

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: software application, simulation software, software resource

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 170 mentions in open access literature.

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

Yoshida-Minato R, et al. (2026) JAG1 expression in papillary thyroid cancer stem-like cells predicts poor prognosis and implicates angiogenesis. *Discover oncology*, 17(1).

Yu H, et al. (2026) Integrated single-cell and spatial transcriptomic profiling decodes lineage plasticity and immune microenvironment remodeling in prostate cancer progression. *Molecular cancer*, 25(1).

Ping Y, et al. (2026) Perivascular mesenchymal cells instruct ST2+ reparative macrophages to promote endovascular injury-induced neointimal hyperplasia in mice. *Nature communications*, 17(1).

Lai Y, et al. (2026) Multi-omics analysis and experimental validation reveal the IRF7-CXCL10 axis as a master regulator of microglial PCD in ischemic stroke. *Cell biology and toxicology*, 42(1).

Peng Y, et al. (2026) Dissecting Heterogeneity Reveals Functional Subpopulation of Stem Cells From Human Exfoliated Deciduous Teeth. *International dental journal*, 76(1), 104014.

Tang S, et al. (2026) Single-cell RNA sequencing analysis reveals the evolution and regulatory features of specialized endothelial cell subsets in non-traumatic osteonecrosis of the femoral head. *Biology direct*, 21(1).

Dai H, et al. (2026) Integrating single-cell multi-omics and machine learning to reveal triaptois heterogeneity in clear cell renal cell carcinoma. *Human genomics*, 20(1).

Han Z, et al. (2026) Single-Nucleus Transcriptome Reveals Cellular Heterogeneity and Transcriptional Response to Heat Stress in Skeletal Muscle. *Journal of cachexia, sarcopenia and muscle*, 17(1), e70217.

Chen J, et al. (2026) Identification of UBE2T as a novel diagnostic biomarker of psoriasis and proliferating UBE2T+ Keratinocyte in psoriasis. *Journal of translational medicine*,

24(1).

Lou S, et al. (2026) Integrated Genome-wide Association and Single-cell Transcriptomic Analysis Identifies OAT as Therapeutic Targets for Periodontitis. *Inflammation*, 49(1).

Sun S, et al. (2026) Single-Nucleus RNA-Seq Reveals Neuroprotective Effects of Acupuncture in Chronic Migraine Through Modulation of Glial Subtypes. *CNS neuroscience & therapeutics*, 32(6), e70981.

Zeng Q, et al. (2026) Intratumoral Tertiary Lymphoid Structures Characterized by a B Cell-Related Signature Elicit Antitumor Effect through HAPLN3 in Hepatocellular Carcinoma. *Cancer immunology research*, 14(5), 771.

Jaiswal S, et al. (2026) Identification of tumor initiating cells and early marker genes in histologically normal colonic mucosa that lead to neoplastic transformation. *Neoplasia* (New York, N.Y.), 75, 101300.

Du H, et al. (2026) Multi-omics analysis identifies stemness-driven molecular subtypes, prognostic signature, epigenetic target APCDD1, and drug candidate Leflunomide in Wilms tumor. *Frontiers in oncology*, 16, 1775326.

Xi Y, et al. (2026) Macrophage efferocytosis mediated by the TP63-RAC2 pathway promotes immunosuppressive remodeling in esophageal cancer. *Cell reports. Medicine*, 7(1), 102529.

Wu C, et al. (2026) The Tumor-to-Endothelial Transfer of FTO Promotes Vascular Remodeling and Metastasis in Nasopharyngeal Carcinoma. *Advanced science* (Weinheim, Baden-Wurtemberg, Germany), 13(8), e09524.

Shi Y, et al. (2026) Integrative single-cell analysis reveals TRIM31+ colorectal tumor cells orchestrating macrophage crosstalk within the cancer-immunity regulome. *Frontiers in immunology*, 17, 1848654.

Liu S, et al. (2026) Exploration of the roles of SSR2 in hepatocellular carcinogenesis based on single-cell transcriptomics and spatial transcriptomics. *Discover oncology*, 17(1).

Zhu J, et al. (2026) Single-cell landscape of piglet lung response with *Actinobacillus pleuropneumoniae*. *Virulence*, 17(1), 2646800.

Chen L, et al. (2026) Single-cell and spatial transcriptome analysis reveals the potential therapeutic targets for testicular sex cord-stromal cell tumor. *Biomarker research*, 14(1).