Xia Shen

List of Publications by Year
in descending order

59 papers	3,823 citations	236925 25 h-index	155660 55 g-index
77 all docs	77 docs citations	77 times ranked	9014 citing authors

#	Article	IF	Citations
1	Genetic mechanisms of critical illness in COVID-19. Nature, 2021, 591, 92-98.	27.8	1,014
2	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. Nature Genetics, 2016, 48, 1462-1472.	21.4	284
3	An update on lipid oxidation and inflammation in cardiovascular diseases. Free Radical Biology and Medicine, 2019, 144, 266-278.	2.9	215
4	Whole-genome sequencing reveals host factors underlying critical COVID-19. Nature, 2022, 607, 97-103.	27.8	174
5	Genomics of 1 million parent lifespans implicates novel pathways and common diseases and distinguishes survival chances. ELife, 2019, 8, .	6.0	170
6	Profiling surface proteins on individual exosomes using a proximity barcoding assay. Nature Communications, 2019, 10, 3854.	12.8	148
7	Natural CMT2 Variation Is Associated With Genome-Wide Methylation Changes and Temperature Seasonality. PLoS Genetics, 2014, 10, e1004842.	3.5	147
8	hglm: A Package for Fitting Hierarchical Generalized Linear Models. R Journal, 2010, 2, 20.	1.8	133
9	Inheritance Beyond Plain Heritability: Variance-Controlling Genes in Arabidopsis thaliana. PLoS Genetics, 2012, 8, e1002839.	3.5	130
10	Genome-wide meta-analysis associates HLA-DQA1/DRB1 and LPA and lifestyle factors with human longevity. Nature Communications, 2017, 8, 910.	12.8	118
11	High-definition likelihood inference of genetic correlations across human complex traits. Nature Genetics, 2020, 52, 859-864.	21.4	114
12	Multivariate discovery and replication of five novel loci associated with Immunoglobulin G N-glycosylation. Nature Communications, 2017, 8, 447.	12.8	102
13	Crowdsourced estimation of cognitive decline and resilience in Alzheimer's disease. Alzheimer's and Dementia, 2016, 12, 645-653.	0.8	72
14	A Novel Generalized Ridge Regression Method for Quantitative Genetics. Genetics, 2013, 193, 1255-1268.	2.9	68
15	Genetic dissection of growth traits in a Chinese indigenous Ã— commercial broiler chicken cross. BMC Genomics, 2013, 14, 151.	2.8	67
16	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
17	Lipids, Apolipoproteins, and the Risk of Parkinson Disease. Circulation Research, 2019, 125, 643-652.	4.5	50
18	Serum Metabolomics Identifies Dysregulated Pathways and Potential Metabolic Biomarkers for Hyperuricemia and Gout. Arthritis and Rheumatology, 2021, 73, 1738-1748.	5.6	49

#	Article	IF	Citations
19	Glucose challenge metabolomics implicates medium-chain acylcarnitines in insulin resistance. Scientific Reports, 2018, 8, 8691.	3.3	47
20	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
21	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
22	Endogenous cholesterol ester hydroperoxides modulate cholesterol levels and inhibit cholesterol uptake in hepatocytes and macrophages. Redox Biology, 2019, 21, 101069.	9.0	38
23	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
24	Mapping the serum proteome to neurological diseases using whole genome sequencing. Nature Communications, 2021, 12, 7042.	12.8	29
25	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
26	Recent development on liquid chromatography-mass spectrometry analysis of oxidized lipids. Free Radical Biology and Medicine, 2019, 144, 16-34.	2.9	28
27	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
28	Fitting Conditional and Simultaneous Autoregressive Spatial Models in hglm. R Journal, 2015, 7, 5.	1.8	27
29	Genetic Regulation of Transcriptional Variation in Natural *Arabidopsis thaliana* Accessions. G3: Genes, Genomes, Genetics, 2016, 6, 2319-2328.	1.8	25
30	Targeted genetic screening in bacteria with a Cas12k-guided transposase. Cell Reports, 2021, 36, 109635.	6.4	24
31	Genetic Landscape of the ACE2 Coronavirus Receptor. Circulation, 2022, 145, 1398-1411.	1.6	20
32	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
33	Genetic and phenotypic analysis of the causal relationship between aging and COVID-19. Communications Medicine, 2021, 1, .	4.2	19
34	The curse of the missing heritability. Frontiers in Genetics, 2013, 4, 225.	2.3	18
35	PASE: a novel method for functional prediction of amino acid substitutions based on physicochemical properties. Frontiers in Genetics, 2013, 4, 21.	2.3	13
36	Pleiotropy Complicates Human Gene Editing: CCR5Î"32 and Beyond. Frontiers in Genetics, 2019, 10, 669.	2.3	13

#	Article	IF	Citations
37	Issues with data transformation in genome-wide association studies for phenotypic variability. F1000Research, 2013, 2, 200.	1.6	12
38	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
39	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
40	A Chinese host genetic study discovered IFNs and causality of laboratory traits on COVID-19 severity. IScience, 2021, 24, 103186.	4.1	10
41	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
42	Changes in Plasma Metabolome Profiles Following Oral Glucose Challenge among Adult Chinese. Nutrients, 2021, 13, 1474.	4.1	8
43	Hierarchical likelihood opens a new way of estimating genetic values using genome-wide dense marker maps. BMC Proceedings, 2011, 5, S14.	1.6	7
44	MAPfastR: Quantitative Trait Loci Mapping in Outbred Line Crosses. G3: Genes, Genomes, Genetics, 2013, 3, 2147-2149.	1.8	7
45	Application of a genomic model for high‐dimensional chemometric analysis. Journal of Chemometrics, 2014, 28, 548-557.	1.3	7
46	qtl.outbred: Interfacing outbred line cross data with the R/qtl mapping software. BMC Research Notes, 2011, 4, 154.	1.4	5
47	Improved Estimation of Phenotypic Correlations Using Summary Association Statistics. Frontiers in Genetics, 2021, 12, 665252.	2.3	5
48	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
49	Nontrivial Replication of Loci Detected by Multi-Trait Methods. Frontiers in Genetics, 2021, 12, 627989.	2.3	4
50	Total genetic contribution assessment across the human genome. Nature Communications, 2021, 12, 2845.	12.8	4
51	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
52	Fusion Gene Detection Using Whole-Exome Sequencing Data in Cancer Patients. Frontiers in Genetics, 2022, 13, 820493.	2.3	3
53	How to deal with genotype uncertainty in variance component quantitative trait loci analyses. Genetical Research, 2011, 93, 333-342.	0.9	2
54	Bivariate genomic analysis identifies a hidden locus associated with bacteria hypersensitive response in Arabidopsis thaliana. Scientific Reports, 2017, 7, 45281.	3.3	2

#	Article	IF	Citations
55	Genetic and phenotypic links between obesity and extracellular vesicles. Human Molecular Genetics, 2022, 31, 3643-3651.	2.9	2
56	RE: The Effect on Melanoma Risk of Genes Previously Associated With Telomere Length. Journal of the National Cancer Institute, 2015, 107, .	6.3	1
57	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
58	Integration of Distinct Analysis Strategies Improves Tissue-Trait Association Identification. Frontiers in Genetics, 2022, 13, 798269.	2.3	0
59	Genetic and Phenotypic Evidence for the Causal Relationship Between Aging and COVID-19. Innovation in Aging, 2021, 5, 330-330.	0.1	0