

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	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. <i>Nature</i> , 2022, 604, 502-508.	27.8	929
2	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
3	Concepts, estimation and interpretation of SNP-based heritability. <i>Nature Genetics</i> , 2017, 49, 1304-1310.	21.4	378
4	Signatures of negative selection in the genetic architecture of human complex traits. <i>Nature Genetics</i> , 2018, 50, 746-753.	21.4	304
5	Identifying gene targets for brain-related traits using transcriptomic and methylomic data from blood. <i>Nature Communications</i> , 2018, 9, 2282.	12.8	294
6	Improved polygenic prediction by Bayesian multiple regression on summary statistics. <i>Nature Communications</i> , 2019, 10, 5086.	12.8	291
7	Integrative analysis of omics summary data reveals putative mechanisms underlying complex traits. <i>Nature Communications</i> , 2018, 9, 918.	12.8	250
8	Genome-wide association study identifies 143 loci associated with 25 hydroxyvitamin D concentration. <i>Nature Communications</i> , 2020, 11, 1647.	12.8	211
9	Genomic Prediction of Hybrid Wheat Performance. <i>Crop Science</i> , 2013, 53, 802-810.	1.8	127
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	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
12	Genomic selection of purebred animals for crossbred performance in the presence of dominant gene action. <i>Genetics Selection Evolution</i> , 2013, 45, 11.	3.0	79
13	Global genetic differentiation of complex traits shaped by natural selection in humans. <i>Nature Communications</i> , 2018, 9, 1865.	12.8	70
14	Dissecting the genetic architecture of frost tolerance in Central European winter wheat. <i>Journal of Experimental Botany</i> , 2013, 64, 4453-4460.	4.8	69
15	Genomic Prediction from Multiple-Trait Bayesian Regression Methods Using Mixture Priors. <i>Genetics</i> , 2018, 209, 89-103.	2.9	61
16	Widespread signatures of natural selection across human complex traits and functional genomic categories. <i>Nature Communications</i> , 2021, 12, 1164.	12.8	50
17	The effect of X-linked dosage compensation on complex trait variation. <i>Nature Communications</i> , 2019, 10, 3009.	12.8	44
18	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

#	ARTICLE	IF	CITATIONS
19	Inference on the Genetic Basis of Eye and Skin Color in an Admixed Population via Bayesian Linear Mixed Models. <i>Genetics</i> , 2017, 206, 1113-1126.	2.9	30
20	Impact of fitting dominance and additive effects on accuracy of genomic prediction of breeding values in layers. <i>Journal of Animal Breeding and Genetics</i> , 2016, 133, 334-346.	2.0	24
21	Genomic breeding value prediction and QTL mapping of QTLMAS2011 data using Bayesian and GBLUP methods. <i>BMC Proceedings</i> , 2012, 6, S7.	1.6	17
22	Tumor Mutational Burden Is Polygenic and Genetically Associated with Complex Traits and Diseases. <i>Cancer Research</i> , 2021, 81, 1230-1239.	0.9	14
23	Extend mixed models to multilayer neural networks for genomic prediction including intermediate omics data. <i>Genetics</i> , 2022, 221, .	2.9	13
24	Analysis of common genetic variation and rare CNVs in the Australian Autism Biobank. <i>Molecular Autism</i> , 2021, 12, 12.	4.9	11
25	A nested mixture model for genomic prediction using whole-genome SNP genotypes. <i>PLoS ONE</i> , 2018, 13, e0194683.	2.5	9
26	Promoter-anchored chromatin interactions predicted from genetic analysis of epigenomic data. <i>Nature Communications</i> , 2020, 11, 2061.	12.8	8