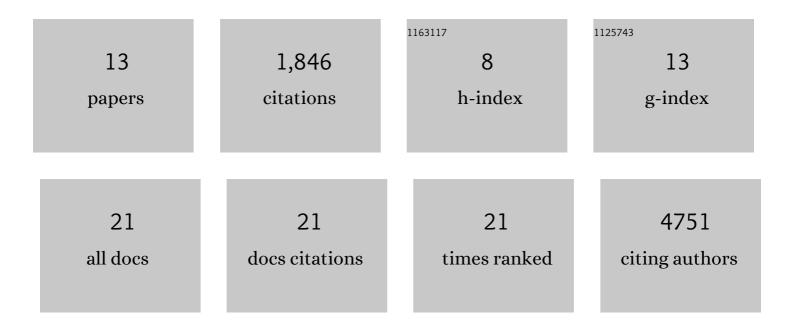
Rounak Dey

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5525819/publications.pdf Version: 2024-02-01



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