

Jin Li

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4133155/publications.pdf>

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	Prediction of potential disease-associated microRNAs based on random walk. <i>Bioinformatics</i> , 2015, 31, 1805-1815.	4.1	175
2	Genome-wide analysis of aberrant methylation of enhancer DNA in human osteoarthritis. <i>BMC Medical Genomics</i> , 2020, 13, 1.	1.5	77
3	A PET imaging approach for determining EGFR mutation status for improved lung cancer patient management. <i>Science Translational Medicine</i> , 2018, 10, .	12.4	66
4	Genome-wide haplotype association study identify TNFRSF1A, CASP7, LRP1B, CDH1 and TG genes associated with Alzheimer's disease in Caribbean Hispanic individuals. <i>Oncotarget</i> , 2015, 6, 42504-42514.	1.8	46
5	EWASdb: epigenome-wide association study database. <i>Nucleic Acids Research</i> , 2019, 47, D989-D993.	14.5	39
6	Genome-wide haplotype association study identify the FGFR2 gene as a risk gene for Acute Myeloid Leukemia. <i>Oncotarget</i> , 2017, 8, 7891-7899.	1.8	34
7	Genome-wide pathway-based association analysis identifies risk pathways associated with Parkinson's disease. <i>Neuroscience</i> , 2017, 340, 398-410.	2.3	23
8	EWAS: epigenome-wide association study software 2.0. <i>Bioinformatics</i> , 2018, 34, 2657-2658.	4.1	23
9	Mining disease genes using integrated protein-protein interaction and gene-gene co-regulation information. <i>FEBS Open Bio</i> , 2015, 5, 251-256.	2.3	16
10	The drug target genes show higher evolutionary conservation than non-target genes. <i>Oncotarget</i> , 2016, 7, 4961-4971.	1.8	16
11	Integrative analysis of genome-wide association studies and gene expression analysis identifies pathways associated with rheumatoid arthritis. <i>Oncotarget</i> , 2016, 7, 8580-8589.	1.8	12
12	MCPPerm: A Monte Carlo Permutation Method for Accurately Correcting the Multiple Testing in a Meta-Analysis of Genetic Association Studies. <i>PLoS ONE</i> , 2014, 9, e89212.	2.5	10
13	eSNPO: An eQTL-based SNP Ontology and SNP functional enrichment analysis platform. <i>Scientific Reports</i> , 2016, 6, 30595.	3.3	9
14	Geometry-Based Molecular Generation With Deep Constrained Variational Autoencoder. <i>IEEE Transactions on Neural Networks and Learning Systems</i> , 2024, PP, 1-10.	11.3	6
15	DBGSA: a novel method of distance-based gene set analysis. <i>Journal of Human Genetics</i> , 2012, 57, 642-653.	2.3	4
16	Computational Prediction of Protein Function Based on Weighted Mapping of Domains and GO Terms. <i>BioMed Research International</i> , 2014, 2014, 1-9.	1.9	3
17	Higher-Order Proximity-Based MiRNA-Disease Associations Prediction. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 501-512.	3.0	3
18	A novel parallel distance metric-based approach for diversified ranking on large graphs. <i>Future Generation Computer Systems</i> , 2018, 88, 79-91.	7.5	2

#	ARTICLE	IF	CITATIONS
19	Genes with stable DNA methylation levels show higher evolutionary conservation than genes with fluctuant DNA methylation levels. <i>Oncotarget</i> , 2015, 6, 40235-40246.	1.8	2
20	Multidimensional Integration Analysis of Autophagy-related Modules in Colorectal Cancer. <i>Letters in Organic Chemistry</i> , 2019, 16, 340-346.	0.5	0