

# Rounak Dey

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5525819/publications.pdf>

Version: 2024-02-01

13  
papers

1,846  
citations

1163117

8  
h-index

1125743

13  
g-index

21  
all docs

21  
docs citations

21  
times ranked

4751  
citing authors

#	ARTICLE	IF	CITATIONS
1	COVID-19 Spread Mapper: a multi-resolution, unified framework and open-source tool. <i>Bioinformatics</i> , 2022, 38, 2661-2663.	4.1	5
2	Group testing via hypergraph factorization applied to COVID-19. <i>Nature Communications</i> , 2022, 13, 1837.	12.8	4
3	Efficient mixed model approach for large-scale genome-wide association studies of ordinal categorical phenotypes. <i>American Journal of Human Genetics</i> , 2021, 108, 825-839.	6.2	25
4	Rejoinder: Regression Models for Understanding COVID-19 Epidemic Dynamics With Incomplete Data. <i>Journal of the American Statistical Association</i> , 2021, 116, 1591-1594.	3.1	1
5	Regression Models for Understanding COVID-19 Epidemic Dynamics With Incomplete Data. <i>Journal of the American Statistical Association</i> , 2021, 116, 1561-1577.	3.1	16
6	Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. <i>Nature Genetics</i> , 2020, 52, 969-983.	21.4	146
7	Fast and robust ancestry prediction using principal component analysis. <i>Bioinformatics</i> , 2020, 36, 3439-3446.	4.1	21
8	A Fast and Accurate Method for Genome-wide Scale Phenome-wide $G \tilde{A} - E$ Analysis and Its Application to UK Biobank. <i>American Journal of Human Genetics</i> , 2019, 105, 1182-1192.	6.2	20
9	Robust meta-analysis of biobank-based genome-wide association studies with unbalanced binary phenotypes. <i>Genetic Epidemiology</i> , 2019, 43, 462-476.	1.3	7
10	Asymptotic properties of principal component analysis and shrinkage-bias adjustment under the generalized spiked population model. <i>Journal of Multivariate Analysis</i> , 2019, 173, 145-164.	1.0	6
11	Biobank-driven genomic discovery yields new insight into atrial fibrillation biology. <i>Nature Genetics</i> , 2018, 50, 1234-1239.	21.4	547
12	Efficiently controlling for case-control imbalance and sample relatedness in large-scale genetic association studies. <i>Nature Genetics</i> , 2018, 50, 1335-1341.	21.4	896
13	A Fast and Accurate Algorithm to Test for Binary Phenotypes and Its Application to PheWAS. <i>American Journal of Human Genetics</i> , 2017, 101, 37-49.	6.2	116