

Kousik Kundu

List of Publications by Year in descending order

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Version: 2024-02-01

22
papers

2,897
citations

566801

15
h-index

676716

22
g-index

32
all docs

32
docs citations

32
times ranked

7824
citing authors

#	ARTICLE	IF	CITATIONS
1	Insights into the genetic architecture of haematological traits from deep phenotyping and whole-genome sequencing for two Mediterranean isolated populations. <i>Scientific Reports</i> , 2022, 12, 1131.	1.6	2
2	Genetic associations at regulatory phenotypes improve fine-mapping of causal variants for 12 immune-mediated diseases. <i>Nature Genetics</i> , 2022, 54, 251-262.	9.4	23
3	Whole-exome sequencing identifies rare genetic variants associated with human plasma metabolites. <i>American Journal of Human Genetics</i> , 2022, 109, 1038-1054.	2.6	17
4	Genetic perturbation of PU.1 binding and chromatin looping at neutrophil enhancers associates with autoimmune disease. <i>Nature Communications</i> , 2021, 12, 2298.	5.8	32
5	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. <i>American Journal of Human Genetics</i> , 2021, 108, 874-893.	2.6	28
6	A map of transcriptional heterogeneity and regulatory variation in human microglia. <i>Nature Genetics</i> , 2021, 53, 861-868.	9.4	115
7	Mitochondrial DNA variants modulate N-formylmethionine, proteostasis and risk of late-onset human diseases. <i>Nature Medicine</i> , 2021, 27, 1564-1575.	15.2	40
8	Whole-genome sequencing in diverse subjects identifies genetic correlates of leukocyte traits: The NHLBI TOPMed program. <i>American Journal of Human Genetics</i> , 2021, 108, 1836-1851.	2.6	14
9	The Polygenic and Monogenic Basis of Blood Traits and Diseases. <i>Cell</i> , 2020, 182, 1214-1231.e11.	13.5	388
10	Tumors induce de novo steroid biosynthesis in T cells to evade immunity. <i>Nature Communications</i> , 2020, 11, 3588.	5.8	54
11	The influence of rare variants in circulating metabolic biomarkers. <i>PLoS Genetics</i> , 2020, 16, e1008605.	1.5	9
12	Shared genetic effects on chromatin and gene expression indicate a role for enhancer priming in immune response. <i>Nature Genetics</i> , 2018, 50, 424-431.	9.4	253
13	Cohort-wide deep whole genome sequencing and the allelic architecture of complex traits. <i>Nature Communications</i> , 2018, 9, 4674.	5.8	33
14	Freiburg RNA tools: a central online resource for RNA-focused research and teaching. <i>Nucleic Acids Research</i> , 2018, 46, W25-W29.	6.5	107
15	An Efficient Semi-supervised Learning Approach to Predict SH2 Domain Mediated Interactions. <i>Methods in Molecular Biology</i> , 2017, 1555, 83-97.	0.4	0
16	<i>GRIN3B</i> missense mutation as an inherited risk factor for schizophrenia: whole-exome sequencing in a family with a familiar history of psychotic disorders. <i>Genetical Research</i> , 2017, 99, e1.	0.3	15
17	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease. <i>Cell</i> , 2016, 167, 1415-1429.e19.	13.5	1,052
18	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. <i>Cell</i> , 2016, 167, 1398-1414.e24.	13.5	573

#	ARTICLE	IF	CITATIONS
19	MoDPepInt: an interactive web server for prediction of modular domain-peptide interactions. <i>Bioinformatics</i> , 2014, 30, 2668-2669.	1.8	37
20	Cluster based prediction of PDZ-peptide interactions. <i>BMC Genomics</i> , 2014, 15, S5.	1.2	16
21	A graph kernel approach for alignment-free domain-peptide interaction prediction with an application to human SH3 domains. <i>Bioinformatics</i> , 2013, 29, i335-i343.	1.8	15
22	Semi-Supervised Prediction of SH2-Peptide Interactions from Imbalanced High-Throughput Data. <i>PLoS ONE</i> , 2013, 8, e62732.	1.1	27