

# Jun Zhong

## List of Publications by Year in descending order

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Version: 2024-02-01

18  
papers

742  
citations

687363

13  
h-index

996975

15  
g-index

18  
all docs

18  
docs citations

18  
times ranked

1753  
citing authors

#	ARTICLE	IF	CITATIONS
1	Hepcidin-regulating iron metabolism genes and pancreatic ductal adenocarcinoma: a pathway analysis of genome-wide association studies. <i>American Journal of Clinical Nutrition</i> , 2021, 114, 1408-1417.	4.7	9
2	A 584Åbp deletion in CTRB2 inhibits chymotrypsin B2 activity and secretion and confers risk of pancreatic cancer. <i>American Journal of Human Genetics</i> , 2021, 108, 1852-1865.	6.2	15
3	Inferred expression regulator activities suggest genes mediating cardiometabolic genetic signals. <i>PLoS Computational Biology</i> , 2021, 17, e1009563.	3.2	3
4	A Transcriptome-Wide Association Study Identifies Novel Candidate Susceptibility Genes for Pancreatic Cancer. <i>Journal of the National Cancer Institute</i> , 2020, 112, 1003-1012.	6.3	59
5	Genome-wide association meta-analysis identifies GP2 gene risk variants for pancreatic cancer. <i>Nature Communications</i> , 2020, 11, 3175.	12.8	34
6	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. <i>Nature Communications</i> , 2020, 11, 3353.	12.8	75
7	Abstract IA-11: An exception to the rule: A coding functional variant at a pancreatic cancer GWAS locus. , 2020, , .		0
8	Cross-sectional Whole-genome Sequencing and Epidemiological Study of Multidrug-resistant <i>Mycobacterium tuberculosis</i> in China. <i>Clinical Infectious Diseases</i> , 2019, 69, 405-413.	5.8	39
9	Abstract 1591: Large-scale transcriptome-wide association study (TWAS) identifies novel candidate susceptibility genes for pancreatic cancer. , 2019, , .		3
10	Abstract 1591: Large-scale transcriptome-wide association study (TWAS) identifies novel candidate susceptibility genes for pancreatic cancer. , 2019, , .		3
11	Genome-wide meta-analysis identifies five new susceptibility loci for pancreatic cancer. <i>Nature Communications</i> , 2018, 9, 556.	12.8	188
12	Pan-Genomic Study of <i>Mycobacterium tuberculosis</i> Reflecting the Primary/Secondary Genes, Generality/Individuality, and the Interconversion Through Copy Number Variations. <i>Frontiers in Microbiology</i> , 2018, 9, 1886.	3.5	35
13	Complete genome sequence of the drought resistance-promoting endophyte <i>Klebsiella</i> sp. LTGPAF-6F. <i>Journal of Biotechnology</i> , 2017, 246, 36-39.	3.8	17
14	Precision methylome characterization of <i>Mycobacterium tuberculosis</i> complex (MTBC) using PacBio single-molecule real-time (SMRT) technology. <i>Nucleic Acids Research</i> , 2016, 44, 730-743.	14.5	124
15	Information Commons for Rice (IC4R). <i>Nucleic Acids Research</i> , 2016, 44, D1172-D1180.	14.5	41
16	Genome sequencing of high-penicillin producing industrial strain of <i>Penicillium chrysogenum</i> . <i>BMC Genomics</i> , 2014, 15, S11.	2.8	41
17	VCGDB: a dynamic genome database of the Chinese population. <i>BMC Genomics</i> , 2014, 15, 265.	2.8	13
18	Systematic analysis of intron size and abundance parameters in diverse lineages. <i>Science China Life Sciences</i> , 2013, 56, 968-974.	4.9	43