

# Resource Summary Report

Generated by PRECISE-TBI on Jul 29, 2026

## Mixed effects association testing for single cells

RRID:SCR\_025632

Type: Tool

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### Proper Citation

Mixed effects association testing for single cells (RRID:SCR\_025632)

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### Resource Information

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

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**Description:** Software tool for testing whether specified covariate influences membership of single cells in any of multiple cellular subsets while accounting for technical confounds and biological variation.

**Abbreviations:** MASC

**Synonyms:** , Mixed-effects modeling of Associations of Single Cells, Mixed-effects Association testing for Single Cells

**Resource Type:** source code, software resource

**Defining Citation:** [PMID:30333237](#)

**Keywords:** specified covariate, influences membership, single cells, multiple cellular subsets, accounting for technical confounds and biological variation,

**Funding:** NIAMSD UH2AR067677;  
NIAID U19AI111224;  
NIAMSD 1R01AR063759;  
NIAMSD R01 AR064850;  
Doris Duke Charitable Foundation ;  
NIAMSD T32 AR007530;  
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Rheumatology Research Foundation Tobe and Stephen Malawista

**Resource Name:** Mixed effects association testing for single cells

**Resource ID:** SCR\_025632

**License:** LGPL v3.0

**Record Creation Time:** 20240816T053258+0000

**Record Last Update:** 20260729T044625+0000

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## Ratings and Alerts

No rating or validation information has been found for Mixed effects association testing for single cells.

No alerts have been found for Mixed effects association testing for single cells.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Bian L, et al. (2025) Single-cell eQTL mapping reveals cell-type-specific genes associated with the risk of gastric cancer. Cell genomics, 5(4), 100812.

Siu JHY, et al. (2025) Early lymph node T follicular helper cell signalling hub drives influenza vaccine response in an ancestrally diverse cohort. EBioMedicine, 122, 106036.