

Jie Zheng

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

95
papers

5,595
citations

29
h-index

74
g-index

110
ext. papers

8,952
ext. citations

8.7
avg, IF

5.26
L-index

#	Paper	IF	Citations
95	Rho GTPase gene expression and breast cancer risk: a Mendelian randomization analysis.. <i>Scientific Reports</i> , 2022 , 12, 1463	4.9	0
94	Using genetic variation to disentangle the complex relationship between food intake and health outcomes. <i>PLoS Genetics</i> , 2022 , 18, e1010162	6	0
93	A Combined Proteomics and Mendelian Randomization Approach to Investigate the Effects of Aspirin-Targeted Proteins on Colorectal Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021 , 30, 564-575	4	2
92	VEuPathDB: the eukaryotic pathogen, vector and host bioinformatics resource center. <i>Nucleic Acids Research</i> , 2021 ,	20.1	22
91	OBO Foundry in 2021: operationalizing open data principles to evaluate ontologies. <i>Database: the Journal of Biological Databases and Curation</i> , 2021 , 2021,	5	7
90	VaximmutorDB: A Web-Based Vaccine Immune Factor Database and Its Application for Understanding Vaccine-Induced Immune Mechanisms. <i>Frontiers in Immunology</i> , 2021 , 12, 639491	8.4	0
89	The causal effects of serum lipids and apolipoproteins on kidney function: multivariable and bidirectional Mendelian-randomization analyses. <i>International Journal of Epidemiology</i> , 2021 , 50, 1569-1579	7.8	4
88	EpiGraphDB: a database and data mining platform for health data science. <i>Bioinformatics</i> , 2021 , 37, 1304-1311	7.1	5
87	Computational Tools for Causal Inference in Genetics. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2021 , 11,	5.4	2
86	Identifying drug targets for neurological and psychiatric disease via genetics and the brain transcriptome. <i>PLoS Genetics</i> , 2021 , 17, e1009224	6	10
85	Transcriptome-wide Mendelian randomization study prioritising novel tissue-dependent genes for glioma susceptibility. <i>Scientific Reports</i> , 2021 , 11, 2329	4.9	0
84	Mendelian randomization for studying the effects of perturbing drug targets. <i>Wellcome Open Research</i> , 2021 , 6, 16	4.8	15
83	Microbiome Metadata Standards: Report of the National Microbiome Data Collaborative Workshop and Follow-On Activities. <i>MSystems</i> , 2021 , 6,	7.6	7
82	Genetic predictors of participation in optional components of UK Biobank. <i>Nature Communications</i> , 2021 , 12, 886	17.4	20
81	Intake of processed meat, but not sodium, is associated with risk of colorectal cancer: Evidence from a large prospective cohort and two-sample Mendelian randomization. <i>Clinical Nutrition</i> , 2021 , 40, 4551-4559	5.9	0
80	CIDO ontology updates and secondary analysis of host responses to COVID-19 infection based on ImmPort reports and literature. <i>Journal of Biomedical Semantics</i> , 2021 , 12, 18	2.2	2
79	A proteome-wide genetic investigation identifies several SARS-CoV-2-exploited host targets of clinical relevance. <i>ELife</i> , 2021 , 10,	8.9	2

78	GWAS META-analysis followed by MENDELIAN randomisation revealed potential control mechanisms for circulating β klotho levels. <i>Human Molecular Genetics</i> , 2021 ,	5.6	1
77	Deciphering osteoarthritis genetics across 826,690 individuals from 9 populations. <i>Cell</i> , 2021 , 184, 4784-4818.e17	5.6	17
76	Trans-ethnic Mendelian-randomization study reveals causal relationships between cardiometabolic factors and chronic kidney disease. <i>International Journal of Epidemiology</i> , 2021 ,	7.8	1
75	piNET: a versatile web platform for downstream analysis and visualization of proteomics data. <i>Nucleic Acids Research</i> , 2020 , 48, W85-W93	20.1	9
74	The Effect of Plasma Lipids and Lipid-Lowering Interventions on Bone Mineral Density: A Mendelian Randomization Study. <i>Journal of Bone and Mineral Research</i> , 2020 , 35, 1224-1235	6.3	19
73	Mendelian Randomization Analysis Reveals a Causal Effect of Urinary Sodium/Urinary Creatinine Ratio on Kidney Function in Europeans. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020 , 8, 662	5.8	0
72	Exploiting horizontal pleiotropy to search for causal pathways within a Mendelian randomization framework. <i>Nature Communications</i> , 2020 , 11, 1010	17.4	23
71	Education, intelligence and Alzheimer's disease: evidence from a multivariable two-sample Mendelian randomization study. <i>International Journal of Epidemiology</i> , 2020 , 49, 1163-1172	7.8	32
70	Introducing M-GCTA a Software Package to Estimate Maternal (or Paternal) Genetic Effects on Offspring Phenotypes. <i>Behavior Genetics</i> , 2020 , 50, 51-66	3.2	5
69	Mendelian randomisation for nutritional psychiatry. <i>Lancet Psychiatry</i> , 2020 , 7, 208-216	23.3	3
68	Circulating Lipoprotein Lipids, Apolipoproteins and Ischemic Stroke. <i>Annals of Neurology</i> , 2020 , 88, 1229-1236	14.36	14
67	Phenome-wide Mendelian randomization mapping the influence of the plasma proteome on complex diseases. <i>Nature Genetics</i> , 2020 , 52, 1122-1131	36.3	75
66	Long-term use of antibiotics and risk of type 2 diabetes in women: a prospective cohort study. <i>International Journal of Epidemiology</i> , 2020 , 49, 1572-1581	7.8	8
65	Validation of Susceptibility Loci for Vitiligo Identified by GWAS in the Chinese Han Population. <i>Frontiers in Genetics</i> , 2020 , 11, 542275	4.5	3
64	Identification of new therapeutic targets for osteoarthritis through genome-wide analyses of UK Biobank data. <i>Nature Genetics</i> , 2019 , 51, 230-236	36.3	143
63	Mendelian Randomization Analysis Reveals a Causal Influence of Circulating Sclerostin Levels on Bone Mineral Density and Fractures. <i>Journal of Bone and Mineral Research</i> , 2019 , 34, 1824-1836	6.3	11
62	OSCI: standardized stem cell ontology representation and use cases for stem cell investigation. <i>BMC Bioinformatics</i> , 2019 , 20, 180	3.6	4
61	Association of Maternal Neurodevelopmental Risk Alleles With Early-Life Exposures. <i>JAMA Psychiatry</i> , 2019 , 76, 834-842	14.5	49

60	Genome Analysis Identification of Genes Involved in Host-Pathogen Protein-Protein Interaction Networks 2019 , 410-424		
59	Appraising the role of previously reported risk factors in epithelial ovarian cancer risk: A Mendelian randomization analysis. <i>PLoS Medicine</i> , 2019 , 16, e1002893	11.6	32
58	A Phenome-Wide Mendelian Randomization Study of Pancreatic Cancer Using Summary Genetic Data. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019 , 28, 2070-2078	4	17
57	Use of Mendelian Randomization to Examine Causal Inference in Osteoporosis. <i>Frontiers in Endocrinology</i> , 2019 , 10, 807	5.7	10
56	ClinEpiDB: an open-access clinical epidemiology database resource encouraging online exploration of complex studies. <i>Gates Open Research</i> , 2019 , 3, 1661	2.4	12
55	ClinEpiDB: an open-access clinical epidemiology database resource encouraging online exploration of complex studies. <i>Gates Open Research</i> , 2019 , 3, 1661	2.4	7
54	Using the MR-Base platform to investigate risk factors and drug targets for thousands of phenotypes. <i>Wellcome Open Research</i> , 2019 , 4, 113	4.8	18
53	Expression of Heat Shock Protein 70 Is Insufficient To Extend Longevity. <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 4197-4207	3.2	2
52	VIO: ontology classification and study of vaccine responses given various experimental and analytical conditions. <i>BMC Bioinformatics</i> , 2019 , 20, 704	3.6	7
51	OHMI: the ontology of host-microbiome interactions. <i>Journal of Biomedical Semantics</i> , 2019 , 10, 25	2.2	4
50	Variation in Serum PCSK9 (Proprotein Convertase Subtilisin/Kexin Type 9), Cardiovascular Disease Risk, and an Investigation of Potential Unanticipated Effects of PCSK9 Inhibition. <i>Circulation Genomic and Precision Medicine</i> , 2019 , 12, e002335	5.2	3
49	MicrobiomeDB: a systems biology platform for integrating, mining and analyzing microbiome experiments. <i>Nucleic Acids Research</i> , 2018 , 46, D684-D691	20.1	26
48	The eXtensible ontology development (XOD) principles and tool implementation to support ontology interoperability. <i>Journal of Biomedical Semantics</i> , 2018 , 9, 3	2.2	32
47	Systematic Mendelian randomization framework elucidates hundreds of CpG sites which may mediate the influence of genetic variants on disease. <i>Human Molecular Genetics</i> , 2018 , 27, 3293-3304	5.6	40
46	Author response: The MR-Base platform supports systematic causal inference across the human phenome 2018 ,		17
45	Use of Mendelian randomization for identifying risk actors for rain umors. <i>Frontiers in Genetics</i> , 2018 , 9, 525	4.5	12
44	PhenoSpD: an integrated toolkit for phenotypic correlation estimation and multiple testing correction using GWAS summary statistics. <i>GigaScience</i> , 2018 , 7,	7.6	27
43	The MR-Base platform supports systematic causal inference across the human phenome. <i>ELife</i> , 2018 , 7,	8.9	1190

42	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases: A Mendelian Randomization Study. <i>JAMA Oncology</i> , 2017 , 3, 636-651	13.4	236
41	Epigenome-wide Association of DNA Methylation in Whole Blood With Bone Mineral Density. <i>Journal of Bone and Mineral Research</i> , 2017 , 32, 1644-1650	6.3	33
40	Shared genetic origin of asthma, hay fever and eczema elucidates allergic disease biology. <i>Nature Genetics</i> , 2017 , 49, 1752-1757	36.3	256
39	Mendelian Randomization Analysis Identifies CpG Sites as Putative Mediators for Genetic Influences on Cardiovascular Disease Risk. <i>American Journal of Human Genetics</i> , 2017 , 101, 590-602	11	44
38	Recent Developments in Mendelian Randomization Studies. <i>Current Epidemiology Reports</i> , 2017 , 4, 330-345	34.5	218
37	HAPRAP: a haplotype-based iterative method for statistical fine mapping using GWAS summary statistics. <i>Bioinformatics</i> , 2017 , 33, 79-86	7.2	4
36	LD Hub: a centralized database and web interface to perform LD score regression that maximizes the potential of summary level GWAS data for SNP heritability and genetic correlation analysis. <i>Bioinformatics</i> , 2017 , 33, 272-279	7.2	541
35	Ontobee: A linked ontology data server to support ontology term dereferencing, linkage, query and integration. <i>Nucleic Acids Research</i> , 2017 , 45, D347-D352	20.1	69
34	The Ontology of Biological and Clinical Statistics (OBCS)-based statistical method standardization and meta-analysis of host responses to yellow fever vaccines. <i>Quantitative Biology</i> , 2017 , 5, 291-301	3.9	2
33	EuPathDB: the eukaryotic pathogen genomics database resource. <i>Nucleic Acids Research</i> , 2017 , 45, D5812-D5911	14.591	141
32	The Ontology of Biological and Clinical Statistics (OBCS)-based statistical method standardization and meta-analysis of host responses to yellow fever vaccines. <i>Quantitative Biology</i> , 2017 , 5, 291-301	3.9	2
31	Regulating the UAS/GAL4 system in adult with Tet-off GAL80 transgenes. <i>PeerJ</i> , 2017 , 5, e4167	3.1	10
30	Identification of 153 new loci associated with heel bone mineral density and functional involvement of GPC6 in osteoporosis. <i>Nature Genetics</i> , 2017 , 49, 1468-1475	36.3	235
29	The Ontology of Biological and Clinical Statistics (OBCS) for standardized and reproducible statistical analysis. <i>Journal of Biomedical Semantics</i> , 2016 , 7, 53	2.2	14
28	VICO: Ontology-based representation and integrative analysis of Vaccination Informed Consent forms. <i>Journal of Biomedical Semantics</i> , 2016 , 7, 20	2.2	7
27	OBIB-a novel ontology for biobanking. <i>Journal of Biomedical Semantics</i> , 2016 , 7, 23	2.2	13
26	Lipids, obesity and gallbladder disease in women: insights from genetic studies using the cardiovascular gene-centric 50K SNP array. <i>European Journal of Human Genetics</i> , 2016 , 24, 106-12	5.3	20
25	Collapsed methylation quantitative trait loci analysis for low frequency and rare variants. <i>Human Molecular Genetics</i> , 2016 , 25, 4339-4349	5.6	7

24	The Ontology for Biomedical Investigations. <i>PLoS ONE</i> , 2016 , 11, e0154556	3.7	143
23	Systematic identification of genetic influences on methylation across the human life course. <i>Genome Biology</i> , 2016 , 17, 61	18.3	331
22	Modeling a microbial community and biodiversity assay with OBO Foundry ontologies: the interoperability gains of a modular approach. <i>Database: the Journal of Biological Databases and Curation</i> , 2015 , 2015,	5	5
21	Ontorat: automatic generation of new ontology terms, annotations, and axioms based on ontology design patterns. <i>Journal of Biomedical Semantics</i> , 2015 , 6, 4	2.2	33
20	Multi-ancestry genome-wide association study of 21,000 cases and 95,000 controls identifies new risk loci for atopic dermatitis. <i>Nature Genetics</i> , 2015 , 47, 1449-1456	36.3	329
19	A Framework for Global Collaborative Data Management for Malaria Research. <i>American Journal of Tropical Medicine and Hygiene</i> , 2015 , 93, 124-132	3.2	9
18	Ontodog: a web-based ontology community view generation tool. <i>Bioinformatics</i> , 2014 , 30, 1340-2	7.2	11
17	CLO: The cell line ontology. <i>Journal of Biomedical Semantics</i> , 2014 , 5, 37	2.2	70
16	Standardized metadata for human pathogen/vector genomic sequences. <i>PLoS ONE</i> , 2014 , 9, e99979	3.7	25
15	Sequential sentinel SNP Regional Association Plots (SSS-RAP): an approach for testing independence of SNP association signals using meta-analysis data. <i>Annals of Human Genetics</i> , 2013 , 77, 67-79	2.2	5
14	The Ontology for Parasite Lifecycle (OPL): towards a consistent vocabulary of lifecycle stages in parasitic organisms. <i>Journal of Biomedical Semantics</i> , 2012 , 3, 5	2.2	4
13	AnnotCompute: annotation-based exploration and meta-analysis of genomics experiments. <i>Database: the Journal of Biological Databases and Curation</i> , 2011 , 2011, bar045	5	4
12	Modeling sample variables with an Experimental Factor Ontology. <i>Bioinformatics</i> , 2010 , 26, 1112-8	7.2	302
11	Modeling biomedical experimental processes with OBI. <i>Journal of Biomedical Semantics</i> , 2010 , 1 Suppl 1, S7	2.2	187
10	Sod2 knockdown in the musculature has whole-organism consequences in <i>Drosophila</i> . <i>Free Radical Biology and Medicine</i> , 2009 , 47, 803-13	7.8	31
9	Characterization of the <i>Drosophila</i> gene-switch system in aging studies: a cautionary tale. <i>Aging Cell</i> , 2008 , 7, 758-70	9.9	68
8	Differential patterns of apoptosis in response to aging in <i>Drosophila</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 12083-8	11.5	70
7	Structural motifs of pituitary adenylate cyclase-activating polypeptide (PACAP) defining PAC1-receptor selectivity. <i>Regulatory Peptides</i> , 1999 , 79, 83-92		15

6	PACAP stimulates transcription of c-Fos and c-Jun and activates the AP-1 transcription factor in rat pancreatic carcinoma cells. <i>Biochemical and Biophysical Research Communications</i> , 1996 , 221, 111-6	3-4	32
5	Pituitary adenylate-cyclase-activating polypeptide stimulates proto-oncogene expression and activates the AP-1 (c-Fos/c-Jun) transcription factor in AR4-2J pancreatic carcinoma cells. <i>FEBS Journal</i> , 1996 , 242, 467-76		20
4	Regulating the UAS/GAL4 system in adult <i>Drosophila</i> with Tet-off GAL80 transgenes		1
3	The MRC IEU OpenGWAS data infrastructure		61
2	Expression of heat shock protein 70 is insufficient to extend <i>Drosophila melanogaster</i> longevity		1
1	MicrobiomeDB: a systems biology platform for integrating, mining and analyzing microbiome experiments		1