

Jianhua Ruan

List of Publications by Year in descending order

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Version: 2024-02-01

79
papers

3,007
citations

257101

24
h-index

174990

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. <i>Nature Biotechnology</i> , 2013, 31, 126-134.	9.4	341
2	Characterization and Identification of MicroRNA Core Promoters in Four Model Species. <i>PLoS Computational Biology</i> , 2007, 3, e37.	1.5	273
3	A general co-expression network-based approach to gene expression analysis: comparison and applications. <i>BMC Systems Biology</i> , 2010, 4, 8.	3.0	226
4	An Iterated loop matching approach to the prediction of RNA secondary structures with pseudoknots. <i>Bioinformatics</i> , 2004, 20, 58-66.	1.8	213
5	Identifying network communities with a high resolution. <i>Physical Review E</i> , 2008, 77, 016104.	0.8	163
6	A novel link prediction algorithm for reconstructing protein-protein interaction networks by topological similarity. <i>Bioinformatics</i> , 2013, 29, 355-364.	1.8	160
7	Cis-regulatory element based targeted gene finding: genome-wide identification of abscisic acid- and abiotic stress-responsive genes in <i>Arabidopsis thaliana</i> . <i>Bioinformatics</i> , 2005, 21, 3074-3081.	1.8	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. <i>Genome Biology</i> , 2008, 9, R148.	13.9	94
10	Alterations in the placental methylome with maternal obesity and evidence for metabolic regulation. <i>PLoS ONE</i> , 2017, 12, e0186115.	1.1	89
11	Enhancer reprogramming driven by high-order assemblies of transcription factors promotes phenotypic plasticity and breast cancer endocrine resistance. <i>Nature Cell Biology</i> , 2020, 22, 701-715.	4.6	84
12	The regulatory repertoire of PLZF and SALL4 in undifferentiated spermatogonia. <i>Development (Cambridge)</i> , 2016, 143, 1893-906.	1.2	69
13	Plasticity of the Systemic Inflammatory Response to Acute Infection during Critical Illness: Development of the Riboleukogram. <i>PLoS ONE</i> , 2008, 3, e1564.	1.1	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. <i>Journal of Biological Chemistry</i> , 2011, 286, 37063-37066.	1.6	68
15	Intratumoral CD56bright natural killer cells are associated with improved survival in bladder cancer. <i>Oncotarget</i> , 2018, 9, 36492-36502.	0.8	60
16	Building and analyzing protein interactome networks by cross-species comparisons. <i>BMC Systems Biology</i> , 2010, 4, 36.	3.0	55
17	Comprehensive methylome analysis of ovarian tumors reveals hedgehog signaling pathway regulators as prognostic DNA methylation biomarkers. <i>Epigenetics</i> , 2013, 8, 624-634.	1.3	51
18	A Network of Conserved Damage Survival Pathways Revealed by a Genomic RNAi Screen. <i>PLoS Genetics</i> , 2009, 5, e1000527.	1.5	47

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19	EpCAM-Regulated Transcription Exerts Influences on Nanomechanical Properties of Endometrial Cancer Cells That Promote Epithelial-to-Mesenchymal Transition. <i>Cancer Research</i> , 2016, 76, 6171-6182.	0.4	46
20	Promoter Hypomethylation of EpCAM-Regulated <i>Bone Morphogenetic Protein</i> Gene Family in Recurrent Endometrial Cancer. <i>Clinical Cancer Research</i> , 2013, 19, 6272-6285.	3.2	37
21	A personalized committee classification approach to improving prediction of breast cancer metastasis. <i>Bioinformatics</i> , 2014, 30, 1858-1866.	1.8	34
22	ILM: a web server for predicting RNA secondary structures with pseudoknots. <i>Nucleic Acids Research</i> , 2004, 32, W146-W149.	6.5	32
23	Manipulation of the Plant Host by the Geminivirus AC2/C2 Protein, a Central Player in the Infection Cycle. <i>Frontiers in Plant Science</i> , 2020, 11, 591.	1.7	32
24	Regulation of adipose oestrogen output by mechanical stress. <i>Nature Communications</i> , 2013, 4, 1821.	5.8	31
25	Pathway Enrichment Analysis with Networks. <i>Genes</i> , 2017, 8, 246.	1.0	30
26	Cell density-dependent transcriptional activation of endocrine-related genes in human adipose tissue-derived stem cells. <i>Experimental Cell Research</i> , 2010, 316, 2087-2098.	1.2	26
27	A Steiner tree-based method for biomarker discovery and classification in breast cancer metastasis. <i>BMC Genomics</i> , 2012, 13, S8.	1.2	25
28	Genetic and Genomic Analyses of RNA Polymerase II-pausing Factor in Regulation of Mammalian Transcription and Cell Growth. <i>Journal of Biological Chemistry</i> , 2011, 286, 36248-36257.	1.6	24
29	A bi-dimensional regression tree approach to the modeling of gene expression regulation. <i>Bioinformatics</i> , 2006, 22, 332-340.	1.8	23
30	Computational modeling of <i>in vivo</i> and <i>in vitro</i> protein-DNA interactions by multiple instance learning. <i>Bioinformatics</i> , 2017, 33, 2097-2105.	1.8	20
31	Genetic suppression reveals DNA repair-independent antagonism between BRCA1 and COBRA1 in mammary gland development. <i>Nature Communications</i> , 2016, 7, 10913.	5.8	19
32	A particle swarm optimization-based algorithm for finding gapped motifs. <i>BioData Mining</i> , 2010, 3, 9.	2.2	16
33	Adipokines Deregulate Cellular Communication via Epigenetic Repression of <i>Gap Junction</i> Loci in Obese Endometrial Cancer. <i>Cancer Research</i> , 2019, 79, 196-208.	0.4	16
34	A systems biology approach to the identification and analysis of transcriptional regulatory networks in osteocytes. <i>BMC Bioinformatics</i> , 2009, 10, S5.	1.2	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. <i>BMC Plant Biology</i> , 2014, 14, 302.	1.6	15

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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. <i>Cancers</i> , 2019, 11, 1910.	1.7	14
40	A novel algorithm for network-based prediction of cancer recurrence. <i>Genomics</i> , 2019, 111, 17-23.	1.3	14
41	A genome-wide cis-regulatory element discovery method based on promoter sequences and gene co-expression networks. <i>BMC Genomics</i> , 2013, 14, S4.	1.2	13
42	Network-Based Single-Cell RNA-Seq Data Imputation Enhances Cell Type Identification. <i>Genes</i> , 2020, 11, 377.	1.0	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. <i>International Journal of Computational Biology and Drug Design</i> , 2009, 2, 323.	0.3	11
46	A Top-Performing Algorithm for the DREAM3 Gene Expression Prediction Challenge. <i>PLoS ONE</i> , 2010, 5, e8944.	1.1	10
47	A structure-based Multiple-Instance Learning approach to predicting in vitro transcription factor-DNA interaction. <i>BMC Genomics</i> , 2015, 16, S3.	1.2	10
48	Systematic identification of functional modules and cis-regulatory elements in <i>Arabidopsis thaliana</i> . <i>BMC Bioinformatics</i> , 2011, 12, S2.	1.2	8
49	Comparative evaluation of network features for the prediction of breast cancer metastasis. <i>BMC Medical Genomics</i> , 2020, 13, 40.	0.7	8
50	2-Hydroxyglutarate destabilizes chromatin regulatory landscape and lineage fidelity to promote cellular heterogeneity. <i>Cell Reports</i> , 2022, 38, 110220.	2.9	8
51	CAGER: classification analysis of gene expression regulation using multiple information sources. <i>BMC Bioinformatics</i> , 2005, 6, 114.	1.2	6
52	An ensemble learning approach to reverse-engineering transcriptional regulatory networks from time-series gene expression data. <i>BMC Genomics</i> , 2009, 10, S8.	1.2	5
53	Logo2PWM: a tool to convert sequence logo to position weight matrix. <i>BMC Genomics</i> , 2017, 18, 709.	1.2	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.	1.2	4
56	Robust edge-based biomarker discovery improves prediction of breast cancer metastasis. BMC Bioinformatics, 2020, 21, 359.	1.2	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.	1.9	4
58	Finding Gapped Motifs by a Novel Evolutionary Algorithm. Lecture Notes in Computer Science, 2010, , 50-61.	1.0	4
59	EGFR-Dependent Regulated Intramembrane Proteolysis of EpCAMâ€™Response. Cancer Research, 2017, 77, 1777-1777.	0.4	3
60	Utilizing networks for differential analysis of chromatin interactions. Journal of Bioinformatics and Computational Biology, 2017, 15, 1740008.	0.3	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.	0.9	2
64	Probabilistic Topic and Role Model for Information Diffusion in Social Network. Lecture Notes in Computer Science, 2018, , 3-15.	1.0	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.	0.7	1
67	The International Conference on Intelligent Biology and Medicine (ICIBM) 2016: from big data to big analytical tools. BMC Bioinformatics, 2017, 18, 405.	1.2	1
68	The International Conference on Intelligent Biology and Medicine (ICIBM) 2018: bioinformatics towards translational applications. BMC Bioinformatics, 2018, 19, 492.	1.2	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

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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.	0.8	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.	0.8	0