Arunabha Majumdar

List of Publications by Year
in descending order

		1307594	1125743
15 papers	308 citations	7 h-index	13 g-index
19 all docs	19 docs citations	19 times ranked	1053 citing authors

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