



# Core Project R03OD034501









## Overview







High-level info about this project.

| Projects        | Name   | Award  | Publications   | Repositories   | Analytics    |
|-----------------|--|--------|----------------|----------------|--------------|
| 1R03OD034501-01 | Integration of GTEx and HuBMAP data to gain population-level cell-type-specific insights | \$315K | 6 publications | 0 repositories | 0 properties |

## Publications

Published works associated with this project.

| ID  | Title  | Authors  | RCR    | SJR   | Citations | Cit./year | Journal   | Published | Updated      |
|---|--|--|--------|-------|-----------|-----------|---|-----------|--------------|
| <a href="#">38168620</a> <br><a href="#">DOI</a>      | scMD facilitates cell type deconvolution using single-cell DNA methylation references.               | Cai, Manqi<br>...2 more...<br>Wang, Jiebiao      | 10.786 | 2.071 | 51        | 51        | Communications biology  | 2024      | Dec 28, 2025 |
| <a href="#">37563770</a> <br><a href="#">DOI</a>  | Transcriptional risk scores in Alzheimer's disease: From pathology to cognition.                     | Pyun, Jung-Min<br>...7 more...<br>Nho, Kwang sik | 1.5    | 3.6   | 8         | 8         | Alzheimer's & dementia : the journal of the Alzheimer's Association | 2024      | Dec 28, 2025 |
| <a href="#">36993280</a> <br><a href="#">DOI</a>  | Accurate estimation of rare cell type fractions from tissue omics data via hierarchical deconvolu... | Huang, Penghui<br>...3 more...<br>Wang, Jiebiao  | 0.297  | 0     | 3         | 1.5       | bioRxiv : the preprint server for biology                           | 2023      | Dec 28, 2025 |

|   |   |   |     |       |   |   |   |      |              |
|---|---|---|-----|-------|---|---|---|------|--------------|
| <a href="#">37577715</a> <br><a href="#">DOI</a>    | scMD: cell type deconvolution using single-cell DNA methylation references.     | Cai, Manqi ...2 more... Wang, Jiebiao     | 0.2 | 0     | 2 | 1 | bioRxiv : the preprint server for biology | 2023 | Dec 28, 2025 |
| <a href="#">39149243</a> <br><a href="#">DOI</a>    | BLEND: Probabilistic Cellular Deconvolution with Automated Reference Selection. | Huang, Penghui ...2 more... Wang, Jiebiao | 0   | 0     | 0 | 0 | bioRxiv : the preprint server for biology | 2024 | Dec 28, 2025 |
| <a href="#">41112940</a> <br><a href="#">DOI</a>  | EMixed: Probabilistic Multi-Omics Cellular Deconvolution of Bulk Omics Data.    | Cai, Manqi ...5 more... Wang, Jiebiao     | 0   | 0.387 | 0 | 0 | Journal of data science : JDS             | 2025 | Dec 28, 2025 |





Notes

RCR [Relative Citation Ratio](#) 

SJR [Scimago Journal Rank](#) 

# </> Repositories

Software repositories associated with this project.

C

Built on Jan 16, 2026

Developed with support from NIH Award [U54 OD036472](#)

| Name    | Description | Tags | Last Commit | Stars | forks | authors | commits | Issues | PRs | Issue Avg | PR Avg | readme | ributing | eof Con. | license | ntrib. | nguages |
|---------|-------------|------|-------------|-------|-------|---------|---------|--------|-----|-----------|--------|--------|----------|----------|---------|--------|---------|
|         |             |      |             |       |       |         |         |        |     |           |        |        |          |          |         |        |         |
| No data |             |      |             |       |       |         |         |        |     |           |        |        |          |          |         |        |         |

## Notes

- Repository For storing, tracking changes to, and collaborating on a piece of software.
- PR "Pull request", a draft change (new feature, bug fix, etc.) to a repo.
- Closed/Open Resolved/unresolved.
- Issue/PR Avg Average time issues/pull requests stay open for before being closed.

Only the main/default branch is considered for metrics like # of commits.

# of dependencies is totaled from all manifests in repo, direct and transitive, e.g. package.json + package-lock.json.

## Analytics

Website metrics associated with this project.

### Notes

Active Users      [Distinct users who visited the website](#) .

New Users      [Users who visited the website for the first time](#) .

Engaged Sessions      [Visits that had significant interaction](#) .

"Top" metrics are measured by number of engaged sessions.