

Ji-Gang Zhang

List of Publications by Year in descending order

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Version: 2024-02-01

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	A Statistical Test for Differential Network Analysis Based on Inference of Gaussian Graphical Model. <i>Scientific Reports</i> , 2019, 9, 10863.	3.3	12
2	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.	3.3	6
3	Metabolomic profiles associated with bone mineral density in US Caucasian women. <i>Nutrition and Metabolism</i> , 2018, 15, 57.	3.0	51
4	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.	2.5	24
5	Mass spectrometry based proteomics profiling of human monocytes. <i>Protein and Cell</i> , 2017, 8, 123-133.	11.0	6
6	Low-, high-coverage, and two-stage DNA sequencing in the design of the genetic association study. <i>Genetic Epidemiology</i> , 2017, 41, 187-197.	1.3	20
7	Quantitative proteomics and integrative network analysis identified novel genes and pathways related to osteoporosis. <i>Journal of Proteomics</i> , 2016, 142, 45-52.	2.4	21
8	Network-based proteomic analysis for postmenopausal osteoporosis in Caucasian females. <i>Proteomics</i> , 2016, 16, 12-28.	2.2	40
9	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, 2119-2126.	2.8	13
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.	2.5	26
11	MicroRNA-mRNA interaction analysis to detect potential dysregulation in complex diseases. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2015, 4, 1.	2.1	10
12	Replication of 6 Obesity Genes in a Meta-Analysis of Genome-Wide Association Studies from Diverse Ancestries. <i>PLoS ONE</i> , 2014, 9, e96149.	2.5	56
13	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-E2399.	3.6	10
14	Population clustering based on copy number variations detected from next generation sequencing data. <i>Journal of Bioinformatics and Computational Biology</i> , 2014, 12, 1450021.	0.8	0
15	Is GSN significant for hip BMD in female Caucasians?. <i>Bone</i> , 2014, 63, 69-75.	2.9	21
16	Multistage genome-wide association meta-analyses identified two new loci for bone mineral density. <i>Human Molecular Genetics</i> , 2014, 23, 1923-1933.	2.9	130
17	CNV-TV: A robust method to discover copy number variation from short sequencing reads. <i>BMC Bioinformatics</i> , 2013, 14, 150.	2.6	38
18	Comparative Studies of Copy Number Variation Detection Methods for Next-Generation Sequencing Technologies. <i>PLoS ONE</i> , 2013, 8, e59128.	2.5	138

#	ARTICLE	IF	CITATIONS
19	Detection of common copy number variation with application to population clustering from next generation sequencing data. , 2012, 2012, 1246-9.		3
20	Fusing Gene Interaction to Improve Disease Discrimination on Classification Analysis. Advancements in Genetic Engineering, 2012, 01, 1000102.	0.1	1