

▶ Core Project R03OD032630

O Details

| Projects | Name | Award | Publications | Repositories | Analytics |
|-----------------|--|--------------|----------------|----------------|--------------|
| 1R03OD032630-01 | Methods to maximize the utility of common fund functional genomic data in multi-ethnic genetic studies | \$335,407.00 | 8 publications | 0 repositories | 0 properties |

Publications

Published works associated with this project.

| ID | Title | Authors | RC R | SJ R | Cita tion s | Cit./ yea r | Journal | Publ ishe d | Updat ed |
|------------|--|-----------------|-----------|---------|-------------------|-------------------|--------------|-------------------|-------------|
| 30643251 🗹 | Association studies of up to 1.2 million individuals yield new insights into the | Mengzhen Liu | 63. 31 | 0 | 1,12 9 | 225. 8 | Nat Genet | 2019 | Dec 28, |

| | genetic etiology | 121 more Scott Vrieze | | | | | | | 2024 (2 weeks ago) |
|-----------------------------------|---|--|-----------|---|-----|------|-------------------|------|---|
| 36477530 乙 | Genetic diversity fuels gene discovery for tobacco and alcohol use. | Gretchen R B Saunders215 more Scott Vrieze | 23. 29 | 0 | 159 | 79.5 | Nature | 2022 | Dec 29, 2024 (2 weeks ago) |
| 36702996 ♂ DOI ♂ | Multi-ancestry transcriptome-wide association analyses yield insights into tobacco use biology an | Fang Chen 88 more Dajiang J Liu | 5.0 4 | 0 | 22 | 22 | Nat Genet | 2023 | Dec 28, 2024 (2 weeks ago) |
| <u>36750564</u> | Multi-ancestry and multi-trait genome-wide association meta-analyses inform clinical risk predict | Chachrit Khunsrirak sakul 16 more Dajiang J Liu | 3.4 8 | 0 | 15 | 15 | Nat Comm un | 2023 | Dec 28, 2024 (2 weeks ago) |
| 35672318 🗹 DOI 🗹 | Integrating 3D genomic and epigenomic data to enhance target gene discovery and drug repurposing | Chachrit Khunsrirak sakul 12 more | 1.8 4 | 0 | 16 | 8 | Nat Comm un | 2022 | Dec 29, 2024 (2 |

| | | Dajiang J Liu | | | | | | | weeks ago) |
|----------------------------|--|---|----------|---|----|-----|----------------------|------|---|
| 35927319 🗗 | Rare genetic variants explain missing heritability in smoking. | Seon- Kyeong Jang 88 more Scott Vrieze | 1.4 3 | 0 | 13 | 6.5 | Nat Hum Behav | 2022 | Dec 29, 2024 (2 weeks ago) |
| <u>35833142</u> ☑ DOI ☑ | Construction and Application of Polygenic Risk Scores in Autoimmune Diseases. | Chachrit Khunsrirak sakul 4 more Dajiang J Liu | 0.8 6 | 0 | 7 | 3.5 | Front Immun ol | 2022 | Dec 29, 2024 (2 weeks ago) |
| 35178743 🖸 DOI 🗗 | Assessing reproducibility of high- throughput experiments in the case of missing data. | Roopali Singh 1 more Qunhua Li | 0.4 5 | 0 | 3 | 1.5 | Stat Med | 2022 | Dec 28, 2024 (2 weeks ago) |

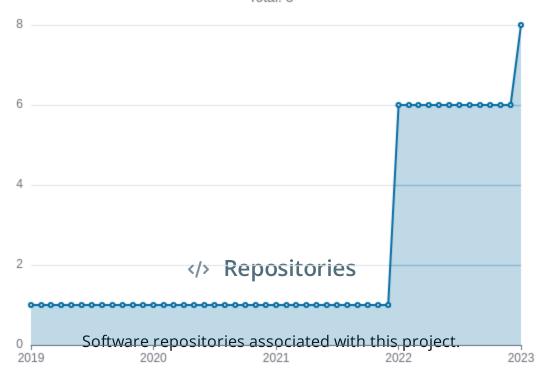
Notes

RCR Relative Citation Ratio

SJR Scimago Journal Rank

Publications (cumulative)





| Name | Description | Stars | Watchers | Forks | Issues | PRs | Commits | Contrib. |
|---------|-------------|-------|----------|-------|--------|-----|---------|----------|
| No data | | | | | | | | |

| Name | Tags | Last Commit | Avg Issue | Avg PR | Languages | License | Readme | Contributing | Dependencies |
|------|------|-------------|-----------|--------|-----------|---------|--------|--------------|--------------|
| | | | | | 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.

Avg Issue/PR 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

Traffic metrics of websites associated with this project.

Notes

Active Users <u>Distinct users who visited the website</u> 2.

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

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

Generated on Jan 10, 2025

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