

Wei Jiang

List of Publications by Year in descending order

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63
papers

2,421
citations

185998

28
h-index

214527

47
g-index

64
all docs

64
docs citations

64
times ranked

3181
citing authors

#	ARTICLE	IF	CITATIONS
1	Single-cell RNA-seq dissects the intratumoral heterogeneity of triple-negative breast cancer based on gene regulatory networks. <i>Molecular Therapy - Nucleic Acids</i> , 2021, 23, 682-690.	2.3	45
2	In silico drug repositioning based on drug-miRNA associations. <i>Briefings in Bioinformatics</i> , 2020, 21, 498-510.	3.2	22
3	Dissecting the m6A methylation affection on afatinib resistance in non-small cell lung cancer. <i>Pharmacogenomics Journal</i> , 2020, 20, 227-234.	0.9	27
4	Circulating Circular RNAs as Biomarkers for the Diagnosis and Prediction of Outcomes in Acute Ischemic Stroke. <i>Stroke</i> , 2020, 51, 319-323.	1.0	98
5	Integrative Analysis of Regulatory Module Reveals Associations of Microgravity with Dysfunctions of Multi-body Systems and Tumorigenesis. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7585.	1.8	5
6	ncRI: a manually curated database for experimentally validated non-coding RNAs in inflammation. <i>BMC Genomics</i> , 2020, 21, 380.	1.2	8
7	Pan-cancer analysis reveals cooperativity of both strands of microRNA that regulate tumorigenesis and patient survival. <i>Nature Communications</i> , 2020, 11, 968.	5.8	57
8	ncEP: A Manually Curated Database for Experimentally Validated ncRNA-encoded Proteins or Peptides. <i>Journal of Molecular Biology</i> , 2020, 432, 3364-3368.	2.0	34
9	Identification of drug resistance associated ncRNAs based on comprehensive heterogeneous network. <i>Life Sciences</i> , 2020, 243, 117256.	2.0	4
10	LncRNA-Encoded Peptide: Functions and Predicting Methods. <i>Frontiers in Oncology</i> , 2020, 10, 622294.	1.3	59
11	Extracellular Vesicle-Mediated Delivery of Circular RNA SCMH1 Promotes Functional Recovery in Rodent and Nonhuman Primate Ischemic Stroke Models. <i>Circulation</i> , 2020, 142, 556-574.	1.6	198
12	D-lnc: a comprehensive database and analytical platform to dissect the modification of drugs on lncRNA expression. <i>RNA Biology</i> , 2019, 16, 1586-1591.	1.5	25
13	MycoResistance: a curated resource of drug resistance molecules in Mycobacteria. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	8
14	LncRNA HCP5 promotes triple negative breast cancer progression as a ceRNA to regulate BIRC3 by sponging miR-219a-5p. <i>Cancer Medicine</i> , 2019, 8, 4389-4403.	1.3	70
15	Drug Resistance-Related Competing Interactions of lncRNA and mRNA across 19 Cancer Types. <i>Molecular Therapy - Nucleic Acids</i> , 2019, 16, 442-451.	2.3	25
16	Identification of transcription factor-miRNA-lncRNA feed-forward loops in breast cancer subtypes. <i>Computational Biology and Chemistry</i> , 2019, 78, 1-7.	1.1	21
17	Pathway enrichment analysis approach based on topological structure and updated annotation of pathway. <i>Briefings in Bioinformatics</i> , 2019, 20, 168-177.	3.2	32
18	Detecting the long non-coding RNA signature related to spinal cord ependymal tumor subtype using a genome-wide methylome analysis approach. <i>Molecular Medicine Reports</i> , 2019, 20, 1531-1540.	1.1	2

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19	Systematical analysis of lncRNA-mRNA competing endogenous RNA network in breast cancer subtypes. <i>Breast Cancer Research and Treatment</i> , 2018, 169, 267-275.	1.1	47
20	Accurate prediction and elucidation of drug resistance based on the robust and reproducible chemoresponse communities. <i>International Journal of Cancer</i> , 2018, 142, 1427-1439.	2.3	3
21	Inferring Novel Autophagy Regulators Based on Transcription Factors and Non-Coding RNAs Coordinated Regulatory Network. <i>Cells</i> , 2018, 7, 194.	1.8	8
22	Prediction of Non-coding RNAs as Drug Targets. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1094, 109-115.	0.8	5
23	Matrix Metalloproteinase-2 Gene rs2287074 Polymorphism is Associated with Brick Tea Skeletal Fluorosis in Tibetans and Kazaks, China. <i>Scientific Reports</i> , 2017, 7, 40086.	1.6	19
24	Molecular classification of prostate adenocarcinoma by the integrated somatic mutation profiles and molecular network. <i>Scientific Reports</i> , 2017, 7, 738.	1.6	12
25	ncDR: a comprehensive resource of non-coding RNAs involved in drug resistance. <i>Bioinformatics</i> , 2017, 33, 4010-4011.	1.8	48
26	Decoding critical long non-coding RNA in ovarian cancer epithelial-to-mesenchymal transition. <i>Nature Communications</i> , 2017, 8, 1604.	5.8	159
27	High expression of PU.1 is associated with Her2 and shorter survival in patients with breast cancer. <i>Oncology Letters</i> , 2017, 14, 8220-8226.	0.8	12
28	Quantitative proteomics reveals the novel co-expression signatures in early brain development for prognosis of glioblastoma multiforme. <i>Oncotarget</i> , 2016, 7, 14161-14171.	0.8	27
29	Dissecting the Origin of Breast Cancer Subtype Stem Cell and the Potential Mechanism of Malignant Transformation. <i>PLoS ONE</i> , 2016, 11, e0165001.	1.1	11
30	Association between vitamin D receptor gene FokI polymorphism and skeletal fluorosis of the brick-tea type fluorosis: a cross sectional, case control study. <i>BMJ Open</i> , 2016, 6, e011980.	0.8	15
31	Large-scale identification of adverse drug reaction-related proteins through a random walk model. <i>Scientific Reports</i> , 2016, 6, 36325.	1.6	19
32	Psmir: a database of potential associations between small molecules and miRNAs. <i>Scientific Reports</i> , 2016, 6, 19264.	1.6	21
33	Systematic dissection of dysregulated transcription factor-miRNA feed-forward loops across tumor types. <i>Briefings in Bioinformatics</i> , 2016, 17, 996-1008.	3.2	54
34	The gain and loss of long noncoding RNA associated-competing endogenous RNAs in prostate cancer. <i>Oncotarget</i> , 2016, 7, 57228-57238.	0.8	43
35	Identification of associations between small molecule drugs and miRNAs based on functional similarity. <i>Oncotarget</i> , 2016, 7, 38658-38669.	0.8	34
36	Systematic Analysis of the Associations between Adverse Drug Reactions and Pathways. <i>BioMed Research International</i> , 2015, 2015, 1-12.	0.9	7

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37	Genome-wide characterization of essential, toxicity-modulating and no-phenotype genes in <i>S. cerevisiae</i> . <i>Gene</i> , 2015, 559, 1-8.	1.0	0
38	Identifying novel associations between small molecules and miRNAs based on integrated molecular networks. <i>Bioinformatics</i> , 2015, 31, 3638-3644.	1.8	72
39	Characterization of proteins in <i>S. cerevisiae</i> with subcellular localizations. <i>Molecular BioSystems</i> , 2015, 11, 1360-1369.	2.9	2
40	Spatiotemporal-specific lncRNAs in the brain, colon, liver and lung of macaque during development. <i>Molecular BioSystems</i> , 2015, 11, 3253-3263.	2.9	43
41	Integrated systems approach identifies risk regulatory pathways and key regulators in coronary artery disease. <i>Journal of Molecular Medicine</i> , 2015, 93, 1381-1390.	1.7	18
42	TMREC: A Database of Transcription Factor and MiRNA Regulatory Cascades in Human Diseases. <i>PLoS ONE</i> , 2015, 10, e0125222.	1.1	22
43	Characterization of TATA-containing genes and TATA-less genes in <i>S. cerevisiae</i> by network topologies and biological properties. <i>Genomics</i> , 2014, 104, 562-571.	1.3	7
44	Analysis and identification of essential genes in humans using topological properties and biological information. <i>Gene</i> , 2014, 551, 138-151.	1.0	22
45	Computational identification of human long intergenic non-coding RNAs using a GA-SVM algorithm. <i>Gene</i> , 2014, 533, 94-99.	1.0	34
46	Characterization of essential genes by topological properties in the perturbation sensitivity network. <i>Biochemical and Biophysical Research Communications</i> , 2014, 448, 473-479.	1.0	10
47	Analysis and identification of toxin targets by topological properties in protein-protein interaction network. <i>Journal of Theoretical Biology</i> , 2014, 349, 82-91.	0.8	16
48	Human proteins characterization with subcellular localizations. <i>Journal of Theoretical Biology</i> , 2014, 358, 61-73.	0.8	11
49	Gene Expression Profiling in Human Lung Development: An Abundant Resource for Lung Adenocarcinoma Prognosis. <i>PLoS ONE</i> , 2014, 9, e105639.	1.1	19
50	Identification of active transcription factor and miRNA regulatory pathways in Alzheimer's disease. <i>Bioinformatics</i> , 2013, 29, 2596-2602.	1.8	66
51	SM2miR: a database of the experimentally validated small molecules' effects on microRNA expression. <i>Bioinformatics</i> , 2013, 29, 409-411.	1.8	175
52	Identification of links between small molecules and miRNAs in human cancers based on transcriptional responses. <i>Scientific Reports</i> , 2012, 2, 282.	1.6	72
53	Association Analysis of IL-17A and IL-17F Polymorphisms in Chinese Han Women with Breast Cancer. <i>PLoS ONE</i> , 2012, 7, e34400.	1.1	92
54	A miRNA Binding Site Single-Nucleotide Polymorphism in the 3'-UTR Region of the IL23R Gene Is Associated with Breast Cancer. <i>PLoS ONE</i> , 2012, 7, e49823.	1.1	42

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55	Topological properties of the drug targets regulated by microRNA in human protein-protein interaction network. <i>Journal of Drug Targeting</i> , 2011, 19, 354-364.	2.1	35
56	Predicting human microRNA precursors based on an optimized feature subset generated by GA-SVM. <i>Genomics</i> , 2011, 98, 73-78.	1.3	53
57	The analysis of the drug targets based on the topological properties in the human protein-protein interaction network. <i>Journal of Drug Targeting</i> , 2009, 17, 524-532.	2.1	101
58	Constructing disease-specific gene networks using pair-wise relevance metric: Application to colon cancer identifies interleukin 8, desmin and enolase 1 as the central elements. <i>BMC Systems Biology</i> , 2008, 2, 72.	3.0	64
59	Familial aggregation analysis of gene expressions. <i>BMC Proceedings</i> , 2007, 1, S49.	1.8	1
60	Inhibition of LXR α signaling by vitamin D receptor: Possible role of VDR in bile acid synthesis. <i>Biochemical and Biophysical Research Communications</i> , 2006, 351, 176-184.	1.0	46
61	A novel model-free approach for reconstruction of time-delayed gene regulatory networks. <i>Science in China Series C: Life Sciences</i> , 2006, 49, 190-200.	1.3	2
62	Reconstruct gene regulatory subnetwork in yeast cell cycle using a novel approach. , 2005, , .		0
63	A robust hybrid between genetic algorithm and support vector machine for extracting an optimal feature gene subset. <i>Genomics</i> , 2005, 85, 16-23.	1.3	112