

Resource Summary Report

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[TraCeR](#)

RRID:SCR_016338

Type: Tool

Proper Citation

TraCeR (RRID:SCR_016338)

Resource Information

URL: <https://github.com/Teichlab/tracer>

Proper Citation: TraCeR (RRID:SCR_016338)

Description: Software application for recovery of T cell receptor (TCR) data from single cell data. Used to reconstruct full-length, paired T cell receptor (TCR) sequences from T lymphocyte single-cell RNA sequence data. Links T cell specificity with functional response by revealing clonal relationships between cells alongside their transcriptional profiles.

Resource Type: simulation software, data processing software, data analysis software, software resource, software application, software toolkit

Defining Citation: [PMID:26950746](#)

Keywords: recovery, receptor, single, cell, data, computation, method, reconstruct, sequence, T lymphocyte, RNA, sequence

Funding: European Research Council ;
the Lister Institute for Preventative Medicine (S.A.T.)

Availability: Free, Available for download, Freely available

Resource Name: TraCeR

Resource ID: SCR_016338

License: Apache licence

Record Creation Time: 20220129T080330+0000

Record Last Update: 20260805T044352+0000

Ratings and Alerts

No rating or validation information has been found for TraCeR .

No alerts have been found for TraCeR .

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

Chin WL, et al. (2025) Coupling of response biomarkers between tumor and peripheral blood in patients undergoing chemoimmunotherapy. *Cell reports. Medicine*, 6(1), 101882.

Zheng C, et al. (2022) Transcriptomic profiles of neoantigen-reactive T cells in human gastrointestinal cancers. *Cancer cell*, 40(4), 410.

Xydia M, et al. (2021) Common clonal origin of conventional T cells and induced regulatory T cells in breast cancer patients. *Nature communications*, 12(1), 1119.

Sun Y, et al. (2021) Single-cell landscape of the ecosystem in early-relapse hepatocellular carcinoma. *Cell*, 184(2), 404.

Chiou SH, et al. (2021) Global analysis of shared T cell specificities in human non-small cell lung cancer enables HLA inference and antigen discovery. *Immunity*, 54(3), 586.

Cheng Y, et al. (2021) Non-terminally exhausted tumor-resident memory HBV-specific T cell responses correlate with relapse-free survival in hepatocellular carcinoma. *Immunity*, 54(8), 1825.

Mathewson ND, et al. (2021) Inhibitory CD161 receptor identified in glioma-infiltrating T cells by single-cell analysis. *Cell*, 184(5), 1281.

Teraguchi S, et al. (2020) Methods for sequence and structural analysis of B and T cell receptor repertoires. *Computational and structural biotechnology journal*, 18, 2000.

Davidson S, et al. (2020) Single-Cell RNA Sequencing Reveals a Dynamic Stromal Niche That Supports Tumor Growth. *Cell reports*, 31(7), 107628.

Carmona SJ, et al. (2020) Deciphering the transcriptomic landscape of tumor-infiltrating CD8 lymphocytes in B16 melanoma tumors with single-cell RNA-Seq. *Oncoimmunology*, 9(1), 1737369.

Li A, et al. (2019) IL-33 Signaling Alters Regulatory T Cell Diversity in Support of Tumor Development. *Cell reports*, 29(10), 2998.

Dulken BW, et al. (2019) Single-cell analysis reveals T cell infiltration in old neurogenic niches. *Nature*, 571(7764), 205.

Zheng C, et al. (2017) Landscape of Infiltrating T Cells in Liver Cancer Revealed by Single-Cell Sequencing. *Cell*, 169(7), 1342.