Kushal K Dey

List of Publications by Year
in descending order

15 papers	1,631 citations	840776 11 h-index	940533 16 g-index
31 all docs	31 docs citations	31 times ranked	3772 citing authors

#	Article	IF	Citations
1	Combining SNP-to-gene linking strategies to identify disease genes and assess disease omnigenicity. Nature Genetics, 2022, 54, 827-836.	21.4	61
2	SNP-to-gene linking strategies reveal contributions of enhancer-related and candidate master-regulator genes to autoimmune disease. Cell Genomics, 2022, 2, 100145.	6.5	19
3	Dispersal syndromes drive the formation of biogeographical regions, illustrated by the case of Wallace's Line. Global Ecology and Biogeography, 2021, 30, 685-696.	5.8	15
4	Genome-wide enhancer maps link risk variants to disease genes. Nature, 2021, 593, 238-243.	27.8	332
5	COVID-19 tissue atlases reveal SARS-CoV-2 pathology and cellular targets. Nature, 2021, 595, 107-113.	27.8	537
6	Improving the trans-ancestry portability of polygenic risk scores by prioritizing variants in predicted cell-type-specific regulatory elements. Nature Genetics, 2020, 52, 1346-1354.	21.4	126
7	Evaluating the informativeness of deep learning annotations for human complex diseases. Nature Communications, 2020, 11, 4703.	12.8	21
8	Improving the informativeness of Mendelian disease-derived pathogenicity scores for common disease. Nature Communications, 2020, 11, 6258.	12.8	8
9	Genetic history from the Middle Neolithic to present on the Mediterranean island of Sardinia. Nature Communications, 2020, 11, 939.	12.8	96
10	Characterizing and inferring quantitative cell cycle phase in single-cell RNA-seq data analysis. Genome Research, 2020, 30, 611-621.	5.5	63
11	Regional influences on community structure across the tropical-temperate divide. Nature Communications, 2019, 10, 2646.	12.8	40
12	Inference and visualization of DNA damage patterns using a grade of membership model. Bioinformatics, 2019, 35, 1292-1298.	4.1	7
13	A new sequence logo plot to highlight enrichment and depletion. BMC Bioinformatics, 2018, 19, 473.	2.6	43
14	Visualizing the structure of RNA-seq expression data using grade of membership models. PLoS Genetics, 2017, 13, e1006599.	3.5	132
15	Learning diagnostic signatures from microarray data using L1-regularized logistic regression. Systems Biomedicine (Austin, Tex), 2013, 1, 240-246.	0.7	2