



# Core Project R03OD032630









## Overview











High-level info about this project.


Projects	Name	Award	Publications	Repositories	Analytics
1R03OD032630-01	Methods to maximize the utility of common fund functional genomic data in multi-ethnic genetic studies	\$335K	9 publications	0 repositories	0 properties

## Publications

Published works associated with this project.

ID	Title	Authors	RC R	SJR	Cita tion s	Cit./ yea r	Journal	Publ ishe d	Upda ted
<a href="#">30643251</a>  <a href="#">DOI</a> 	Association studies of up to 1.2 million individuals yield new insights into the genetic etiology...	Liu, Mengzhen ...123 more... Vrieze, Scott	64. 94 3	16. 58 6	1,44 2	206	Nature genetics	2019	Feb 1, 2026
<a href="#">36477530</a>  <a href="#">DOI</a> 	Genetic diversity fuels gene discovery for tobacco and alcohol use.	Saunders, Gretchen R B ...217 more... Vrieze, Scott	30. 74 1	18. 28 8	356	89	Nature	2022	Feb 1, 2026
<a href="#">36750564</a>  <a href="#">DOI</a> 	Multi-ancestry and multi-trait genome-wide association meta-analyses inform clinical risk predict...	Khunsriraks akul, Chachrit ...16 more... Liu, Dajiang J	4.4 27	4.7 61	44	14.6 67	Nature communica tions	2023	Feb 1, 2026

<a href="#">36702996</a>  <a href="#">DOI</a> 	Multi-ancestry transcriptome-wide association analyses yield insights into tobacco use biology an...	Chen, Fang ...88 more... Liu, Dajiang J	3.8 65	16. 58 6	41	13.6 67	Nature genetics	2023	Feb 1, 2026
<a href="#">35672318</a>  <a href="#">DOI</a> 	Integrating 3D genomic and epigenomic data to enhance target gene discovery and drug repurposing ...	Khunsriraks akul, Chachrit ...12 more... Liu, Dajiang J	2.1 6	4.7 61	33	8.25	Nature communica tions	2022	Feb 1, 2026
<a href="#">35927319</a>  <a href="#">DOI</a> 	Rare genetic variants explain missing heritability in smoking.	Jang, Seon- Kyeong ...88 more... Vrieze, Scott	1.5 38	5.5 37	21	5.25	Nature human behaviour	2022	Feb 1, 2026
<a href="#">35833142</a>  <a href="#">DOI</a> 	Construction and Application of Polygenic Risk Scores in Autoimmune Diseases.	Khunsriraks akul, Chachrit ...4 more... Liu, Dajiang J	0.9 8	1.9 41	13	3.25	Frontiers in immunolog y	2022	Feb 1, 2026
<a href="#">38918381</a>  <a href="#">DOI</a> 	Dissecting heritability, environmental risk, and air pollution causal effects using > 50 milli...	McGuire, Daniel ...8 more... Jiang, Bibo	0.8 39	4.7 61	2	1	Nature communica tions	2024	Feb 1, 2026

35178743   
DOI 

Assessing reproducibility of high-throughput experiments in the case of missing data.

Singh,  
Roopali  
...1 more...  
Li, Qunhua

0.4  
96

1.2  
68

6

1.5

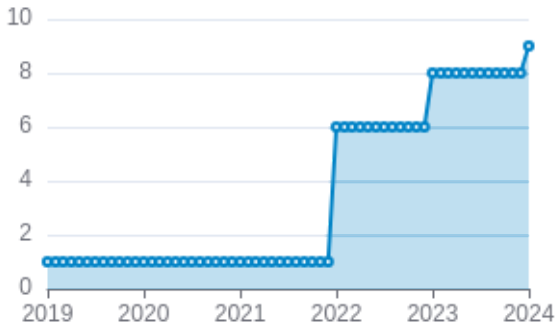
Statistics in  
medicine

2022

Feb  
1,  
2026

Publications (cumulative)

Total: 9



Notes

RCR [Relative Citation Ratio](#) 

SJR [Scimago Journal Rank](#) 

# </> Repositories

Software repositories associated with this project.

Name	Description	Tags	Last Commit	Stars	Forks	Watchers	Commits	Issues	PRs	Issue Avg	PR Avg	Readme	Contributing	Code of Con.	License	Contrib.	Languages

Built on Feb 1, 2026

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

## 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.