

Debashree Ray

List of Publications by Year in descending order

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Version: 2024-02-01

24
papers

1,063
citations

840776

11
h-index

642732

23
g-index

34
all docs

34
docs citations

34
times ranked

1994
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide association studies of 27 accelerometry-derived physical activity measurements identified novel loci and genetic mechanisms. <i>Genetic Epidemiology</i> , 2022, 46, 122-138.	1.3	7
2	Benchmarking statistical methods for analyzing parent-child dyads in genetic association studies. <i>Genetic Epidemiology</i> , 2022, 46, 266-284.	1.3	2
3	Meta-analysis under imbalance in measurement of confounders in cohort studies using only summary-level data. <i>BMC Medical Research Methodology</i> , 2022, 22, 143.	3.1	2
4	Lessons from SARS-CoV-2 in India: A data-driven framework for pandemic resilience. <i>Science Advances</i> , 2022, 8, .	10.3	16
5	Detecting Gene-Environment Interaction for Maternal Exposures Using Case-Parent Trios Ascertained Through a Case With Non-Syndromic Orofacial Cleft. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 621018.	3.7	2
6	Incorporating false negative tests in epidemiological models for SARS-CoV-2 transmission and reconciling with seroprevalence estimates. <i>Scientific Reports</i> , 2021, 11, 9748.	3.3	16
7	The trans-ancestral genomic architecture of glycemic traits. <i>Nature Genetics</i> , 2021, 53, 840-860.	21.4	341
8	COVID-19 Pandemic in India: Through the Lens of Modeling. <i>Global Health, Science and Practice</i> , 2021, 9, 220-228.	1.7	12
9	A comparison of five epidemiological models for transmission of SARS-CoV-2 in India. <i>BMC Infectious Diseases</i> , 2021, 21, 533.	2.9	31
10	Estimating the wave 1 and wave 2 infection fatality rates from SARS-CoV-2 in India. <i>BMC Research Notes</i> , 2021, 14, 262.	1.4	22
11	Pleiotropy method reveals genetic overlap between orofacial clefts at multiple novel loci from GWAS of multi-ethnic trios. <i>PLoS Genetics</i> , 2021, 17, e1009584.	3.5	18
12	Discussion on "The timing and effectiveness of implementing mild interventions of COVID-19 in large industrial regions via a synthetic control method" by Tian <i>et al.</i> <i>Statistics and Its Interface</i> , 2021, 14, 25-28.	0.3	0
13	Effect of non-normality and low count variants on cross-phenotype association tests in GWAS. <i>European Journal of Human Genetics</i> , 2020, 28, 300-312.	2.8	12
14	Comprehensive public health evaluation of lockdown as a non-pharmaceutical intervention on COVID-19 spread in India: national trends masking state-level variations. <i>BMJ Open</i> , 2020, 10, e041778.	1.9	41
15	Predictions, Role of Interventions and Effects of a Historic National Lockdown in India's Response to the the COVID-19 Pandemic: Data Science Call to Arms. , 2020, 2020, .		75
16	A powerful method for pleiotropic analysis under composite null hypothesis identifies novel shared loci between Type 2 Diabetes and Prostate Cancer. <i>PLoS Genetics</i> , 2020, 16, e1009218.	3.5	49
17	Exome sequencing of Finnish isolates enhances rare-variant association power. <i>Nature</i> , 2019, 572, 323-328.	27.8	161
18	The Evolving Field of Genetic Epidemiology: From Familial Aggregation to Genomic Sequencing. <i>American Journal of Epidemiology</i> , 2019, 188, 2069-2077.	3.4	6

#	ARTICLE	IF	CITATIONS
19	Methods for meta-analysis of multiple traits using GWAS summary statistics. <i>Genetic Epidemiology</i> , 2018, 42, 134-145.	1.3	61
20	A novel association test for multiple secondary phenotypes from a case-control GWAS. <i>Genetic Epidemiology</i> , 2017, 41, 413-426.	1.3	10
21	USAT: A Unified Score-Based Association Test for Multiple Phenotype-Genotype Analysis. <i>Genetic Epidemiology</i> , 2016, 40, 20-34.	1.3	42
22	A Bayesian Partitioning Model for the Detection of Multilocus Effects in Case-Control Studies. <i>Human Heredity</i> , 2015, 79, 69-79.	0.8	4
23	Global Individual Ancestry Using Principal Components for Family Data. <i>Human Heredity</i> , 2015, 80, 1-11.	0.8	6
24	A Rapid Gene-Based Genome-Wide Association Test with Multivariate Traits. <i>Human Heredity</i> , 2013, 76, 53-63.	0.8	17