Jianxin Shi

List of Publications by Year
in descending order

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		50276	32842
101	19,668	46	100
papers	citations	h-index	g-index

105	105	105	30791
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Sex-Dependent Shared and Nonshared Genetic Architecture Across Mood and Psychotic Disorders. Biological Psychiatry, 2022, 91, 102-117.	1.3	61
2	Clinical Implications of Inter- and Intratumor Heterogeneity of Immune Cell Markers in Lung Cancer. Journal of the National Cancer Institute, 2022, 114, 280-289.	6.3	8
3	Dissecting the Shared Genetic Architecture of Suicide Attempt, Psychiatric Disorders, and Known Risk Factors. Biological Psychiatry, 2022, 91, 313-327.	1.3	114
4	Mid-term follow-up surgical results in 284 cases of clival chordomas: the risk factors for outcome and tumor recurrence. Neurosurgical Review, 2022, 45, 1451-1462.	2.4	13
5	Multi-Trait Genetic Analysis Identifies Autoimmune Loci Associated with Cutaneous Melanoma. Journal of Investigative Dermatology, 2022, 142, 1607-1616.	0.7	11
6	SUITOR: Selecting the number of mutational signatures through cross-validation. PLoS Computational Biology, 2022, 18, e1009309.	3.2	1
7	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	27.8	929
8	fast.adonis: a computationally efficient non-parametric multivariate analysis of microbiome data for large-scale studies. Bioinformatics Advances, 2022, 2, .	2.4	2
9	Rare germline deleterious variants increase susceptibility for lung cancer. Human Molecular Genetics, 2022, 31, 3558-3565.	2.9	5
10	A Penalized Regression Framework for Building Polygenic Risk Models Based on Summary Statistics From Genome-Wide Association Studies and Incorporating External Information. Journal of the American Statistical Association, 2021, 116, 133-143.	3.1	13
11	Whole genome sequencing of skull-base chordoma reveals genomic alterations associated with recurrence and chordoma-specific survival. Nature Communications, 2021, 12, 757.	12.8	55
12	Sub-multiplicative interaction between polygenic risk score and household coal use in relation to lung adenocarcinoma among never-smoking women in Asia. Environment International, 2021, 147, 105975.	10.0	12
13	Associations of fecal microbial profiles with breast cancer and nonmalignant breast disease in the Ghana Breast Health Study. International Journal of Cancer, 2021, 148, 2712-2723.	5.1	33
14	Modeling Longitudinal Microbiome Compositional Data: A Two-Part Linear Mixed Model with Shared Random Effects. Statistics in Biosciences, 2021, 13, 243-266.	1.2	2
15	The association between genetically determined ABO blood types and major depressive disorder. Psychiatry Research, 2021, 299, 113837.	3.3	4
16	A 584Âbp deletion in CTRB2 inhibits chymotrypsin B2 activity and secretion and confers risk of pancreatic cancer. American Journal of Human Genetics, 2021, 108, 1852-1865.	6.2	15
17	Transcriptome-based polygenic score links depression-related corticolimbic gene expression changes to sex-specific brain morphology and depression risk. Neuropsychopharmacology, 2021, 46, 2304-2311.	5.4	5
18	Genomic and evolutionary classification of lung cancer in never smokers. Nature Genetics, 2021, 53, 1348-1359.	21.4	81

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19	Cell-type-specific meQTLs extend melanoma GWAS annotation beyond eQTLs and inform melanocyte gene-regulatory mechanisms. American Journal of Human Genetics, 2021, 108, 1631-1646.	6.2	12
20	MYC DNA Methylation in Prostate Tumor Tissue is Associated with Gleason Score. Genes, 2021, 12, 12.	2.4	6
21	Inferred expression regulator activities suggest genes mediating cardiometabolic genetic signals. PLoS Computational Biology, 2021, 17, e1009563.	3.2	3
22	Comparison of fecal and oral collection methods for studies of the human microbiota in two Iranian cohorts. BMC Microbiology, 2021, 21, 324.	3.3	4
23	Comparison of somatic mutation landscapes in Chinese versus European breast cancer patients. Human Genetics and Genomics Advances, 2021, 3, 100076.	1.7	3
24	Potential Genetic Overlap Between Insomnia and Sleep Symptoms in Major Depressive Disorder: A Polygenic Risk Score Analysis. Frontiers in Psychiatry, 2021, 12, 734077.	2.6	2
25	Tuberculosis infection and lung adenocarcinoma: Mendelian randomization and pathway analysis of genome-wide association study data from never-smoking Asian women. Genomics, 2020, 112, 1223-1232.	2.9	15
26	Classical Human Leukocyte Antigen Alleles and C4 Haplotypes Are Not Significantly Associated With Depression. Biological Psychiatry, 2020, 87, 419-430.	1.3	27
27	A Transcriptome-Wide Association Study Identifies Novel Candidate Susceptibility Genes for Pancreatic Cancer. Journal of the National Cancer Institute, 2020, 112, 1003-1012.	6.3	59
28	Oral microbial community composition is associated with pancreatic cancer: A caseâ€control study in Iran. Cancer Medicine, 2020, 9, 797-806.	2.8	42
29	Allele-specific open chromatin in human iPSC neurons elucidates functional disease variants. Science, 2020, 369, 561-565.	12.6	77
30	Genetic and epigenetic intratumor heterogeneity impacts prognosis of lung adenocarcinoma. Nature Communications, 2020, 11, 2459.	12.8	77
31	The genomic and epigenomic evolutionary history of papillary renal cell carcinomas. Nature Communications, 2020, 11, 3096.	12.8	19
32	Minimal phenotyping yields genome-wide association signals of low specificity for major depression. Nature Genetics, 2020, 52, 437-447.	21.4	207
33	Comparison of Oral Microbiota Collected Using Multiple Methods and Recommendations for New Epidemiologic Studies. MSystems, 2020, 5, .	3.8	17
34	Genome-Wide Association Study Data Reveal Genetic Susceptibility to Chronic Inflammatory Intestinal Diseases and Pancreatic Ductal Adenocarcinoma Risk. Cancer Research, 2020, 80, 4004-4013.	0.9	5
35	Genome-wide association meta-analyses combining multiple risk phenotypes provide insights into the genetic architecture of cutaneous melanoma susceptibility. Nature Genetics, 2020, 52, 494-504.	21.4	138
36	Comparison of Methods To Collect Fecal Samples for Microbiome Studies Using Whole-Genome Shotgun Metagenomic Sequencing. MSphere, 2020, 5, .	2.9	23

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37	Contribution of Common Genetic Variants to Familial Aggregation of Disease and Implications for Sequencing Studies. PLoS Genetics, 2019, 15, e1008490.	3.5	8
38	Mammographic breast density and its association with urinary estrogens and the fecal microbiota in postmenopausal women. PLoS ONE, 2019, 14, e0216114.	2.5	12
39	SummaryAUC: a tool for evaluating the performance of polygenic risk prediction models in validation datasets with only summary level statistics. Bioinformatics, 2019, 35, 4038-4044.	4.1	15
40	THREE AUTHORS REPLY. American Journal of Epidemiology, 2019, 188, 809-810.	3.4	0
41	Genome-wide Burden of Rare Short Deletions Is Enriched in Major Depressive Disorder in Four Cohorts. Biological Psychiatry, 2019, 85, 1065-1073.	1.3	25
42	The respiratory tract microbiome and its relationship to lung cancer and environmental exposures found in rural china. Environmental and Molecular Mutagenesis, 2019, 60, 617-623.	2.2	22
43	Reproducibility, stability, and accuracy of microbial profiles by fecal sample collection method in three distinct populations. PLoS ONE, 2019, 14, e0224757.	2.5	19
44	Immune gene expression profiling reveals heterogeneity in luminal breast tumors. Breast Cancer Research, 2019, 21, 147.	5.0	43
45	Temporal Variability of Oral Microbiota over 10 Months and the Implications for Future Epidemiologic Studies. Cancer Epidemiology Biomarkers and Prevention, 2018, 27, 594-600.	2.5	24
46	Quantification of Human Microbiome Stability Over 6 Months: Implications for Epidemiologic Studies. American Journal of Epidemiology, 2018, 187, 1282-1290.	3.4	20
47	Open chromatin dynamics reveals stage-specific transcriptional networks in hiPSC-based neurodevelopmental model. Stem Cell Research, 2018, 29, 88-98.	0.7	18
48	Postmenopausal breast cancer and oestrogen associations with the IgA-coated and IgA-noncoated faecal microbiota. British Journal of Cancer, 2018, 118, 471-479.	6.4	82
49	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. Nature Genetics, 2018, 50, 668-681.	21.4	2,224
50	Characterising cis-regulatory variation in the transcriptome of histologically normal and tumour-derived pancreatic tissues. Gut, 2018, 67, 521-533.	12.1	26
51	Post-Selection Inference Following Aggregate Level Hypothesis Testing in Large-Scale Genomic Data. Journal of the American Statistical Association, 2018, 113, 1770-1783.	3.1	14
52	Cell-typeâ€“specific eQTL of primary melanocytes facilitates identification of melanoma susceptibility genes. Genome Research, 2018, 28, 1621-1635.	5.5	67
53	Combining common genetic variants and non-genetic risk factors to predict risk of cutaneous melanoma. Human Molecular Genetics, 2018, 27, 4145-4156.	2.9	34
54	Genome-wide Association for Major Depression Through Age at Onset Stratification: Major Depressive Disorder Working Group of the Psychiatric Genomics Consortium. Biological Psychiatry, 2017, 81, 325-335.	1.3	175

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55	Comparison of Fecal Collection Methods for Microbiota Studies in Bangladesh. Applied and Environmental Microbiology, 2017, 83, .	3.1	50
56	Allele-specific expression reveals interactions between genetic variation and environment. Nature Methods, 2017, 14, 699-702.	19.0	135
57	An Analysis of Two Genome-wide Association Meta-analyses Identifies a New Locus for Broad Depression Phenotype. Biological Psychiatry, 2017, 82, 322-329.	1.3	84
58	Inherited variation in circadian rhythm genes and risks of prostate cancer and three other cancer sites in combined cancer consortia. International Journal of Cancer, 2017, 141, 1794-1802.	5.1	28
59	Open Chromatin Profiling in hiPSC-Derived Neurons Prioritizes Functional Noncoding Psychiatric Risk Variants and Highlights Neurodevelopmental Loci. Cell Stem Cell, 2017, 21, 305-318.e8.	11.1	106
60	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. Nature Genetics, 2017, 49, 27-35.	21.4	838
61	Parental Origin of Interstitial Duplications at 15q11.2-q13.3 in Schizophrenia and Neurodevelopmental Disorders. PLoS Genetics, 2016, 12, e1005993.	3.5	51
62	Colorectal Cancer and the Human Gut Microbiome: Reproducibility with Whole-Genome Shotgun Sequencing. PLoS ONE, 2016, 11, e0155362.	2.5	249
63	Impact of the X Chromosome and sex on regulatory variation. Genome Research, 2016, 26, 768-777.	5.5	88
64	Association between GWAS-identified lung adenocarcinoma susceptibility loci andEGFRmutations in never-smoking Asian women, and comparison with findings from Western populations. Human Molecular Genetics, 2016, 26, ddw414.	2.9	50
65	Developing and evaluating polygenic risk prediction models for stratified disease prevention. Nature Reviews Genetics, 2016, 17, 392-406.	16.3	559
66	Fecal Microbiome in Epidemiologic Studiesâ€"Response. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 870-871.	2.5	4
67	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	27.8	1,204
68	Rare Germline Copy Number Variations and Disease Susceptibility in Familial Melanoma. Journal of Investigative Dermatology, 2016, 136, 2436-2443.	0.7	13
69	An investigation of the association of genetic susceptibility risk with somatic mutation burden in breast cancer. British Journal of Cancer, 2016, 115, 752-760.	6.4	16
70	Genetic variants linked to education predict longevity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13366-13371.	7.1	110
71	Allergy associations with the adult fecal microbiota: Analysis of the American Gut Project. EBioMedicine, 2016, 3, 172-179.	6.1	154
72	MEGSA: A Powerful and Flexible Framework for Analyzing Mutual Exclusivity of Tumor Mutations. American Journal of Human Genetics, 2016, 98, 442-455.	6.2	40

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73	Collecting Fecal Samples for Microbiome Analyses in Epidemiology Studies. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 407-416.	2.5	154
74	A Powerful Procedure for Pathway-Based Meta-analysis Using Summary Statistics Identifies 43 Pathways Associated with Type II Diabetes in European Populations. PLoS Genetics, 2016, 12, e1006122.	3.5	34
75	Winner's Curse Correction and Variable Thresholding Improve Performance of Polygenic Risk Modeling Based on Genome-Wide Association Study Summary-Level Data. PLoS Genetics, 2016, 12, e1006493.	3.5	98
76	Somatic Genomics and Clinical Features of Lung Adenocarcinoma: A Retrospective Study. PLoS Medicine, 2016, 13, e1002162.	8.4	148
77	Fecal Microbiota, Fecal Metabolome, and Colorectal Cancer Interrelations. PLoS ONE, 2016, 11, e0152126.	2.5	157
78	Fecal Microbiota Characteristics of Patients with Colorectal Adenoma Detected by Screening: A Population-based Study. EBioMedicine, 2015, 2, 597-603.	6.1	59
79	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
80	Joint Analysis of Psychiatric Disorders Increases Accuracy of Risk Prediction for Schizophrenia, Bipolar Disorder, and Major Depressive Disorder. American Journal of Human Genetics, 2015, 96, 283-294.	6.2	225
81	Investigation of the Association Between the Fecal Microbiota and Breast Cancer in Postmenopausal Women: a Population-Based Case-Control Pilot Study. Journal of the National Cancer Institute, 2015, 107, .	6.3	257
82	An Apela RNA-Containing Negative Feedback Loop Regulates p53-Mediated Apoptosis in Embryonic Stem Cells. Cell Stem Cell, 2015, 16, 669-683.	11.1	78
83	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	6.2	1,098
84	Deciphering associations for lung cancer risk through imputation and analysis of 12â€‰316 cases and 16â€‰831 controls. European Journal of Human Genetics, 2015, 23, 1723-1728.	2.8	22
85	VTET: a variable threshold exact test for identifying disease-associated copy number variations enriched in short genomic regions. Frontiers in Genetics, 2014, 5, 53.	2.3	2
86	Fecal metabolomics: assay performance and association with colorectal cancer. Carcinogenesis, 2014, 35, 2089-2096.	2.8	117
87	A Rare Functional Noncoding Variant at the GWAS-Implicated MIR137/MIR2682 Locus Might Confer Risk to Schizophrenia and Bipolar Disorder. American Journal of Human Genetics, 2014, 95, 744-753.	6.2	91
88	Diversity and Composition of the Adult Fecal Microbiome Associated with History of Cesarean Birth or Appendectomy: Analysis of the American Gut Project. EBioMedicine, 2014, 1, 167-172.	6.1	74
89	A fast multilocus test with adaptive SNP selection for large-scale genetic-association studies. European Journal of Human Genetics, 2014, 22, 696-702.	2.8	19
90	Rare missense variants in POT1 predispose to familial cutaneous malignant melanoma. Nature Genetics, 2014, 46, 482-486.	21.4	283

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91	Characterizing the genetic basis of transcriptome diversity through RNA-sequencing of 922 individuals. Genome Research, 2014, 24, 14-24.	5.5	547
92	Genetic polymorphisms in the 9p21 region associated with risk of multiple cancers. Carcinogenesis, 2014, 35, 2698-2705.	2.8	67
93	Characterizing the genetic basis of methylome diversity in histologically normal human lung tissue. Nature Communications, 2014, 5, 3365.	12.8	123
94	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	21.4	1,818
95	Leveraging local identity-by-descent increases the power of case/control GWAS with related individuals. Annals of Applied Statistics, 2014, 8, 974-998.	1.1	0
96	Inherited Variation at Chromosome 12p13.33, Including RAD52, Influences the Risk of Squamous Cell Lung Carcinoma. Cancer Discovery, 2012, 2, 131-139.	9.4	54
97	An Integrative Segmentation Method for Detecting Germline Copy Number Variations in SNP Arrays. Genetic Epidemiology, 2012, 36, 373-383.	1.3	4
98	Copy Number Variants in Schizophrenia: Confirmation of Five Previous Findings and New Evidence for 3q29 Microdeletions and VIPR2 Duplications. American Journal of Psychiatry, 2011, 168, 302-316.	7.2	398
99	Genomeâ€wide association studies of pigmentation and skin cancer: a review and metaâ€analysis. Pigment Cell and Melanoma Research, 2010, 23, 587-606.	3.3	108
100	Common variants on chromosome 6p22.1 are associated with schizophrenia. Nature, 2009, 460, 753-757.	27.8	1,063
101	Statistical corrections of linkage data suggest predominantly cis regulations of gene expression. BMC Proceedings, 2007, 1, S145.	1.6	3