Jianhua Ruan

List of Publications by Year
in descending order

79 papers	3,007 citations	257450 24 h-index	175258 52 g-index
88 all docs	88 docs citations	88 times ranked	4898 citing authors

#	Article	IF	Citations
1	Evaluation of methods for modeling transcription factor sequence specificity. Nature Biotechnology, 2013, 31, 126-134.	17.5	341
2	Characterization and Identification of MicroRNA Core Promoters in Four Model Species. PLoS Computational Biology, 2007, 3, e37.	3.2	273
3	A general co-expression network-based approach to gene expression analysis: comparison and applications. BMC Systems Biology, 2010, 4, 8.	3.0	226
4	An Iterated loop matching approach to the prediction of RNA secondary structures with pseudoknots. Bioinformatics, 2004, 20, 58-66.	4.1	213
5	Identifying network communities with a high resolution. Physical Review E, 2008, 77, 016104.	2.1	163
6	A novel link prediction algorithm for reconstructing proteinâ€"protein interaction networks by topological similarity. Bioinformatics, 2013, 29, 355-364.	4.1	160
7	Cis-regulatory element based targeted gene finding: genome-wide identification of abscisic acid- and abiotic stress-responsive genes in Arabidopsis thaliana. Bioinformatics, 2005, 21, 3074-3081.	4.1	151
8	An Efficient Spectral Algorithm for Network Community Discovery and Its Applications to Biological and Social Networks. , 2007, , .		97
9	Variations in the transcriptome of Alzheimer's disease reveal molecular networks involved in cardiovascular diseases. Genome Biology, 2008, 9, R148.	9.6	94
10	Alterations in the placental methylome with maternal obesity and evidence for metabolic regulation. PLoS ONE, 2017, 12, e0186115.	2.5	89
11	Enhancer reprogramming driven by high-order assemblies of transcription factors promotes phenotypic plasticity and breast cancer endocrine resistance. Nature Cell Biology, 2020, 22, 701-715.	10.3	84
12	The regulatory repertoire of PLZF and SALL4 in undifferentiated spermatogonia. Development (Cambridge), 2016, 143, 1893-906.	2.5	69
13	Plasticity of the Systemic Inflammatory Response to Acute Infection during Critical Illness: Development of the Riboleukogram. PLoS ONE, 2008, 3, e1564.	2.5	68
14	Genomic Analyses of the RNA-binding Protein Hu Antigen R (HuR) Identify a Complex Network of Target Genes and Novel Characteristics of Its Binding Sites. Journal of Biological Chemistry, 2011, 286, 37063-37066.	3.4	68
15	Intratumoral CD56bright natural killer cells are associated with improved survival in bladder cancer. Oncotarget, 2018, 9, 36492-36502.	1.8	60
16	Building and analyzing protein interactome networks by cross-species comparisons. BMC Systems Biology, 2010, 4, 36.	3.0	55
17	Comprehensive methylome analysis of ovarian tumors reveals hedgehog signaling pathway regulators as prognostic DNA methylation biomarkers. Epigenetics, 2013, 8, 624-634.	2.7	51
18	A Network of Conserved Damage Survival Pathways Revealed by a Genomic RNAi Screen. PLoS Genetics, 2009, 5, e1000527.	3.5	47

#	Article	IF	Citations
19	EpCAM-Regulated Transcription Exerts Influences on Nanomechanical Properties of Endometrial Cancer Cells That Promote Epithelial-to-Mesenchymal Transition. Cancer Research, 2016, 76, 6171-6182.	0.9	46
20	Promoter Hypomethylation of EpCAM-Regulated Bone Morphogenetic Protein Gene Family in Recurrent Endometrial Cancer. Clinical Cancer Research, 2013, 19, 6272-6285.	7.0	37
21	A personalized committee classification approach to improving prediction of breast cancer metastasis. Bioinformatics, 2014, 30, 1858-1866.	4.1	34
22	ILM: a web server for predicting RNA secondary structures with pseudoknots. Nucleic Acids Research, 2004, 32, W146-W149.	14.5	32
23	Manipulation of the Plant Host by the Geminivirus AC2/C2 Protein, a Central Player in the Infection Cycle. Frontiers in Plant Science, 2020, 11, 591.	3.6	32
24	Regulation of adipose oestrogen output by mechanical stress. Nature Communications, 2013, 4, 1821.	12.8	31
25	Pathway Enrichment Analysis with Networks. Genes, 2017, 8, 246.	2.4	30
26	Cell density-dependent transcriptional activation of endocrine-related genes in human adipose tissue-derived stem cells. Experimental Cell Research, 2010, 316, 2087-2098.	2.6	26
27	A Steiner tree-based method for biomarker discovery and classification in breast cancer metastasis. BMC Genomics, 2012, 13, S8.	2.8	25
28	Genetic and Genomic Analyses of RNA Polymerase II-pausing Factor in Regulation of Mammalian Transcription and Cell Growth. Journal of Biological Chemistry, 2011, 286, 36248-36257.	3.4	24
29	A bi-dimensional regression tree approach to the modeling of gene expression regulation. Bioinformatics, 2006, 22, 332-340.	4.1	23
30	Computational modeling of in vivo and in vitro protein-DNA interactions by multiple instance learning. Bioinformatics, 2017, 33, 2097-2105.	4.1	20
31	Genetic suppression reveals DNA repair-independent antagonism between BRCA1 and COBRA1 in mammary gland development. Nature Communications, 2016, 7, 10913.	12.8	19
32	A particle swarm optimization-based algorithm for finding gapped motifs. BioData Mining, 2010, 3, 9.	4.0	16
33	Adipokines Deregulate Cellular Communication via Epigenetic Repression of Gap Junction Loci in Obese Endometrial Cancer. Cancer Research, 2019, 79, 196-208.	0.9	16
34	A systems biology approach to the identification and analysis of transcriptional regulatory networks in osteocytes. BMC Bioinformatics, 2009, 10, S5.	2.6	15
35	An ensemble approach for drug side effect prediction. , 2013, , 440-445.		15
36	Altered expression of Arabidopsis genes in response to a multifunctional geminivirus pathogenicity protein. BMC Plant Biology, 2014, 14, 302.	3.6	15

#	Article	IF	Citations
37	Semi-Supervised Multi-Label Feature Selection by Preserving Feature-Label Space Consistency. , 2018, , .		15
38	A Particle Swarm Optimization algorithm for finding DNA sequence motifs. , 2008, , .		14
39	Spatial EGFR Dynamics and Metastatic Phenotypes Modulated by Upregulated EphB2 and Src Pathways in Advanced Prostate Cancer. Cancers, 2019, 11, 1910.	3.7	14
40	A novel algorithm for network-based prediction of cancer recurrence. Genomics, 2019, 111, 17-23.	2.9	14
41	A genome-wide cis-regulatory element discovery method based on promoter sequences and gene co-expression networks. BMC Genomics, 2013, 14, S4.	2.8	13
42	Network-Based Single-Cell RNA-Seq Data Imputation Enhances Cell Type Identification. Genes, 2020, 11, 377.	2.4	13
43	Network-based pathway enrichment analysis. , 2013, , 218-221.		12
44	A Fully Automated Method for Discovering Community Structures in High Dimensional Data. , 2009, , 968-973.		11
45	A novel swarm intelligence algorithm for finding DNA motifs. International Journal of Computational Biology and Drug Design, 2009, 2, 323.	0.3	11
46	A Top-Performing Algorithm for the DREAM3 Gene Expression Prediction Challenge. PLoS ONE, 2010, 5, e8944.	2.5	10
47	A structure-based Multiple-Instance Learning approach to predicting in vitrotranscription factor-DNA interaction. BMC Genomics, 2015, 16, S3.	2.8	10
48	Systematic identification of functional modules and cis-regulatory elements in Arabidopsis thaliana. BMC Bioinformatics, 2011, 12, S2.	2.6	8
49	Comparative evaluation of network features for the prediction of breast cancer metastasis. BMC Medical Genomics, 2020, 13, 40.	1.5	8
50	2-Hydroxyglutarate destabilizes chromatin regulatory landscape and lineage fidelity to promote cellular heterogeneity. Cell Reports, 2022, 38, 110220.	6.4	8
51	CAGER: classification analysis of gene expression regulation using multiple information sources. BMC Bioinformatics, 2005, 6, 114.	2.6	6
52	An ensemble learning approach to reverse-engineering transcriptional regulatory networks from time-series gene expression data. BMC Genomics, 2009, 10, S8.	2.8	5
53	Logo2PWM: a tool to convert sequence logo to position weight matrix. BMC Genomics, 2017, 18, 709.	2.8	5
54	Identification of biomarkers in breast cancer metastasis by integrating protein-protein interaction network and gene expression data. , 2011, , .		4

#	Article	IF	Citations
55	The International Conference on Intelligent Biology and Medicine (ICIBM) 2016: summary and innovation in genomics. BMC Genomics, 2017, 18, 703.	2.8	4
56	Robust edge-based biomarker discovery improves prediction of breast cancer metastasis. BMC Bioinformatics, 2020, 21, 359.	2.6	4
57	Construction and Evaluation of Robust Interpretation Models for Breast Cancer Metastasis Prediction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 1344-1353.	3.0	4
58	Finding Gapped Motifs by a Novel Evolutionary Algorithm. Lecture Notes in Computer Science, 2010, , 50-61.	1.3	4
59	EGFR-Dependent Regulated Intramembrane Proteolysis of EpCAMâ€"Response. Cancer Research, 2017, 77, 1777-1777.	0.9	3
60	Utilizing networks for differential analysis of chromatin interactions. Journal of Bioinformatics and Computational Biology, 2017, 15, 1740008.	0.8	3
61	Network-based classification of recurrent endometrial cancers using high-throughput DNA methylation data. , 2012, , .		2
62	A random walk based approach for improving protein-protein interaction network and protein complex prediction. , 2012, , .		2
63	Frontiers in Integrative Genomics and Translational Bioinformatics. BioMed Research International, 2015, 2015, 1-3.	1.9	2
64	Probabilistic Topic and Role Model for Information Diffusion in Social Network. Lecture Notes in Computer Science, 2018, , 3-15.	1.3	2
65	Promoter prediction based on a multiple instance learning scheme. , 2010, , .		1
66	Fully automated protein complex prediction based on topological similarity and community structure. Proteome Science, 2013, 11, S9.	1.7	1
67	The International Conference on Intelligent Biology and Medicine (ICIBM) 2016: from big data to big analytical tools. BMC Bioinformatics, 2017, 18, 405.	2.6	1
68	The International Conference on Intelligent Biology and Medicine (ICIBM) 2018: bioinformatics towards translational applications. BMC Bioinformatics, 2018, 19, 492.	2.6	1
69	A Novel Multiple Classifier Generation and Combination Framework Based on Fuzzy Clustering and Individualized Ensemble Construction. , 2019, , .		1
70	A genome-wide cis-regulatory element discovery method based on promoter sequences and gene co-expression networks. , 2012, , .		1
71	A novel approach for cancer outcome prediction using personalized classifier. , 2012, , .		1
72	Computational Methods for Transcriptional Regulatory Networks. , 2013, , 468-473.		0

#	Article	IF	Citations
73	Structure-based prediction of drug side effects using a novel classification algorithm. International Journal of Computational Biology and Drug Design, 2016, 9, 87.	0.3	0
74	The International Conference on Intelligent Biology and Medicine (ICIBM) 2016: putting systems biology to work. BMC Systems Biology, 2017, 11, 88.	3.0	0
75	An integrative approach to transcriptional co-regulatory network construction and characterization in Arabidopsis. , 2018, , .		0
76	Probabilistic Margin-Aware Multi-Label Feature Selection by Preserving Spatial Consistency. , 2019, , .		0
77	Spatial mapping of single cells in the Drosophila embryo from transcriptomic data based on topological consistency. F1000Research, 2020, 9, 1014.	1.6	0
78	Functional evaluation and analysis of predicted miRNA-mRNA regulatory network. , 2012, , .		0
79	Spatial mapping of single cells in the Drosophila embryo from transcriptomic data based on topological consistency. F1000Research, 2020, 9, 1014.	1.6	0