

Sayantana Das

List of Publications by Year in descending order

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Version: 2024-02-01

22
papers

8,343
citations

516710

16
h-index

677142

22
g-index

26
all docs

26
docs citations

26
times ranked

18413
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|-----------|
| 1 | Meta-imputation: An efficient method to combine genotype data after imputation with multiple reference panels. <i>American Journal of Human Genetics</i> , 2022, 109, 1007-1015. | 6.2 | 15 |
| 2 | Insights From a Large-Scale Whole-Genome Sequencing Study of Systolic Blood Pressure, Diastolic Blood Pressure, and Hypertension. <i>Hypertension</i> , 2022, 79, 1656-1667. | 2.7 | 12 |
| 3 | Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. <i>Nature</i> , 2021, 590, 290-299. | 27.8 | 1,069 |
| 4 | Genomewide Association Studies of <i>LRRK2</i> Modifiers of Parkinson's Disease. <i>Annals of Neurology</i> , 2021, 90, 76-88. | 5.3 | 30 |
| 5 | Whole-genome association analyses of sleep-disordered breathing phenotypes in the NHLBI TOPMed program. <i>Genome Medicine</i> , 2021, 13, 136. | 8.2 | 16 |
| 6 | A population-specific reference panel for improved genotype imputation in African Americans. <i>Communications Biology</i> , 2021, 4, 1269. | 4.4 | 15 |
| 7 | Inherited causes of clonal haematopoiesis in 97,691 whole genomes. <i>Nature</i> , 2020, 586, 763-768. | 27.8 | 376 |
| 8 | 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 |
| 9 | Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. <i>Nature Communications</i> , 2020, 11, 6417. | 12.8 | 39 |
| 10 | Exploring various polygenic risk scores for skin cancer in the phenomes of the Michigan genomics initiative and the UK Biobank with a visual catalog: PRSWeb. <i>PLoS Genetics</i> , 2019, 15, e1008202. | 3.5 | 28 |
| 11 | Narrow-sense heritability estimation of complex traits using identity-by-descent information. <i>Heredity</i> , 2018, 121, 616-630. | 2.6 | 20 |
| 12 | Comparison of methods that use whole genome data to estimate the heritability and genetic architecture of complex traits. <i>Nature Genetics</i> , 2018, 50, 737-745. | 21.4 | 205 |
| 13 | Genetic signature to provide robust risk assessment of psoriatic arthritis development in psoriasis patients. <i>Nature Communications</i> , 2018, 9, 4178. | 12.8 | 95 |
| 14 | Genotype Imputation from Large Reference Panels. <i>Annual Review of Genomics and Human Genetics</i> , 2018, 19, 73-96. | 6.2 | 158 |
| 15 | Large scale meta-analysis characterizes genetic architecture for common psoriasis associated variants. <i>Nature Communications</i> , 2017, 8, 15382. | 12.8 | 251 |
| 16 | Improving power of association tests using multiple sets of imputed genotypes from distributed reference panels. <i>Genetic Epidemiology</i> , 2017, 41, 744-755. | 1.3 | 27 |
| 17 | Exome-wide association study reveals novel psoriasis susceptibility locus at TNFSF15 and rare protective alleles in genes contributing to type I IFN signalling. <i>Human Molecular Genetics</i> , 2017, 26, 4301-4313. | 2.9 | 41 |
| 18 | Next-generation genotype imputation service and methods. <i>Nature Genetics</i> , 2016, 48, 1284-1287. | 21.4 | 2,828 |

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|----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|-----------|
| 19 | A reference panel of 64,976 haplotypes for genotype imputation. <i>Nature Genetics</i> , 2016, 48, 1279-1283. | 21.4 | 2,421 |
| 20 | Enhanced meta-analysis and replication studies identify five new psoriasis susceptibility loci. <i>Nature Communications</i> , 2015, 6, 7001. | 12.8 | 156 |
| 21 | Genome-wide Association Analysis of Psoriatic Arthritis and Cutaneous Psoriasis Reveals Differences in Their Genetic Architecture. <i>American Journal of Human Genetics</i> , 2015, 97, 816-836. | 6.2 | 245 |
| 22 | Fine mapping of eight psoriasis susceptibility loci. <i>European Journal of Human Genetics</i> , 2015, 23, 844-853. | 2.8 | 25 |