

Jin Li

List of Publications by Year in descending order

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Version: 2024-02-01

20
papers

634
citations

759233

12
h-index

752698

20
g-index

22
all docs

22
docs citations

22
times ranked

1244
citing authors

#	ARTICLE	IF	CITATIONS
1	Geometry-Based Molecular Generation With Deep Constrained Variational Autoencoder. IEEE Transactions on Neural Networks and Learning Systems, 2024, PP, 1-10.	11.3	6
2	Higher-Order Proximity-Based MiRNA-Disease Associations Prediction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 501-512.	3.0	3
3	Genome-wide analysis of aberrant methylation of enhancer DNA in human osteoarthritis. BMC Medical Genomics, 2020, 13, 1.	1.5	77
4	EWASdb: epigenome-wide association study database. Nucleic Acids Research, 2019, 47, D989-D993.	14.5	39
5	Multidimensional Integration Analysis of Autophagy-related Modules in Colorectal Cancer. Letters in Organic Chemistry, 2019, 16, 340-346.	0.5	0
6	A PET imaging approach for determining EGFR mutation status for improved lung cancer patient management. Science Translational Medicine, 2018, 10, .	12.4	66
7	EWAS: epigenome-wide association study software 2.0. Bioinformatics, 2018, 34, 2657-2658.	4.1	23
8	A novel parallel distance metric-based approach for diversified ranking on large graphs. Future Generation Computer Systems, 2018, 88, 79-91.	7.5	2
9	Genome-wide pathway-based association analysis identifies risk pathways associated with Parkinson's disease. Neuroscience, 2017, 340, 398-410.	2.3	23
10	Genome-wide haplotype association study identify the FGFR2 gene as a risk gene for Acute Myeloid Leukemia. Oncotarget, 2017, 8, 7891-7899.	1.8	34
11	eSNPO: An eQTL-based SNP Ontology and SNP functional enrichment analysis platform. Scientific Reports, 2016, 6, 30595.	3.3	9
12	The drug target genes show higher evolutionary conservation than non-target genes. Oncotarget, 2016, 7, 4961-4971.	1.8	16
13	Integrative analysis of genome-wide association studies and gene expression analysis identifies pathways associated with rheumatoid arthritis. Oncotarget, 2016, 7, 8580-8589.	1.8	12
14	Prediction of potential disease-associated microRNAs based on random walk. Bioinformatics, 2015, 31, 1805-1815.	4.1	175
15	Mining disease genes using integrated protein-protein interaction and gene-gene co-regulation information. FEBS Open Bio, 2015, 5, 251-256.	2.3	16
16	Genes with stable DNA methylation levels show higher evolutionary conservation than genes with fluctuant DNA methylation levels. Oncotarget, 2015, 6, 40235-40246.	1.8	2
17	Genome-wide haplotype association study identify TNFRSF1A, CASP7, LRP1B, CDH1 and TG genes associated with Alzheimer's disease in Caribbean Hispanic individuals. Oncotarget, 2015, 6, 42504-42514.	1.8	46
18	MCPPerm: A Monte Carlo Permutation Method for Accurately Correcting the Multiple Testing in a Meta-Analysis of Genetic Association Studies. PLoS ONE, 2014, 9, e89212.	2.5	10

#	ARTICLE	IF	CITATIONS
19	Computational Prediction of Protein Function Based on Weighted Mapping of Domains and GO Terms. BioMed Research International, 2014, 2014, 1-9.	1.9	3
20	DBGSA: a novel method of distance-based gene set analysis. Journal of Human Genetics, 2012, 57, 642-653.	2.3	4