

# Wei Jiang

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/536204/publications.pdf>

Version: 2024-02-01

26  
papers

497  
citations

759233

12  
h-index

713466

21  
g-index

30  
all docs

30  
docs citations

30  
times ranked

899  
citing authors

#	ARTICLE	IF	CITATIONS
1	Autophagy mediates the beneficial effect of hypoxic preconditioning on bone marrow mesenchymal stem cells for the therapy of myocardial infarction. <i>Stem Cell Research and Therapy</i> , 2017, 8, 89.	5.5	63
2	Interactions Between Enhanced Polygenic Risk Scores and Lifestyle for Cardiovascular Disease, Diabetes, and Lipid Levels. <i>Circulation Genomic and Precision Medicine</i> , 2021, 14, e003128.	3.6	61
3	Autophagy regulates the apoptosis of bone marrow-derived mesenchymal stem cells under hypoxic condition via AMP-activated protein kinase/mammalian target of rapamycin pathway. <i>Cell Biology International</i> , 2016, 40, 671-685.	3.0	47
4	Intracarotid transplantation of autologous adipose-derived mesenchymal stem cells significantly improves neurological deficits in rats after MCAo. <i>Journal of Materials Science: Materials in Medicine</i> , 2014, 25, 1357-1366.	3.6	40
5	Medical Group Structural Integration May Not Ensure That Care Is Integrated, From The Patient's Perspective. <i>Health Affairs</i> , 2017, 36, 885-892.	5.2	35
6	Leveraging effect size distributions to improve polygenic risk scores derived from summary statistics of genome-wide association studies. <i>PLoS Computational Biology</i> , 2020, 16, e1007565.	3.2	32
7	MicroRNA-18a Decreases Choroidal Endothelial Cell Proliferation and Migration by Inhibiting HIF1A Expression. <i>Medical Science Monitor</i> , 2015, 21, 1642-1647.	1.1	28
8	Autophagy inhibits high glucose induced cardiac microvascular endothelial cells apoptosis by mTOR signal pathway. <i>Apoptosis: an International Journal on Programmed Cell Death</i> , 2017, 22, 1510-1523.	4.9	25
9	Comparison of methods for estimating genetic correlation between complex traits using GWAS summary statistics. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	24
10	Controlling the joint local false discovery rate is more powerful than meta-analysis methods in joint analysis of summary statistics from multiple genome-wide association studies. <i>Bioinformatics</i> , 2017, 33, 500-507.	4.1	21
11	Power estimation and sample size determination for replication studies of genome-wide association studies. <i>BMC Genomics</i> , 2016, 17, 3.	2.8	17
12	Xolik: finding cross-linked peptides with maximum paired scores in linear time. <i>Bioinformatics</i> , 2019, 35, 251-257.	4.1	16
13	A Set of Efficient Methods to Generate High-Dimensional Binary Data With Specified Correlation Structures. <i>American Statistician</i> , 2021, 75, 310-322.	1.6	15
14	Leveraging LD eigenvalue regression to improve the estimation of SNP heritability and confounding inflation. <i>American Journal of Human Genetics</i> , 2022, 109, 802-811.	6.2	12
15	PBOOST: a GPU-based tool for parallel permutation tests in genome-wide association studies. <i>Bioinformatics</i> , 2015, 31, 1460-1462.	4.1	11
16	A network approach to exploring the functional basis of gene-gene epistatic interactions in disease susceptibility. <i>Bioinformatics</i> , 2018, 34, 1741-1749.	4.1	11
17	From One-Cell to Tissue: Reprogramming, Cell Differentiation and Tissue Engineering. <i>BioScience</i> , 2015, 65, 468-475.	4.9	10
18	Region-based interaction detection in genome-wide case-control studies. <i>BMC Medical Genomics</i> , 2019, 12, 133.	1.5	7

#	ARTICLE	IF	CITATIONS
19	Comparison of peripheral iridectomy methods for posterior chamber phakic intraocular lens implantation in patients with brown irides. BMC Ophthalmology, 2016, 16, 51.	1.4	4
20	M-DATA: A statistical approach to jointly analyzing de novo mutations for multiple traits. PLoS Genetics, 2021, 17, e1009849.	3.5	4
21	A novel transcriptional risk score for risk prediction of complex human diseases. Genetic Epidemiology, 2021, 45, 811-820.	1.3	3
22	Network assisted analysis of de novo variants using protein-protein interaction information identified 46 candidate genes for congenital heart disease. PLoS Genetics, 2022, 18, e1010252.	3.5	3
23	Overrepresentation of highly functional T regulatory cells in patients with nonfunctioning pituitary adenoma. Human Immunology, 2020, 81, 314-319.	2.4	2
24	Jointly determining significance levels of primary and replication studies by controlling the false discovery rate in two-stage genome-wide association studies. Statistical Methods in Medical Research, 2018, 27, 2795-2808.	1.5	1
25	Protective effect of aldehyde dehydrogenase 2 against rat corneal dysfunction caused by streptozotocin-induced type I diabetes. Experimental Biology and Medicine, 2021, 246, 1740-1749.	2.4	1
26	A Preliminary Exploration of Stroop Task's Role in Fatigue Measurement for Air Traffic Controllers. , 2021, , .		0