

Jian Zeng

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1821529/publications.pdf>

Version: 2024-02-01

26
papers

4,181
citations

361413

20
h-index

526287

27
g-index

41
all docs

41
docs citations

41
times ranked

7028
citing authors

#	ARTICLE	IF	CITATIONS
1	Extend mixed models to multilayer neural networks for genomic prediction including intermediate omics data. <i>Genetics</i> , 2022, 221, .	2.9	13
2	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. <i>Nature</i> , 2022, 604, 502-508.	27.8	929
3	Genome-wide analyses of behavioural traits are subject to bias by misreports and longitudinal changes. <i>Nature Communications</i> , 2021, 12, 20211.	12.8	40
4	Widespread signatures of natural selection across human complex traits and functional genomic categories. <i>Nature Communications</i> , 2021, 12, 1164.	12.8	50
5	Analysis of common genetic variation and rare CNVs in the Australian Autism Biobank. <i>Molecular Autism</i> , 2021, 12, 12.	4.9	11
6	A Comparison of Ten Polygenic Score Methods for Psychiatric Disorders Applied Across Multiple Cohorts. <i>Biological Psychiatry</i> , 2021, 90, 611-620.	1.3	103
7	Tumor Mutational Burden Is Polygenic and Genetically Associated with Complex Traits and Diseases. <i>Cancer Research</i> , 2021, 81, 1230-1239.	0.9	14
8	Promoter-anchored chromatin interactions predicted from genetic analysis of epigenomic data. <i>Nature Communications</i> , 2020, 11, 2061.	12.8	8
9	Genome-wide association study identifies 143 loci associated with 25 hydroxyvitamin D concentration. <i>Nature Communications</i> , 2020, 11, 1647.	12.8	211
10	Genotype-by-environment interactions inferred from genetic effects on phenotypic variability in the UK Biobank. <i>Science Advances</i> , 2019, 5, eaaw3538.	10.3	123
11	The effect of X-linked dosage compensation on complex trait variation. <i>Nature Communications</i> , 2019, 10, 3009.	12.8	44
12	Improved polygenic prediction by Bayesian multiple regression on summary statistics. <i>Nature Communications</i> , 2019, 10, 5086.	12.8	291
13	Integrative analysis of omics summary data reveals putative mechanisms underlying complex traits. <i>Nature Communications</i> , 2018, 9, 918.	12.8	250
14	Signatures of negative selection in the genetic architecture of human complex traits. <i>Nature Genetics</i> , 2018, 50, 746-753.	21.4	304
15	Genomic Prediction from Multiple-Trait Bayesian Regression Methods Using Mixture Priors. <i>Genetics</i> , 2018, 209, 89-103.	2.9	61
16	Global genetic differentiation of complex traits shaped by natural selection in humans. <i>Nature Communications</i> , 2018, 9, 1865.	12.8	70
17	Genome-wide association analyses identify 143 risk variants and putative regulatory mechanisms for type 2 diabetes. <i>Nature Communications</i> , 2018, 9, 2941.	12.8	570
18	Identifying gene targets for brain-related traits using transcriptomic and methylomic data from blood. <i>Nature Communications</i> , 2018, 9, 2282.	12.8	294

#	ARTICLE	IF	CITATIONS
19	A nested mixture model for genomic prediction using whole-genome SNP genotypes. PLoS ONE, 2018, 13, e0194683.	2.5	9
20	Inference on the Genetic Basis of Eye and Skin Color in an Admixed Population via Bayesian Linear Mixed Models. Genetics, 2017, 206, 1113-1126.	2.9	30
21	Concepts, estimation and interpretation of SNP-based heritability. Nature Genetics, 2017, 49, 1304-1310.	21.4	378
22	Impact of fitting dominance and additive effects on accuracy of genomic prediction of breeding values in layers. Journal of Animal Breeding and Genetics, 2016, 133, 334-346.	2.0	24
23	Genomic selection of purebred animals for crossbred performance in the presence of dominant gene action. Genetics Selection Evolution, 2013, 45, 11.	3.0	79
24	Dissecting the genetic architecture of frost tolerance in Central European winter wheat. Journal of Experimental Botany, 2013, 64, 4453-4460.	4.8	69
25	Genomic Prediction of Hybrid Wheat Performance. Crop Science, 2013, 53, 802-810.	1.8	127
26	Genomic breeding value prediction and QTL mapping of QTLMAS2011 data using Bayesian and GBLUP methods. BMC Proceedings, 2012, 6, S7.	1.6	17