

Resource Summary Report

Generated by [NIF](#) on Aug 29, 2026

MetaMarkers

RRID:SCR_027104

Type: Tool

Proper Citation

MetaMarkers (RRID:SCR_027104)

Resource Information

URL: <https://github.com/gillislabs/MetaMarkers>

Proper Citation: MetaMarkers (RRID:SCR_027104)

Description: Software R package to efficiently compute robust markers across single-cell datasets. Robust marker signatures from single-cell data.

Synonyms: Gillis lab MetaMarkers

Resource Type: software resource, source code

Keywords: compute robust markers, across single-cell datasets, markers, dataset, marker signatures, single-cell data,

Availability: Free, Available for download, Freely available

Resource Name: MetaMarkers

Resource ID: SCR_027104

License: MIT license

Record Creation Time: 20250627T054457+0000

Record Last Update: 20260829T183504+0000

Ratings and Alerts

No rating or validation information has been found for MetaMarkers.

No alerts have been found for MetaMarkers.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Werner JM, et al. (2024) Meta-analysis of single-cell RNA sequencing co-expression in human neural organoids reveals their high variability in recapitulating primary tissue. PLoS biology, 22(12), e3002912.

Werner JM, et al. (2023) Preservation of co-expression defines the primary tissue fidelity of human neural organoids. bioRxiv : the preprint server for biology.

Kawaguchi RK, et al. (2023) Learning single-cell chromatin accessibility profiles using meta-analytic marker genes. Briefings in bioinformatics, 24(1).

Novella-Rausell C, et al. (2023) A comprehensive mouse kidney atlas enables rare cell population characterization and robust marker discovery. iScience, 26(6), 106877.

Suresh H, et al. (2023) Comparative single-cell transcriptomic analysis of primate brains highlights human-specific regulatory evolution. Nature ecology & evolution, 7(11), 1930.

Fischer S, et al. (2022) Defining the extent of gene function using ROC curvature. Bioinformatics (Oxford, England), 38(24), 5390.