

Xia Shen

List of Publications by Year in descending order

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Version: 2024-02-01

59
papers

3,823
citations

236612

25
h-index

155451

55
g-index

77
all docs

77
docs citations

77
times ranked

9014
citing authors

#	ARTICLE	IF	CITATIONS
1	Different Isocaloric Meals and Adiposity Modify Energy Expenditure and Clinical and Metabolomic Biomarkers During Resting and Exercise States in a Randomized Crossover Acute Trial of Normal-Weight and Overweight/Obese Men. <i>Journal of Nutrition</i> , 2022, 152, 1118-1129.	1.3	5
2	SARS-CoV-2 causes a significant stress response mediated by small RNAs in the blood of COVID-19 patients. <i>Molecular Therapy - Nucleic Acids</i> , 2022, 27, 751-762.	2.3	12
3	Fusion Gene Detection Using Whole-Exome Sequencing Data in Cancer Patients. <i>Frontiers in Genetics</i> , 2022, 13, 820493.	1.1	3
4	Genetic and phenotypic links between obesity and extracellular vesicles. <i>Human Molecular Genetics</i> , 2022, 31, 3643-3651.	1.4	2
5	Integration of Distinct Analysis Strategies Improves Tissue-Trait Association Identification. <i>Frontiers in Genetics</i> , 2022, 13, 798269.	1.1	0
6	Whole-genome sequencing reveals host factors underlying critical COVID-19. <i>Nature</i> , 2022, 607, 97-103.	13.7	174
7	Genetic Landscape of the ACE2 Coronavirus Receptor. <i>Circulation</i> , 2022, 145, 1398-1411.	1.6	20
8	Nontrivial Replication of Loci Detected by Multi-Trait Methods. <i>Frontiers in Genetics</i> , 2021, 12, 627989.	1.1	4
9	Changes in Plasma Metabolome Profiles Following Oral Glucose Challenge among Adult Chinese. <i>Nutrients</i> , 2021, 13, 1474.	1.7	8
10	Total genetic contribution assessment across the human genome. <i>Nature Communications</i> , 2021, 12, 2845.	5.8	4
11	Targeted genetic screening in bacteria with a Cas12k-guided transposase. <i>Cell Reports</i> , 2021, 36, 109635.	2.9	24
12	Improved Estimation of Phenotypic Correlations Using Summary Association Statistics. <i>Frontiers in Genetics</i> , 2021, 12, 665252.	1.1	5
13	Serum Metabolomics Identifies Dysregulated Pathways and Potential Metabolic Biomarkers for Hyperuricemia and Gout. <i>Arthritis and Rheumatology</i> , 2021, 73, 1738-1748.	2.9	49
14	A Chinese host genetic study discovered IFNs and causality of laboratory traits on COVID-19 severity. <i>IScience</i> , 2021, 24, 103186.	1.9	10
15	Non-inferiority in cancer clinical trials was associated with more lenient margins and higher hypothesized outcome event rates. <i>Journal of Clinical Epidemiology</i> , 2021, 139, 214-221.	2.4	1
16	Genetic mechanisms of critical illness in COVID-19. <i>Nature</i> , 2021, 591, 92-98.	13.7	1,014
17	Genetic and phenotypic analysis of the causal relationship between aging and COVID-19. <i>Communications Medicine</i> , 2021, 1, .	1.9	19
18	Mapping the serum proteome to neurological diseases using whole genome sequencing. <i>Nature Communications</i> , 2021, 12, 7042.	5.8	29

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19	Physician-Confirmed and Administrative Definitions of Stroke in UK Biobank Reflect the Same Underlying Genetic Trait. <i>Frontiers in Neurology</i> , 2021, 12, 787107.	1.1	4
20	Genetic and Phenotypic Evidence for the Causal Relationship Between Aging and COVID-19. <i>Innovation in Aging</i> , 2021, 5, 330-330.	0.0	0
21	Identification of potential candidate genes and pathways in atrioventricular nodal reentry tachycardia by whole-exome sequencing. <i>Clinical and Translational Medicine</i> , 2020, 10, 238-257.	1.7	10
22	High-definition likelihood inference of genetic correlations across human complex traits. <i>Nature Genetics</i> , 2020, 52, 859-864.	9.4	114
23	Lipids, Apolipoproteins, and the Risk of Parkinson Disease. <i>Circulation Research</i> , 2019, 125, 643-652.	2.0	50
24	Pleiotropy Complicates Human Gene Editing: CCR5 ^{Δ32} and Beyond. <i>Frontiers in Genetics</i> , 2019, 10, 669.	1.1	13
25	The genetic interplay between body mass index, breast size and breast cancer risk: a Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , 2019, 48, 781-794.	0.9	37
26	Effects of Calcium, Magnesium, and Potassium Concentrations on Ventricular Repolarization in Unselected Individuals. <i>Journal of the American College of Cardiology</i> , 2019, 73, 3118-3131.	1.2	27
27	Profiling surface proteins on individual exosomes using a proximity barcoding assay. <i>Nature Communications</i> , 2019, 10, 3854.	5.8	148
28	Recent development on liquid chromatography-mass spectrometry analysis of oxidized lipids. <i>Free Radical Biology and Medicine</i> , 2019, 144, 16-34.	1.3	28
29	An update on lipid oxidation and inflammation in cardiovascular diseases. <i>Free Radical Biology and Medicine</i> , 2019, 144, 266-278.	1.3	215
30	Endogenous cholesterol ester hydroperoxides modulate cholesterol levels and inhibit cholesterol uptake in hepatocytes and macrophages. <i>Redox Biology</i> , 2019, 21, 101069.	3.9	38
31	Genomics of 1 million parent lifespans implicates novel pathways and common diseases and distinguishes survival chances. <i>ELife</i> , 2019, 8, .	2.8	170
32	MR-PheWAS: exploring the causal effect of SUA level on multiple disease outcomes by using genetic instruments in UK Biobank. <i>Annals of the Rheumatic Diseases</i> , 2018, 77, 1039-1047.	0.5	57
33	Glucose challenge metabolomics implicates medium-chain acylcarnitines in insulin resistance. <i>Scientific Reports</i> , 2018, 8, 8691.	1.6	47
34	Bivariate genomic analysis identifies a hidden locus associated with bacteria hypersensitive response in <i>Arabidopsis thaliana</i> . <i>Scientific Reports</i> , 2017, 7, 45281.	1.6	2
35	Genome-wide meta-analysis associates HLA-DQA1/DRB1 and LPA and lifestyle factors with human longevity. <i>Nature Communications</i> , 2017, 8, 910.	5.8	118
36	Multivariate discovery and replication of five novel loci associated with Immunoglobulin G N-glycosylation. <i>Nature Communications</i> , 2017, 8, 447.	5.8	102

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37	A Selection Operator for Summary Association Statistics Reveals Allelic Heterogeneity of Complex Traits. <i>American Journal of Human Genetics</i> , 2017, 101, 903-912.	2.6	9
38	Genetic Regulation of Transcriptional Variation in Natural <i>Arabidopsis thaliana</i> Accessions. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2319-2328.	0.8	25
39	Crowdsourced estimation of cognitive decline and resilience in Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2016, 12, 645-653.	0.4	72
40	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. <i>Nature Genetics</i> , 2016, 48, 1462-1472.	9.4	284
41	Effects of number of training generations on genomic prediction for various traits in a layer chicken population. <i>Genetics Selection Evolution</i> , 2016, 48, 22.	1.2	19
42	A Genome-Wide Association Analysis Reveals Epistatic Cancellation of Additive Genetic Variance for Root Length in <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2015, 11, e1005541.	1.5	38
43	RE: The Effect on Melanoma Risk of Genes Previously Associated With Telomere Length. <i>Journal of the National Cancer Institute</i> , 2015, 107, .	3.0	1
44	Identification of quantitative genetic components of fitness variation in farmed, hybrid and native salmon in the wild. <i>Heredity</i> , 2015, 115, 47-55.	1.2	45
45	Fitting Conditional and Simultaneous Autoregressive Spatial Models in hglm. <i>R Journal</i> , 2015, 7, 5.	0.7	27
46	Natural CMT2 Variation Is Associated With Genome-Wide Methylation Changes and Temperature Seasonality. <i>PLoS Genetics</i> , 2014, 10, e1004842.	1.5	147
47	Application of a genomic model for high-dimensional chemometric analysis. <i>Journal of Chemometrics</i> , 2014, 28, 548-557.	0.7	7
48	Genetic dissection of growth traits in a Chinese indigenous $\tilde{\text{A}}$ - commercial broiler chicken cross. <i>BMC Genomics</i> , 2013, 14, 151.	1.2	67
49	A Novel Generalized Ridge Regression Method for Quantitative Genetics. <i>Genetics</i> , 2013, 193, 1255-1268.	1.2	68
50	MAPfastR: Quantitative Trait Loci Mapping in Outbred Line Crosses. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 2147-2149.	0.8	7
51	PASE: a novel method for functional prediction of amino acid substitutions based on physicochemical properties. <i>Frontiers in Genetics</i> , 2013, 4, 21.	1.1	13
52	Beware of risk for increased false positive rates in genome-wide association studies for phenotypic variability. <i>Frontiers in Genetics</i> , 2013, 4, 93.	1.1	28
53	The curse of the missing heritability. <i>Frontiers in Genetics</i> , 2013, 4, 225.	1.1	18
54	Issues with data transformation in genome-wide association studies for phenotypic variability. <i>F1000Research</i> , 2013, 2, 200.	0.8	12

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55	Inheritance Beyond Plain Heritability: Variance-controlling Genes in Arabidopsis thaliana. PLoS Genetics, 2012, 8, e1002839.	1.5	130
56	qtl.outbred: Interfacing outbred line cross data with the R/qtl mapping software. BMC Research Notes, 2011, 4, 154.	0.6	5
57	Hierarchical likelihood opens a new way of estimating genetic values using genome-wide dense marker maps. BMC Proceedings, 2011, 5, S14.	1.8	7
58	How to deal with genotype uncertainty in variance component quantitative trait loci analyses. Genetical Research, 2011, 93, 333-342.	0.3	2
59	hglm: A Package for Fitting Hierarchical Generalized Linear Models. R Journal, 2010, 2, 20.	0.7	133