

# Arunabha Majumdar

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5081044/publications.pdf>

Version: 2024-02-01

15  
papers

308  
citations

1307594

7  
h-index

1125743

13  
g-index

19  
all docs

19  
docs citations

19  
times ranked

1053  
citing authors

#	ARTICLE	IF	CITATIONS
1	Competing analytical strategies of combining associated SNPs for estimating genetic risks. <i>Journal of Genetics</i> , 2022, 101, 1.	0.7	0
2	Competing analytical strategies of combining associated SNPs for estimating genetic risks.. <i>Journal of Genetics</i> , 2022, 101, .	0.7	0
3	Leveraging expression from multiple tissues using sparse canonical correlation analysis and aggregate tests improves the power of transcriptome-wide association studies. <i>PLoS Genetics</i> , 2021, 17, e1008973.	3.5	35
4	Leveraging eQTLs to identify individual-level tissue of interest for a complex trait. <i>PLoS Computational Biology</i> , 2021, 17, e1008915.	3.2	3
5	Large-scale cross-cancer fine-mapping of the 5p15.33 region reveals multiple independent signals. <i>Human Genetics and Genomics Advances</i> , 2021, 2, 100041.	1.7	6
6	A two-step approach to testing overall effect of gene-environment interaction for multiple phenotypes. <i>Bioinformatics</i> , 2021, 36, 5640-5648.	4.1	4
7	A summary-statistics-based approach to examine the role of serotonin transporter promoter tandem repeat polymorphism in psychiatric phenotypes. <i>European Journal of Human Genetics</i> , 2021, , .	2.8	4
8	Optimized design of single-cell RNA sequencing experiments for cell-type-specific eQTL analysis. <i>Nature Communications</i> , 2020, 11, 5504.	12.8	39
9	Accurate estimation of SNP-heritability from biobank-scale data irrespective of genetic architecture. <i>Nature Genetics</i> , 2019, 51, 1244-1251.	21.4	69
10	An efficient Bayesian meta-analysis approach for studying cross-phenotype genetic associations. <i>PLoS Genetics</i> , 2018, 14, e1007139.	3.5	40
11	Cis-eQTL-based trans-ethnic meta-analysis reveals novel genes associated with breast cancer risk. <i>PLoS Genetics</i> , 2017, 13, e1006690.	3.5	61
12	Determining Which Phenotypes Underlie a Pleiotropic Signal. <i>Genetic Epidemiology</i> , 2016, 40, 366-381.	1.3	15
13	Semiparametric Allelic Tests for Mapping Multiple Phenotypes: Binomial Regression and Mahalanobis Distance. <i>Genetic Epidemiology</i> , 2015, 39, 635-650.	1.3	16
14	Association mapping of blood pressure levels in a longitudinal framework using binomial regression. <i>BMC Proceedings</i> , 2014, 8, S74.	1.6	2
15	A Novel Bayesian Semiparametric Algorithm for Inferring Population Structure and Adjusting for Case-Control Association Tests. <i>Biometrics</i> , 2013, 69, 164-173.	1.4	5