Tianyuan Lu

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/5107424/publications.pdf

Version: 2024-02-01

25	293	1039406	996533
papers	citations	9 h-index	15 g-index

32	32	32	301
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Reshuffling of the ancestral core-eudicot genome shaped chromatin topology and epigenetic modification in Panax. Nature Communications, 2022, 13, 1902.	5.8	30
2	Polygenic risk score as a possible tool for identifying familial monogenic causes of complex diseases. Genetics in Medicine, 2022, 24, 1545-1555.	1.1	12
3	Genetic and Epigenetic Signatures Associated with the Divergence of Aquilegia Species. Genes, 2022, 13, 793.	1.0	0
4	Capturing additional genetic risk from family history for improved polygenic risk prediction. Communications Biology, 2022, 5, .	2.0	6
5	Individuals with common diseases but with a low polygenic risk score could be prioritized for rare variant screening. Genetics in Medicine, 2021, 23, 508-515.	1.1	39
6	Improved prediction of fracture risk leveraging a genome-wide polygenic risk score. Genome Medicine, 2021, 13, 16.	3.6	35
7	A Polygenic Risk Score to Predict Future Adult Short Stature Among Children. Journal of Clinical Endocrinology and Metabolism, 2021, 106, 1918-1928.	1.8	19
8	Evolutionary Contribution of Duplicated Genes to Genome Evolution in the Ginseng Species Complex. Genome Biology and Evolution, 2021, 13, .	1.1	4
9	Detecting cord blood cell type-specific epigenetic associations with gestational diabetes mellitus and early childhood growth. Clinical Epigenetics, 2021, 13, 131.	1.8	5
10	Block coordinate descent algorithm improves variable selection and estimation in errorâ€inâ€variables regression. Genetic Epidemiology, 2021, 45, 874-890.	0.6	5
11	H3K27M in Gliomas Causes a One-Step Decrease in H3K27 Methylation and Reduced Spreading within the Constraints of H3K36 Methylation. Cell Reports, 2020, 33, 108390.	2.9	50
12	Investigating transcriptome-wide sex dimorphism by multi-level analysis of single-cell RNA sequencing data in ten mouse cell types. Biology of Sex Differences, 2020, 11, 61.	1.8	19
13	Simultaneous SNP selection and adjustment for population structure in high dimensional prediction models. PLoS Genetics, 2020, 16, e1008766.	1.5	5
14	Polygenic risk for coronary heart disease acts through atherosclerosis in type 2 diabetes. Cardiovascular Diabetology, 2020, 19, 12.	2.7	23
15	Title is missing!. , 2020, 16, e1008766.		0
16	Title is missing!. , 2020, 16, e1008766.		0
17	Title is missing!. , 2020, 16, e1008766.		0
18	Title is missing!. , 2020, 16, e1008766.		0

#	Article	IF	Citations
19	Title is missing!. , 2020, 16, e1008766.		0
20	Title is missing!. , 2020, 16, e1008766.		0
21	Identifying Causes of Fracture Beyond Bone Mineral Density: Evidence From Human Genetics. Journal of Bone and Mineral Research, 2020, 37, 1592-1602.	3.1	5
22	Whole-genome bisulfite sequencing in systemic sclerosis provides novel targets to understand disease pathogenesis. BMC Medical Genomics, 2019, 12, 144.	0.7	22
23	Rapid Divergence Followed by Adaptation to Contrasting Ecological Niches of Two Closely Related Columbine SpeciesAquilegia japonicaandA. oxysepala. Genome Biology and Evolution, 2019, 11, 919-930.	1.1	7
24	Indirect effect inference and application to GAW20 data. BMC Genetics, 2018, 19, 67.	2.7	3
25	Take a Step Down and Beware of H3K36me2: The H3K27m Mutation in Glioma Directs H3K27 Methylation. SSRN Electronic Journal, 0, , .	0.4	0