

Ji-Gang Zhang

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/10778460/ji-gang-zhang-publications-by-year.pdf>

Version: 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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

20
papers

473
citations

11
h-index

20
g-index

20
ext. papers

566
ext. citations

3.9
avg, IF

3.1
L-index

#	Paper	IF	Citations
20	Genetic risk factors identified in populations of European descent do not improve the prediction of osteoporotic fracture and bone mineral density in Chinese populations. <i>Scientific Reports</i> , 2019 , 9, 6086	4.9	4
19	A Statistical Test for Differential Network Analysis Based on Inference of Gaussian Graphical Model. <i>Scientific Reports</i> , 2019 , 9, 10863	4.9	5
18	Metabolomic profiles associated with bone mineral density in US Caucasian women. <i>Nutrition and Metabolism</i> , 2018 , 15, 57	4.6	30
17	Multivariate analysis of genomics data to identify potential pleiotropic genes for type 2 diabetes, obesity and dyslipidemia using Meta-CCA and gene-based approach. <i>PLoS ONE</i> , 2018 , 13, e0201173	3.7	8
16	Mass spectrometry based proteomics profiling of human monocytes. <i>Protein and Cell</i> , 2017 , 8, 123-133	7.2	3
15	Low-, high-coverage, and two-stage DNA sequencing in the design of the genetic association study. <i>Genetic Epidemiology</i> , 2017 , 41, 187-197	2.6	15
14	Network-based proteomic analysis for postmenopausal osteoporosis in Caucasian females. <i>Proteomics</i> , 2016 , 16, 12-28	4.8	28
13	Quantitative proteomics and integrative network analysis identified novel genes and pathways related to osteoporosis. <i>Journal of Proteomics</i> , 2016 , 142, 45-52	3.9	16
12	MicroRNA-mRNA interaction analysis to detect potential dysregulation in complex diseases. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2015 , 4, 1	1.6	7
11	Genome-wide Survey of Runs of Homozygosity Identifies Recessive Loci for Bone Mineral Density in Caucasian and Chinese Populations. <i>Journal of Bone and Mineral Research</i> , 2015 , 30, 2119-26	6.3	11
10	Attenuated monocyte apoptosis, a new mechanism for osteoporosis suggested by a transcriptome-wide expression study of monocytes. <i>PLoS ONE</i> , 2015 , 10, e0116792	3.7	19
9	Multistage genome-wide association meta-analyses identified two new loci for bone mineral density. <i>Human Molecular Genetics</i> , 2014 , 23, 1923-33	5.6	113
8	Replication of 6 obesity genes in a meta-analysis of genome-wide association studies from diverse ancestries. <i>PLoS ONE</i> , 2014 , 9, e96149	3.7	45
7	Integrative analysis of GWASs, human protein interaction, and gene expression identified gene modules associated with BMDs. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2014 , 99, E2392-9	5.6	7
6	Population clustering based on copy number variations detected from next generation sequencing data. <i>Journal of Bioinformatics and Computational Biology</i> , 2014 , 12, 1450021	1	
5	Is GSN significant for hip BMD in female Caucasians?. <i>Bone</i> , 2014 , 63, 69-75	4.7	16
4	CNV-TV: a robust method to discover copy number variation from short sequencing reads. <i>BMC Bioinformatics</i> , 2013 , 14, 150	3.6	31

3	Comparative studies of copy number variation detection methods for next-generation sequencing technologies. <i>PLoS ONE</i> , 2013 , 8, e59128	3.7	112
2	Detection of common copy number variation with application to population clustering from next generation sequencing data. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference</i> , 2012 , 2012, 1246-9	0.9	2
1	Fusing Gene Interaction to Improve Disease Discrimination on Classification Analysis. <i>Advancements in Genetic Engineering</i> , 2012 , 1, 1000102		1