et al. (2025) Human pluripotent stem cell-derived skin organoids enabled pathophysiological model of *Mycobacterium tuberculosis* infection. *Nature communications*, 16(1), 10831.

An Y, et al. (2025) Inhibition of programmed cell death by melanoma cell subpopulations reveals mechanisms of melanoma metastasis and potential therapeutic targets. *Discover oncology*, 16(1), 62.

Jia T, et al. (2025) Multi-omics profiling identifies TNFRSF18 as a novel marker of exhausted CD8⁺ T cells and reveals tumour-immune dynamics in colorectal cancer. *Clinical and translational medicine*, 15(8), e70425.

Gao Y, et al. (2025) Single-cell RNA sequencing reveals the intra-tumoral heterogeneity and immune microenvironment of small cell carcinoma of the ovary, hypercalcemic type. *Journal of ovarian research*, 18(1), 76.

Zhao G, et al. (2025) Integrating single-cell sequencing and clinical insights to explore malignant transformation in odontogenic keratocyst. *Computational and structural biotechnology journal*, 27, 1158.

Rodriguez-Sevilla JJ, et al. (2025) Natural killer cells' functional impairment drives the immune escape of pre-malignant clones in early-stage myelodysplastic syndromes. *Nature communications*, 16(1), 3450.

Lin J, et al. (2025) Unraveling the oxidative stress landscape in diabetic foot ulcers: insights from bulk RNA and single-cell RNA sequencing data. *Biology direct*, 20(1), 79.

Liu C, et al. (2025) Unravelling NK cell subset dynamics and specific gene signatures post-ibrutinib therapy in chronic lymphocytic leukaemia via single-cell transcriptomics. *BMC cancer*, 25(1), 745.