

# Jianhua Ruan

## List of Publications by Year in descending order

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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	Construction and Evaluation of Robust Interpretation Models for Breast Cancer Metastasis Prediction. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 1344-1353.	1.9	4
2	2-Hydroxyglutarate destabilizes chromatin regulatory landscape and lineage fidelity to promote cellular heterogeneity. <i>Cell Reports</i> , 2022, 38, 110220.	2.9	8
3	Robust edge-based biomarker discovery improves prediction of breast cancer metastasis. <i>BMC Bioinformatics</i> , 2020, 21, 359.	1.2	4
4	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
5	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
6	Comparative evaluation of network features for the prediction of breast cancer metastasis. <i>BMC Medical Genomics</i> , 2020, 13, 40.	0.7	8
7	Network-Based Single-Cell RNA-Seq Data Imputation Enhances Cell Type Identification. <i>Genes</i> , 2020, 11, 377.	1.0	13
8	Spatial mapping of single cells in the Drosophila embryo from transcriptomic data based on topological consistency. <i>F1000Research</i> , 2020, 9, 1014.	0.8	0
9	Spatial mapping of single cells in the Drosophila embryo from transcriptomic data based on topological consistency. <i>F1000Research</i> , 2020, 9, 1014.	0.8	0
10	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
11	A Novel Multiple Classifier Generation and Combination Framework Based on Fuzzy Clustering and Individualized Ensemble Construction. , 2019, , .		1
12	Probabilistic Margin-Aware Multi-Label Feature Selection by Preserving Spatial Consistency. , 2019, , .		0
13	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
14	A novel algorithm for network-based prediction of cancer recurrence. <i>Genomics</i> , 2019, 111, 17-23.	1.3	14
15	The International Conference on Intelligent Biology and Medicine (ICIBM) 2018: bioinformatics towards translational applications. <i>BMC Bioinformatics</i> , 2018, 19, 492.	1.2	1
16	Semi-Supervised Multi-Label Feature Selection by Preserving Feature-Label Space Consistency. , 2018, , .		15
17	An integrative approach to transcriptional co-regulatory network construction and characterization in Arabidopsis. , 2018, , .		0
18	Probabilistic Topic and Role Model for Information Diffusion in Social Network. <i>Lecture Notes in Computer Science</i> , 2018, , 3-15.	1.0	2

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19	Intratumoral CD56bright natural killer cells are associated with improved survival in bladder cancer. <i>Oncotarget</i> , 2018, 9, 36492-36502.	0.8	60
20	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
21	EGFR-Dependent Regulated Intramembrane Proteolysis of EpCAM <sup>+</sup> Response. <i>Cancer Research</i> , 2017, 77, 1777-1777.	0.4	3
22	Utilizing networks for differential analysis of chromatin interactions. <i>Journal of Bioinformatics and Computational Biology</i> , 2017, 15, 1740008.	0.3	3
23	The International Conference on Intelligent Biology and Medicine (ICIBM) 2016: from big data to big analytical tools. <i>BMC Bioinformatics</i> , 2017, 18, 405.	1.2	1
24	Pathway Enrichment Analysis with Networks. <i>Genes</i> , 2017, 8, 246.	1.0	30
25	Alterations in the placental methylome with maternal obesity and evidence for metabolic regulation. <i>PLoS ONE</i> , 2017, 12, e0186115.	1.1	89
26	The International Conference on Intelligent Biology and Medicine (ICIBM) 2016: putting systems biology to work. <i>BMC Systems Biology</i> , 2017, 11, 88.	3.0	0
27	The International Conference on Intelligent Biology and Medicine (ICIBM) 2016: summary and innovation in genomics. <i>BMC Genomics</i> , 2017, 18, 703.	1.2	4
28	Logo2PWM: a tool to convert sequence logo to position weight matrix. <i>BMC Genomics</i> , 2017, 18, 709.	1.2	5
29	The regulatory repertoire of PLZF and SALL4 in undifferentiated spermatogonia. <i>Development (Cambridge)</i> , 2016, 143, 1893-906.	1.2	69
30	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
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	Structure-based prediction of drug side effects using a novel classification algorithm. <i>International Journal of Computational Biology and Drug Design</i> , 2016, 9, 87.	0.3	0
33	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
34	Frontiers in Integrative Genomics and Translational Bioinformatics. <i>BioMed Research International</i> , 2015, 2015, 1-3.	0.9	2
35	Altered expression of Arabidopsis genes in response to a multifunctional geminivirus pathogenicity protein. <i>BMC Plant Biology</i> , 2014, 14, 302.	1.6	15
36	A personalized committee classification approach to improving prediction of breast cancer metastasis. <i>Bioinformatics</i> , 2014, 30, 1858-1866.	1.8	34

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37	A genome-wide cis-regulatory element discovery method based on promoter sequences and gene co-expression networks. BMC Genomics, 2013, 14, S4.	1.2	13
38	Evaluation of methods for modeling transcription factor sequence specificity. Nature Biotechnology, 2013, 31, 126-134.	9.4	341
39	Computational Methods for Transcriptional Regulatory Networks. , 2013, , 468-473.		0
40	An ensemble approach for drug side effect prediction. , 2013, , 440-445.		15
41	A novel link prediction algorithm for reconstructing protein-protein interaction networks by topological similarity. Bioinformatics, 2013, 29, 355-364.	1.8	160
42	Regulation of adipose oestrogen output by mechanical stress. Nature Communications, 2013, 4, 1821.	5.8	31
43	Fully automated protein complex prediction based on topological similarity and community structure. Proteome Science, 2013, 11, S9.	0.7	1
44	Comprehensive methylome analysis of ovarian tumors reveals hedgehog signaling pathway regulators as prognostic DNA methylation biomarkers. Epigenetics, 2013, 8, 624-634.	1.3	51
45	Promoter Hypomethylation of EpCAM-Regulated <i>Bone Morphogenetic Protein</i> Gene Family in Recurrent Endometrial Cancer. Clinical Cancer Research, 2013, 19, 6272-6285.	3.2	37
46	Network-based pathway enrichment analysis. , 2013, , 218-221.		12
47	Network-based classification of recurrent endometrial cancers using high-throughput DNA methylation data. , 2012, , .		2
48	A random walk based approach for improving protein-protein interaction network and protein complex prediction. , 2012, , .		2
49	A Steiner tree-based method for biomarker discovery and classification in breast cancer metastasis. BMC Genomics, 2012, 13, S8.	1.2	25
50	A genome-wide cis-regulatory element discovery method based on promoter sequences and gene co-expression networks. , 2012, , .		1
51	A novel approach for cancer outcome prediction using personalized classifier. , 2012, , .		1
52	Functional evaluation and analysis of predicted miRNA-mRNA regulatory network. , 2012, , .		0
53	Identification of biomarkers in breast cancer metastasis by integrating protein-protein interaction network and gene expression data. , 2011, , .		4
54	Systematic identification of functional modules and cis-regulatory elements in Arabidopsis thaliana. BMC Bioinformatics, 2011, 12, S2.	1.2	8

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55	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
56	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
57	Building and analyzing protein interactome networks by cross-species comparisons. <i>BMC Systems Biology</i> , 2010, 4, 36.	3.0	55
58	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
59	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
60	A particle swarm optimization-based algorithm for finding gapped motifs. <i>BioData Mining</i> , 2010, 3, 9.	2.2	16
61	A Top-Performing Algorithm for the DREAM3 Gene Expression Prediction Challenge. <i>PLoS ONE</i> , 2010, 5, e8944.	1.1	10
62	Promoter prediction based on a multiple instance learning scheme. , 2010, , .		1
63	Finding Gapped Motifs by a Novel Evolutionary Algorithm. <i>Lecture Notes in Computer Science</i> , 2010, , 50-61.	1.0	4
64	A Network of Conserved Damage Survival Pathways Revealed by a Genomic RNAi Screen. <i>PLoS Genetics</i> , 2009, 5, e1000527.	1.5	47
65	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
66	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
67	A Fully Automated Method for Discovering Community Structures in High Dimensional Data. , 2009, , 968-973.		11
68	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
69	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
70	A Particle Swarm Optimization algorithm for finding DNA sequence motifs. , 2008, , .		14
71	Identifying network communities with a high resolution. <i>Physical Review E</i> , 2008, 77, 016104.	0.8	163
72	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

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73	Characterization and Identification of MicroRNA Core Promoters in Four Model Species. PLoS Computational Biology, 2007, 3, e37.	1.5	273
74	An Efficient Spectral Algorithm for Network Community Discovery and Its Applications to Biological and Social Networks. , 2007, , .		97
75	A bi-dimensional regression tree approach to the modeling of gene expression regulation. Bioinformatics, 2006, 22, 332-340.	1.8	23
76	CAGER: classification analysis of gene expression regulation using multiple information sources. BMC Bioinformatics, 2005, 6, 114.	1.2	6
77	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.	1.8	151
78	An Iterated loop matching approach to the prediction of RNA secondary structures with pseudoknots. Bioinformatics, 2004, 20, 58-66.	1.8	213
79	ILM: a web server for predicting RNA secondary structures with pseudoknots. Nucleic Acids Research, 2004, 32, W146-W149.	6.5	32