

# **▶** Core Project R03OD034501

### O Details

| Projects        | Name   | Award        | Publications   | Repositories   | Analytics    |
|-----------------|--|--------------|----------------|----------------|--------------|
| 1R03OD034501-01 | Integration of GTEx and HuBMAP data to gain population-level cell-type-specific insights | \$314,739.00 | 5 publications | 0 repositories | 0 properties |

## Publications

Published works associated with this project.

| ID                                | Title  | Author<br>s       | R<br>C<br>R | SJ<br>R | Cita<br>tion<br>s | Cit./<br>yea<br>r | Journal | Publi<br>shed | Updat<br>ed |
|-----------------------------------|--|-------------------|-------------|---------|-------------------|-------------------|---------|---------------|-------------|
| 36993280 <b>♂</b><br>DOI <b>♂</b> | Accurate estimation of rare cell type fractions from tissue omics data via | Penghu<br>i Huang |             | 0       | 1                 | 1                 | bioRxiv | 2,02<br>3     | Oct<br>26,  |

|                                   | hierarchical deconvolu   | 3<br>more<br>Jiebiao<br>Wang                          |   |           |   |   |                                |           | 2024<br>(3<br>weeks<br>ago)               |
|-----------------------------------|--|---|---|-----------|---|---|--------------------------------|-----------|---|
| 38168620 <b>♂</b><br>DOI <b>♂</b> | scMD facilitates cell type deconvolution using single-cell DNA methylation references. | Manqi<br>Cai<br>2<br>more<br>Jiebiao<br>Wang          | 0 | 2.0<br>9  | 1 | 1 | Communica<br>tions<br>Biology  | 2,02<br>4 | Oct<br>26,<br>2024<br>(3<br>weeks<br>ago) |
| 37563770 🗷<br>DOI 🗹               | Transcriptional risk scores in Alzheimer's disease: From pathology to cognition.       | Jung-<br>Min<br>Pyun<br>7<br>more<br>Kwangs<br>ik Nho | 0 | 3.2<br>26 | 2 | 2 | Alzheimer's<br>and<br>Dementia | 2,02<br>4 | Oct<br>26,<br>2024<br>(3<br>weeks<br>ago) |
| 37577715 🗗<br>DOI 🗗               | scMD: cell type deconvolution using single-cell DNA methylation references.            | Manqi<br>Cai<br>2<br>more<br>Jiebiao<br>Wang          | 0 | 0         | 0 | 0 | bioRxiv                        | 2,02<br>3 | Oct<br>26,<br>2024<br>(3<br>weeks<br>ago) |
| 39149243 🗹<br>DOI 🗹               | BLEND: Probabilistic Cellular<br>Deconvolution with Automated Reference<br>Selection.  | Penghu<br>i Huang<br>2                                | 0 | 0         | 0 | 0 | bioRxiv                        | 2,02<br>4 | Oct<br>26,<br>2024                        |

| more    | (3    |
|---------|-------|
| Jiebiao | weeks |
| Wang    | ago)  |

#### Notes

RCR Relative Citation Ratio

SJR Scimago Journal Rank

## </> Repositories



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

Traffic metrics of websites associated with this project.

Active Users <u>Distinct users who visited the website</u> **.** 

New Users <u>Users who visited the website for the first time</u> **.** 

Engaged Sessions <u>Visits that had significant interaction</u> **?**.

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

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