

# Cuiping Pan

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6296589/publications.pdf>

Version: 2024-02-01

21  
papers

1,831  
citations

687363

13  
h-index

794594

19  
g-index

22  
all docs

22  
docs citations

22  
times ranked

4431  
citing authors

#	ARTICLE	IF	CITATIONS
1	Hummingbird: efficient performance prediction for executing genomic applications in the cloud. <i>Bioinformatics</i> , 2021, 37, 2537-2543.	4.1	4
2	Response by Pan and Tsao to Letter Regarding Article, "Genetic Architecture of Abdominal Aortic Aneurysm in the Million Veteran Program" <i>Circulation</i> , 2021, 143, e873-e874.	1.6	1
3	Swarm: A federated cloud framework for large-scale variant analysis. <i>PLoS Computational Biology</i> , 2021, 17, e1008977.	3.2	2
4	Trellis for efficient data and task management in the VA Million Veteran Program. <i>Scientific Reports</i> , 2021, 11, 23229.	3.3	2
5	Genetic Architecture of Abdominal Aortic Aneurysm in the Million Veteran Program. <i>Circulation</i> , 2020, 142, 1633-1646.	1.6	78
6	Genotyping Array Design and Data Quality Control in the Million Veteran Program. <i>American Journal of Human Genetics</i> , 2020, 106, 535-548.	6.2	118
7	Decoding the Genomics of Abdominal Aortic Aneurysm. <i>Cell</i> , 2018, 174, 1361-1372.e10.	28.9	68
8	Cloud-based interactive analytics for terabytes of genomic variants data. <i>Bioinformatics</i> , 2017, 33, 3709-3715.	4.1	9
9	Sequence to Medical Phenotypes: A Framework for Interpretation of Human Whole Genome DNA Sequence Data. <i>PLoS Genetics</i> , 2015, 11, e1005496.	3.5	23
10	APC-dependent degradation of separase associated but not free securin. <i>EMBO Journal</i> , 2014, 33, 1134-1147.	7.8	57
11	Clinical Interpretation and Implications of Whole-Genome Sequencing. <i>JAMA - Journal of the American Medical Association</i> , 2014, 311, 1035.	7.4	398
12	Comprehensive whole-genome sequencing of an early-stage primary myelofibrosis patient defines low mutational burden and non-recurrent candidate genes. <i>Haematologica</i> , 2013, 98, 1689-1696.	3.5	10
13	Detecting and annotating genetic variations using the HugeSeq pipeline. <i>Nature Biotechnology</i> , 2012, 30, 226-229.	17.5	104
14	Whole Genome Sequence Analysis of Primary Myelofibrosis. <i>Blood</i> , 2012, 120, 2863-2863.	1.4	0
15	Quantitative Proteome and Transcriptome Analysis of the Archaeon <i>Thermoplasma acidophilum</i> Cultured under Aerobic and Anaerobic Conditions. <i>Journal of Proteome Research</i> , 2010, 9, 4839-4850.	3.7	42
16	Global Effects of Kinase Inhibitors on Signaling Networks Revealed by Quantitative Phosphoproteomics. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 2796-2808.	3.8	194
17	Comparative Proteomic Phenotyping of Cell Lines and Primary Cells to Assess Preservation of Cell Type-specific Functions. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 443-450.	3.8	426
18	Quantitative phosphoproteome analysis of a mouse liver cell line reveals specificity of phosphatase inhibitors. <i>Proteomics</i> , 2008, 8, 4534-4546.	2.2	93

#	ARTICLE	IF	CITATIONS
19	Integral and Associated Lysosomal Membrane Proteins. <i>Traffic</i> , 2007, 8, 1676-1686.	2.7	166
20	Dynamic scaling behavior of human brain electroencephalogram. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2006, 364, 315-323.	2.6	7
21	Detrended fluctuation analysis of human brain electroencephalogram. <i>Physics Letters, Section A: General, Atomic and Solid State Physics</i> , 2004, 329, 130-135.	2.1	26