

# Resource Summary Report

Generated by [dkNET](#) on Aug 17, 2026

## starCAT

RRID:SCR\_028475

Type: Tool

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### Proper Citation

starCAT (RRID:SCR\_028475)

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### Resource Information

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

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**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 toolkit, source code, software resource

**Defining Citation:** [PMID:38746317](#)

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

**Funding:** NIAID P01AI148102;  
NHGRI U01HG012009;  
NIAMS R01AR063759;  
NHGRI R56HG013083;  
NHGRI T32HG002295;  
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:** 20260815T183322+0000

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## Ratings and Alerts

No rating or validation information has been found for starCAT.

No alerts have been found for starCAT.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 1 mentions in open access literature.

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

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.