Ji-Gang Zhang

List of Publications by Year
in descending order

20 papers	626 citations	840776 11 h-index	839539 18 g-index
20 all docs	20 docs citations	20 times ranked	1359 citing authors

#	Article	IF	Citations
1	Comparative Studies of Copy Number Variation Detection Methods for Next-Generation Sequencing Technologies. PLoS ONE, 2013, 8, e59128.	2.5	138
2	Multistage genome-wide association meta-analyses identified two new loci for bone mineral density. Human Molecular Genetics, 2014, 23, 1923-1933.	2.9	130
3	Replication of 6 Obesity Genes in a Meta-Analysis of Genome-Wide Association Studies from Diverse Ancestries. PLoS ONE, 2014, 9, e96149.	2.5	56
4	Metabolomic profiles associated with bone mineral density in US Caucasian women. Nutrition and Metabolism, 2018, 15, 57.	3.0	51
5	Network–based proteomic analysis for postmenopausal osteoporosis in Caucasian females. Proteomics, 2016, 16, 12-28.	2.2	40
6	CNV-TV: A robust method to discover copy number variation from short sequencing reads. BMC Bioinformatics, 2013, 14, 150.	2.6	38
7	Attenuated Monocyte Apoptosis, a New Mechanism for Osteoporosis Suggested by a Transcriptome-Wide Expression Study of Monocytes. PLoS ONE, 2015, 10, e0116792.	2.5	26
8	Multivariate analysis of genomics data to identify potential pleiotropic genes for type 2 diabetes, obesity and dyslipidemia using Meta-CCA and gene-based approach. PLoS ONE, 2018, 13, e0201173.	2.5	24
9	Is GSN significant for hip BMD in female Caucasians?. Bone, 2014, 63, 69-75.	2.9	21
10	Quantitative proteomics and integrative network analysis identified novel genes and pathways related to osteoporosis. Journal of Proteomics, 2016, 142, 45-52.	2.4	21
11	Low-, high-coverage, and two-stage DNA sequencing in the design of the genetic association study. Genetic Epidemiology, 2017, 41, 187-197.	1.3	20
12	Genome-Wide Survey of Runs of Homozygosity Identifies Recessive Loci for Bone Mineral Density in Caucasian and Chinese Populations. Journal of Bone and Mineral Research, 2015, 30, 2119-2126.	2.8	13
13	A Statistical Test for Differential Network Analysis Based on Inference of Gaussian Graphical Model. Scientific Reports, 2019, 9, 10863.	3.3	12
14	Integrative Analysis of GWASs, Human Protein Interaction, and Gene Expression Identified Gene Modules Associated With BMDs. Journal of Clinical Endocrinology and Metabolism, 2014, 99, E2392-E2399.	3.6	10
15	MicroRNA–mRNA interaction analysis to detect potential dysregulation in complex diseases. Network Modeling Analysis in Health Informatics and Bioinformatics, 2015, 4, 1.	2.1	10
16	Mass spectrometry based proteomics profiling of human monocytes. Protein and Cell, 2017, 8, 123-133.	11.0	6
17	Genetic risk factors identified in populations of European descent do not improve the prediction of osteoporotic fracture and bone mineral density in Chinese populations. Scientific Reports, 2019, 9, 6086.	3.3	6
18	Detection of common copy number variation with application to population clustering from next generation sequencing data. , 2012, 2012, 1246-9.		3

#	Article	IF	Citations
19	Fusing Gene Interaction to Improve Disease Discrimination on Classification Analysis. Advancements in Genetic Engineering, 2012, 01, 1000102.	0.1	1
20	Population clustering based on copy number variations detected from next generation sequencing data. Journal of Bioinformatics and Computational Biology, 2014, 12, 1450021.	0.8	0