

Resource Summary Report

Generated by [RRID](#) on Sep 20, 2026

starCAT

RRID:SCR_028475

Type: Tool

Proper Citation

starCAT (RRID:SCR_028475)

Resource Information

URL: <https://github.com/immunogenomics/starCAT>

Proper Citation: starCAT (RRID:SCR_028475)

Description: Software pipeline that improves T cell characterization by simultaneously quantifying predefined gene expression programs (scRNA-Seq) capturing activation states and cellular subsets. Used to score cells based on a fixed, multidataset catalog of Gene Expression Programs from any tissues or cell-type.

Synonyms: starCellAnnoTator, starCellAnnoTator (starCAT)

Resource Type: software resource, software toolkit, source code

Defining Citation: [PMID:38746317](#)

Keywords: T cell characterization, simultaneously quantifying predefined gene expression programs, gene expression programs,

Funding: NHGRI R56HG013083;
NHGRI T32HG002295;
NHGRI U01HG012009;
NIAID P01AI148102;
NIAMS R01AR063759;
NIAMS T32AR007530

Availability: Free, Available for download, Freely available

Resource Name: starCAT

Resource ID: SCR_028475

License: MIT license

Record Creation Time: 20260522T053905+0000

Record Last Update: 20260919T200132+0000

Ratings and Alerts

No rating or validation information has been found for starCAT.

No alerts have been found for starCAT.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Fan X, et al. (2026) A Perturb-seq screen guided by species divergence uncovers pathways for collateral artery formation. bioRxiv : the preprint server for biology.