Xia Shen

List of Publications by Year
in descending order

59 papers	3,823 citations	236912 25 h-index	155644 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. Journal of Nutrition, 2022, 152, 1118-1129.	2.9	5
2	SARS-CoV-2 causes a significant stress response mediated by small RNAs in the blood of COVID-19 patients. Molecular Therapy - Nucleic Acids, 2022, 27, 751-762.	5.1	12
3	Fusion Gene Detection Using Whole-Exome Sequencing Data in Cancer Patients. Frontiers in Genetics, 2022, 13, 820493.	2.3	3
4	Genetic and phenotypic links between obesity and extracellular vesicles. Human Molecular Genetics, 2022, 31, 3643-3651.	2.9	2
5	Integration of Distinct Analysis Strategies Improves Tissue-Trait Association Identification. Frontiers in Genetics, 2022, 13, 798269.	2.3	0
6	Whole-genome sequencing reveals host factors underlying critical COVID-19. Nature, 2022, 607, 97-103.	27.8	174
7	Genetic Landscape of the ACE2 Coronavirus Receptor. Circulation, 2022, 145, 1398-1411.	1.6	20
8	Nontrivial Replication of Loci Detected by Multi-Trait Methods. Frontiers in Genetics, 2021, 12, 627989.	2.3	4
9	Changes in Plasma Metabolome Profiles Following Oral Glucose Challenge among Adult Chinese. Nutrients, 2021, 13, 1474.	4.1	8
10	Total genetic contribution assessment across the human genome. Nature Communications, 2021, 12, 2845.	12.8	4
11	Targeted genetic screening in bacteria with a Cas12k-guided transposase. Cell Reports, 2021, 36, 109635.	6.4	24
12	Improved Estimation of Phenotypic Correlations Using Summary Association Statistics. Frontiers in Genetics, 2021, 12, 665252.	2.3	5
13	Serum Metabolomics Identifies Dysregulated Pathways and Potential Metabolic Biomarkers for Hyperuricemia and Gout. Arthritis and Rheumatology, 2021, 73, 1738-1748.	5.6	49
14	A Chinese host genetic study discovered IFNs and causality of laboratory traits on COVID-19 severity. IScience, 2021, 24, 103186.	4.1	10
15	Non-inferiority in cancer clinical trials was associated with more lenient margins and higher hypothesized outcome event rates. Journal of Clinical Epidemiology, 2021, 139, 214-221.	5.0	1
16	Genetic mechanisms of critical illness in COVID-19. Nature, 2021, 591, 92-98.	27.8	1,014
17	Genetic and phenotypic analysis of the causal relationship between aging and COVID-19. Communications Medicine, 2021, 1, .	4.2	19
18	Mapping the serum proteome to neurological diseases using whole genome sequencing. Nature Communications, 2021, 12, 7042.	12.8	29

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19	Physician-Confirmed and Administrative Definitions of Stroke in UK Biobank Reflect the Same Underlying Genetic Trait. Frontiers in Neurology, 2021, 12, 787107.	2.4	4
20	Genetic and Phenotypic Evidence for the Causal Relationship Between Aging and COVID-19. Innovation in Aging, 2021, 5, 330-330.	0.1	0
21	Identification of potential candidate genes and pathways in atrioventricular nodal reentry tachycardia by whole‐exome sequencing. Clinical and Translational Medicine, 2020, 10, 238-257.	4.0	10
22	High-definition likelihood inference of genetic correlations across human complex traits. Nature Genetics, 2020, 52, 859-864.	21.4	114
23	Lipids, Apolipoproteins, and the Risk of Parkinson Disease. Circulation Research, 2019, 125, 643-652.	4.5	50
24	Pleiotropy Complicates Human Gene Editing: CCR5Î"32 and Beyond. Frontiers in Genetics, 2019, 10, 669.	2.3	13
25	The genetic interplay between body mass index, breast size and breast cancer risk: a Mendelian randomization analysis. International Journal of Epidemiology, 2019, 48, 781-794.	1.9	37
26	Effects of Calcium, Magnesium, and Potassium Concentrations on Ventricular Repolarization in Unselected Individuals. Journal of the American College of Cardiology, 2019, 73, 3118-3131.	2.8	27
27	Profiling surface proteins on individual exosomes using a proximity barcoding assay. Nature Communications, 2019, 10, 3854.	12.8	148
28	Recent development on liquid chromatography-mass spectrometry analysis of oxidized lipids. Free Radical Biology and Medicine, 2019, 144, 16-34.	2.9	28
29	An update on lipid oxidation and inflammation in cardiovascular diseases. Free Radical Biology and Medicine, 2019, 144, 266-278.	2.9	215
30	Endogenous cholesterol ester hydroperoxides modulate cholesterol levels and inhibit cholesterol uptake in hepatocytes and macrophages. Redox Biology, 2019, 21, 101069.	9.0	38
31	Genomics of 1 million parent lifespans implicates novel pathways and common diseases and distinguishes survival chances. ELife, 2019, 8, .	6.0	170
32	MR-PheWAS: exploring the causal effect of SUA level on multiple disease outcomes by using genetic instruments in UK Biobank. Annals of the Rheumatic Diseases, 2018, 77, 1039-1047.	0.9	57
33	Glucose challenge metabolomics implicates medium-chain acylcarnitines in insulin resistance. Scientific Reports, 2018, 8, 8691.	3.3	47
34	Bivariate genomic analysis identifies a hidden locus associated with bacteria hypersensitive response in Arabidopsis thaliana. Scientific Reports, 2017, 7, 45281.	3.3	2
35	Genome-wide meta-analysis associates HLA-DQA1/DRB1 and LPA and lifestyle factors with human longevity. Nature Communications, 2017, 8, 910.	12.8	118
36	Multivariate discovery and replication of five novel loci associated with Immunoglobulin G N-glycosylation. Nature Communications, 2017, 8, 447.	12.8	102

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37	A Selection Operator for Summary Association Statistics Reveals Allelic Heterogeneity of Complex Traits. American Journal of Human Genetics, 2017, 101, 903-912.	6.2	9
38	Genetic Regulation of Transcriptional Variation in Natural <i>Arabidopsis thaliana</i> Accessions. G3: Genes, Genomes, Genetics, 2016, 6, 2319-2328.	1.8	25
39	Crowdsourced estimation of cognitive decline and resilience in Alzheimer's disease. Alzheimer's and Dementia, 2016, 12, 645-653.	0.8	72
40	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. Nature Genetics, 2016, 48, 1462-1472.	21.4	284
41	Effects of number of training generations on genomic prediction for various traits in a layer chicken population. Genetics Selection Evolution, 2016, 48, 22.	3.0	19
42	A Genome-Wide Association Analysis Reveals Epistatic Cancellation of Additive Genetic Variance for Root Length in Arabidopsis thaliana. PLoS Genetics, 2015, 11, e1005541.	3.5	38
43	RE: The Effect on Melanoma Risk of Genes Previously Associated With Telomere Length. Journal of the National Cancer Institute, 2015, 107, .	6.3	1
44	Identification of quantitative genetic components of fitness variation in farmed, hybrid and native salmon in the wild. Heredity, 2015, 115, 47-55.	2.6	45
45	Fitting Conditional and Simultaneous Autoregressive Spatial Models in hglm. R Journal, 2015, 7, 5.	1.8	27
46	Natural CMT2 Variation Is Associated With Genome-Wide Methylation Changes and Temperature Seasonality. PLoS Genetics, 2014, 10, e1004842.	3.5	147
47	Application of a genomic model for highâ€dimensional chemometric analysis. Journal of Chemometrics, 2014, 28, 548-557.	1.3	7
48	Genetic dissection of growth traits in a Chinese indigenous Ã— commercial broiler chicken cross. BMC Genomics, 2013, 14, 151.	2.8	67
49	A Novel Generalized Ridge Regression Method for Quantitative Genetics. Genetics, 2013, 193, 1255-1268.	2.9	68
50	MAPfastR: Quantitative Trait Loci Mapping in Outbred Line Crosses. G3: Genes, Genomes, Genetics, 2013, 3, 2147-2149.	1.8	7
51	PASE: a novel method for functional prediction of amino acid substitutions based on physicochemical properties. Frontiers in Genetics, 2013, 4, 21.	2.3	13
52	Beware of risk for increased false positive rates in genome-wide association studies for phenotypic variability. Frontiers in Genetics, 2013, 4, 93.	2.3	28
53	The curse of the missing heritability. Frontiers in Genetics, 2013, 4, 225.	2.3	18
54	Issues with data transformation in genome-wide association studies for phenotypic variability. F1000Research, 2013, 2, 200.	1.6	12

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55	Inheritance Beyond Plain Heritability: Variance-Controlling Genes in Arabidopsis thaliana. PLoS Genetics, 2012, 8, e1002839.	3.5	130
56	qtl.outbred: Interfacing outbred line cross data with the R/qtl mapping software. BMC Research Notes, 2011, 4, 154.	1.4	5
57	Hierarchical likelihood opens a new way of estimating genetic values using genome-wide dense marker maps. BMC Proceedings, 2011, 5, S14.	1.6	7
58	How to deal with genotype uncertainty in variance component quantitative trait loci analyses. Genetical Research, 2011, 93, 333-342.	0.9	2
59	hglm: A Package for Fitting Hierarchical Generalized Linear Models. R Journal, 2010, 2, 20.	1.8	133