

Weixiong Zhang

List of Publications by Year in descending order

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139
papers

7,678
citations

57758

44
h-index

58581

82
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146
all docs

146
docs citations

146
times ranked

10118
citing authors

#	ARTICLE	IF	CITATIONS
1	Graph Triple-Attention Network for Disease-Related LncRNA Prediction. IEEE Journal of Biomedical and Health Informatics, 2022, 26, 2839-2849.	6.3	14
2	Chromosome-scale genome assembly provides insights into speciation of allotetraploid and massive biomass accumulation of elephant grass (<i>Pennisetum purpureum</i> Schum.). Molecular Ecology Resources, 2022, 22, 2363-2378.	4.8	11
3	Response to: Significance and stability of deep learning-based identification of subtypes within major psychiatric disorders. Molecular Psychiatry (2022). Molecular Psychiatry, 2022, 27, 3569-3570.	7.9	2
4	Identifying and validating subtypes within major psychiatric disorders based on frontal-posterior functional imbalance via deep learning. Molecular Psychiatry, 2021, 26, 2991-3002.	7.9	40
5	ARPM-net: A novel CNN-based adversarial method with Markov random field enhancement for prostate and organs at risk segmentation in pelvic CT images. Medical Physics, 2021, 48, 227-237.	3.0	18
6	Robust Detection of Link Communities With Summary Description in Social Networks. IEEE Transactions on Knowledge and Data Engineering, 2021, 33, 2737-2749.	5.7	23
7	A Survey of Community Detection Approaches: From Statistical Modeling to Deep Learning. IEEE Transactions on Knowledge and Data Engineering, 2021, , 1-1.	5.7	118
8	Canonical and Interior Circular RNAs Function as Competing Endogenous RNAs in Psoriatic Skin. International Journal of Molecular Sciences, 2021, 22, 5182.	4.1	8
9	Semi-supervised semantic segmentation of prostate and organs-at-risk on 3D pelvic CT images. Biomedical Physics and Engineering Express, 2021, 7, 065023.	1.2	5
10	GmoDetector: An accurate and efficient GMO identification approach and its applications. Food Research International, 2021, 149, 110662.	6.2	3
11	Weaving attention U-net: A novel hybrid CNN and attention-based method for organs-at-risk segmentation in head and neck CT images. Medical Physics, 2021, 48, 7052-7062.	3.0	15
12	Identification of MicroRNAs and Natural Antisense Transcript-Originated Endogenous siRNAs from Small-RNA Sequencing Data. Methods in Molecular Biology, 2021, 2170, 125-131.	0.9	0
13	Inferring Disease-Associated microRNAs in Heterogeneous Networks with Node Attributes. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 1019-1031.	3.0	18
14	Interior circular RNA. RNA Biology, 2020, 17, 87-97.	3.1	22
15	Effects of early cold stress on gene expression in <i>Chlamydomonas reinhardtii</i> . Genomics, 2020, 112, 1128-1138.	2.9	27
16	Modeling with Node Popularities for Autonomous Overlapping Community Detection. ACM Transactions on Intelligent Systems and Technology, 2020, 11, 1-23.	4.5	9
17	Community-Centric Graph Convolutional Network for Unsupervised Community Detection. , 2020, , .		36
18	Predicting gamma passing rates for portal dosimetry-based IMRT QA using machine learning. Medical Physics, 2019, 46, 4666-4675.	3.0	69

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19	Application of high-throughput amplicon sequencing-based SSR genotyping in genetic background screening. BMC Genomics, 2019, 20, 444.	2.8	10
20	Autonomous Semantic Community Detection via Adaptively Weighted Low-rank Approximation. ACM Transactions on Multimedia Computing, Communications and Applications, 2019, 15, 1-22.	4.3	6
21	Network-Specific Variational Auto-Encoder for Embedding in Attribute Networks. , 2019, , .		26
22	New class of transcription factors controls flagellar assembly by recruiting RNA polymerase II in <i>Chlamydomonas</i> . Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 4435-4440.	7.1	14
23	A non-negative matrix factorization based method for predicting disease-associated miRNAs in miRNA-disease bilayer network. Bioinformatics, 2018, 34, 267-277.	4.1	48
24	Transcriptional insights into the pyramided resistance to rice bacterial blight. Scientific Reports, 2018, 8, 12358.	3.3	5
25	A Fast Algorithm for Generalized Arc Consistency of the Alldifferent Constraint. , 2018, , .		4
26	Integrative Network Embedding via Deep Joint Reconstruction. , 2018, , .		13
27	An accurate and efficient method for large-scale SSR genotyping and applications. Nucleic Acids Research, 2017, 45, e88-e88.	14.5	47
28	Identification of leader and self-organizing communities in complex networks. Scientific Reports, 2017, 7, 704.	3.3	7
29	Detecting and characterizing microRNAs of diverse genomic origins via miRvial. Nucleic Acids Research, 2017, 45, e176-e176.	14.5	6
30	An efficient algorithm for finding all possible input nodes for controlling complex networks. Scientific Reports, 2017, 7, 10677.	3.3	12
31	Comprehensive definition of genome features in <i>Spirodela polyrhiza</i> by high-depth physical mapping and short-read DNA sequencing strategies. Plant Journal, 2017, 89, 617-635.	5.7	115
32	MicroRNA-like RNAs from the same miRNA precursors play a role in cassava chilling responses. Scientific Reports, 2017, 7, 17135.	3.3	9
33	Latitudinal Clines of the Human Vitamin D Receptor and Skin Color Genes. G3: Genes, Genomes, Genetics, 2016, 6, 1251-1266.	1.8	23
34	Large-scale rewiring of innate immunity circuitry and microRNA regulation during initial rice blast infection. Scientific Reports, 2016, 6, 25493.	3.3	27
35	The complete parsimony haplotype inference problem and algorithms based on integer programming, branch-and-bound and Boolean satisfiability. Journal of Discrete Algorithms, 2016, 37, 68-83.	0.7	1
36	<i>Bacillus cereus</i> AR156 primes induced systemic resistance by suppressing miR825/825* and activating defense-related genes in <i>Arabidopsis</i> . Journal of Integrative Plant Biology, 2016, 58, 426-439.	8.5	53

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37	Endogenous Small-Noncoding RNAs and Potential Functions in Desiccation Tolerance in <i>Physcomitrella Patens</i> . <i>Scientific Reports</i> , 2016, 6, 30118.	3.3	13
38	Expansion and stress responses of AP2/EREBP superfamily in <i>Brachypodium Distachyon</i> . <i>Scientific Reports</i> , 2016, 6, 21623.	3.3	82
39	Identification of hybrid node and link communities in complex networks. <i>Scientific Reports</i> , 2015, 5, 8638.	3.3	36
40	Rice Xa21 primed genes and pathways that are critical for combating bacterial blight infection. <i>Scientific Reports</i> , 2015, 5, 12165.	3.3	36
41	Potential functions of microRNAs in starch metabolism and development revealed by miRNA transcriptome profiling of cassava cultivars and their wild progenitor. <i>BMC Plant Biology</i> , 2015, 15, 33.	3.6	49
42	Human gephyrin is encompassed within giant functional noncoding yin-yang sequences. <i>Nature Communications</i> , 2015, 6, 6534.	12.8	15
43	Ten Simple Rules for Writing Research Papers. <i>PLoS Computational Biology</i> , 2014, 10, e1003453.	3.2	18
44	Allele-Specific Network Reveals Combinatorial Interaction That Transcends Small Effects in Psoriasis GWAS. <i>PLoS Computational Biology</i> , 2014, 10, e1003766.	3.2	25
45	A meta-analysis revealed insights into the sources, conservation and impact of microRNA 5'-isoforms in four model species. <i>Nucleic Acids Research</i> , 2014, 42, 1427-1441.	14.5	23
46	Identifying Cis-Regulatory Elements and Modules Using Conditional Random Fields. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 73-82.	3.0	3
47	Cassava genome from a wild ancestor to cultivated varieties. <i>Nature Communications</i> , 2014, 5, 5110.	12.8	230
48	Endogenous small-noncoding RNAs and their roles in chilling response and stress acclimation in Cassava. <i>BMC Genomics</i> , 2014, 15, 634.	2.8	46
49	Chilling acclimation provides immunity to stress by altering regulatory networks and inducing genes with protective functions in Cassava. <i>BMC Plant Biology</i> , 2014, 14, 207.	3.6	47
50	MicroRNAs in normal and psoriatic skin. <i>Physiological Genomics</i> , 2014, 46, 113-122.	2.3	28
51	A Marginalized Denoising Method for Link Prediction in Relational Data. , 2014, , .		11
52	Systems and Evolutionary Characterization of MicroRNAs and Their Underlying Regulatory Networks in Soybean Cotyledons. <i>PLoS ONE</i> , 2014, 9, e86153.	2.5	37
53	DNA methylation polymorphism and stability in Chinese indica hybrid rice. <i>Science China Life Sciences</i> , 2013, 56, 1097-1106.	4.9	8
54	A SAT-based approach to cost-sensitive temporally expressive planning. <i>ACM Transactions on Intelligent Systems and Technology</i> , 2013, 5, 1-35.	4.5	2

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55	Integrative Analysis Using Module-Guided Random Forests Reveals Correlated Genetic Factors Related to Mouse Weight. PLoS Computational Biology, 2013, 9, e1002956.	3.2	24
56	Noncanonical microRNAs and endogenous siRNAs in normal and psoriatic human skin. Human Molecular Genetics, 2013, 22, 737-748.	2.9	43
57	Do transgenesis and marker-assisted backcross breeding produce substantially equivalent plants? - A comparative study of transgenic and backcross rice carrying bacterial blight resistant gene Xa21. BMC Genomics, 2013, 14, 738.	2.8	24
58	SeqTar: an effective method for identifying microRNA guided cleavage sites from degradome of polyadenylated transcripts in plants. Nucleic Acids Research, 2012, 40, e28-e28.	14.5	94
59	Genome-wide analysis of plant nat-siRNAs reveals insights into their distribution, biogenesis and function. Genome Biology, 2012, 13, R20.	9.6	120
60	Discovering link communities in complex networks by exploiting link dynamics. Journal of Statistical Mechanics: Theory and Experiment, 2012, 2012, P10015.	2.3	18
61	Structural features based genome-wide characterization and prediction of nucleosome organization. BMC Bioinformatics, 2012, 13, 49.	2.6	13
62	Noncanonical MicroRNAs and Endogenous siRNAs in Lytic Infection of Murine Gammaherpesvirus. PLoS ONE, 2012, 7, e47863.	2.5	20
63	Identification of MicroRNAs and Natural Antisense Transcript-Originated Endogenous siRNAs from Small-RNA Deep Sequencing Data. Methods in Molecular Biology, 2012, 883, 221-227.	0.9	6
64	Behavioral plasticity in honey bees is associated with differences in brain microRNA transcriptome. Genes, Brain and Behavior, 2012, 11, 660-670.	2.2	87
65	Deep sequencing of small RNAs from human skin reveals major alterations in the psoriasis miRNAome. Human Molecular Genetics, 2011, 20, 4025-4040.	2.9	213
66	Bacteria-responsive microRNAs regulate plant innate immunity by modulating plant hormone networks. Plant Molecular Biology, 2011, 75, 93-105.	3.9	237
67	Deep sequencing of small RNA libraries reveals dynamic regulation of conserved and novel microRNAs and microRNA-stars during silkworm development. BMC Genomics, 2010, 11, 52.	2.8	178
68	Analysis of Alzheimer's disease severity across brain regions by topological analysis of gene co-expression networks. BMC Systems Biology, 2010, 4, 136.	3.0	77
69	A general co-expression network-based approach to gene expression analysis: comparison and applications. BMC Systems Biology, 2010, 4, 8.	3.0	226
70	Transcriptome-wide identification of microRNA targets in rice. Plant Journal, 2010, 62, 742-759.	5.7	370
71	siRNAs from miRNA sites mediate DNA methylation of target genes. Nucleic Acids Research, 2010, 38, 6883-6894.	14.5	153
72	Conservation and divergence of microRNAs and their functions in Euphorbiaceous plants. Nucleic Acids Research, 2010, 38, 981-995.	14.5	110

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73	Identification of Novel MicroRNA-Like Molecules Generated from Herpesvirus and Host tRNA Transcripts. Journal of Virology, 2010, 84, 10344-10353.	3.4	79
74	ANIMAL MICRORNA TARGET PREDICTION USING DIVERSE SEQUENCE-SPECIFIC DETERMINANTS. Journal of Bioinformatics and Computational Biology, 2010, 08, 763-788.	0.8	21
75	Promoter prediction based on a multiple instance learning scheme. , 2010, , .		1
76	SplittingHeirs. , 2010, , .		2
77	Multiple distinct small RNAs originate from the same microRNA precursors. Genome Biology, 2010, 11, R81.	9.6	118
78	A SAT Based Effective Algorithm for the Directed Hamiltonian Cycle Problem. Lecture Notes in Computer Science, 2010, , 216-227.	1.3	1
79	Gene Reachability Using Page Ranking on Gene Co-expression Networks. , 2010, , 557-568.		0
80	How frugal is mother nature with haplotypes?. Bioinformatics, 2009, 25, 68-74.	4.1	10
81	Cloning, characterization and expression analysis of porcine microRNAs. BMC Genomics, 2009, 10, 65.	2.8	94
82	An ensemble learning approach to reverse-engineering transcriptional regulatory networks from time-series gene expression data. BMC Genomics, 2009, 10, S8.	2.8	5
83	Cloning and characterization of small RNAs from <i>Medicago truncatula</i> reveals four novel legume-specific microRNA families. New Phytologist, 2009, 184, 85-98.	7.3	162
84	Long-distance mutual exclusion for planning. Artificial Intelligence, 2009, 173, 365-391.	5.8	15
85	Genetic Control of Human Brain Transcript Expression in Alzheimer Disease. American Journal of Human Genetics, 2009, 84, 445-458.	6.2	290
86	Integrating Gene Expression and Phenotypic Information to Analyze Alzheimer's Disease. Journal of Alzheimer's Disease, 2009, 16, 73-84.	2.6	10
87	Complete Parsimony Haplotype Inference Problem and Algorithms. Lecture Notes in Computer Science, 2009, , 337-348.	1.3	3
88	Identification of novel and candidate miRNAs in rice by high throughput sequencing. BMC Plant Biology, 2008, 8, 25.	3.6	436
89	Variations in the transcriptome of Alzheimer's disease reveal molecular networks involved in cardiovascular diseases. Genome Biology, 2008, 9, R148.	9.6	94
90	Identification of cold-inducible microRNAs in plants by transcriptome analysis. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2008, 1779, 780-788.	1.9	272

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91	Genome-wide identification and analysis of small RNAs originated from natural antisense transcripts in <i>Oryza sativa</i> . <i>Genome Research</i> , 2008, 19, 70-78.	5.5	107
92	MicroRNA prediction with a novel ranking algorithm based on random walks. <i>Bioinformatics</i> , 2008, 24, i50-i58.	4.1	70
93	Identifying network communities with a high resolution. <i>Physical Review E</i> , 2008, 77, 016104.	2.1	163
94	Plasticity of the Systemic Inflammatory Response to Acute Infection during Critical Illness: Development of the Riboleukogram. <i>PLoS ONE</i> , 2008, 3, e1564.	2.5	68
95	PlantQTL-GE: a database system for identifying candidate genes in rice and <i>Arabidopsis</i> by gene expression and QTL information. <i>Nucleic Acids Research</i> , 2007, 35, D879-D882.	14.5	24
96	Characterization and Identification of MicroRNA Core Promoters in Four Model Species. <i>PLoS Computational Biology</i> , 2007, 3, e37.	3.2	273
97	An Efficient Spectral Algorithm for Network Community Discovery and Its Applications to Biological and Social Networks. , 2007, , .		97
98	Gene expression profiling and machine learning to understand and predict primary graft dysfunction. , 2007, , .		0
99	Expression Profiling of Human Donor Lungs to Understand Primary Graft Dysfunction After Lung Transplantation. <i>American Journal of Transplantation</i> , 2007, 7, 2396-2405.	4.7	37
100	An Iterative Method for Selecting Degenerate Multiplex PCR Primers. <i>Methods in Molecular Biology</i> , 2007, 402, 245-267.	0.9	11
101	A steganalysis-based approach to comprehensive identification and characterization of functional regulatory elements. <i>Genome Biology</i> , 2006, 7, R49.	9.6	25
102	Data Mining Methods for Modeling Gene Expression Regulation and Their Applications. <i>IEEE International Conference on Data Mining</i> , 2006, , .	0.0	0
103	Cut-and-solve: An iterative search strategy for combinatorial optimization problems. <i>Artificial Intelligence</i> , 2006, 170, 714-738.	5.8	60
104	A bi-dimensional regression tree approach to the modeling of gene expression regulation. <i>Bioinformatics</i> , 2006, 22, 332-340.	4.1	23
105	An Efficient Hybrid Strategy for Temporal Planning. <i>Lecture Notes in Computer Science</i> , 2006, , 273-287.	1.3	3
106	Identification and Evaluation of Functional Modules in Gene Co-expression Networks. <i>Lecture Notes in Computer Science</i> , 2006, , 57-76.	1.3	5
107	MaxSolver: An efficient exact algorithm for (weighted) maximum satisfiability. <i>Artificial Intelligence</i> , 2005, 164, 47-80.	5.8	46
108	Distributed stochastic search and distributed breakout: properties, comparison and applications to constraint optimization problems in sensor networks. <i>Artificial Intelligence</i> , 2005, 161, 55-87.	5.8	177

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109	CAGER: classification analysis of gene expression regulation using multiple information sources. BMC Bioinformatics, 2005, 6, 114.	2.6	6
110	Frontier search. Journal of the ACM, 2005, 52, 715-748.	2.2	63
111	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
112	WordSpy: identifying transcription factor binding motifs by building a dictionary and learning a grammar. Nucleic Acids Research, 2005, 33, W412-W416.	14.5	45
113	Computational Characterization and Identification of Core Promoters of MicroRNA Genes in C. elegans, H. sapiens and A. thaliana. , 2005, , 235-248.		0
114	An Iterated loop matching approach to the prediction of RNA secondary structures with pseudoknots. Bioinformatics, 2004, 20, 58-66.	4.1	213
115	ILM: a web server for predicting RNA secondary structures with pseudoknots. Nucleic Acids Research, 2004, 32, W146-W149.	14.5	32
116	Average-case analysis of best-first search in two representative directed acyclic graphs. Artificial Intelligence, 2004, 155, 183-206.	5.8	8
117	Configuration landscape analysis and backbone guided local search.. Artificial Intelligence, 2004, 158, 1-26.	5.8	64
118	Efficient Strategies for (Weighted) Maximum Satisfiability. Lecture Notes in Computer Science, 2004, , 690-705.	1.3	12
119	Distributed breakout algorithm for distributed constraint optimization problems -- DBArelax. , 2003, , .		4
120	Distributed problem solving in sensor networks. , 2002, , .		19
121	Iterative state-space reduction for flexible computation. Artificial Intelligence, 2001, 126, 109-138.	5.8	3
122	Heuristic search in artificial intelligence. Artificial Intelligence, 2001, 129, 1-4.	5.8	7
123	Phase Transitions and Backbones of 3-SAT and Maximum 3-SAT. Lecture Notes in Computer Science, 2001, , 153-167.	1.3	24
124	The Asymmetric Traveling Salesman Problem: Algorithms, Instance Generators, and Tests. Lecture Notes in Computer Science, 2001, , 32-59.	1.3	72
125	Towards Flexible Teamwork in Persistent Teams: Extended Report. Autonomous Agents and Multi-Agent Systems, 2000, 3, 159-183.	2.1	29
126	State-Space Search. , 1999, , .		17

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127	A note on the complexity of the asymmetric traveling salesman problem. Operations Research Letters, 1997, 20, 31-38.	0.7	6
128	A study of complexity transitions on the asymmetric traveling salesman problem. Artificial Intelligence, 1996, 81, 223-239.	5.8	71
129	Epsilon-transformation: exploiting phase transitions to solve combinatorial optimization problems. Artificial Intelligence, 1996, 81, 297-325.	5.8	15
130	Performance of linear-space search algorithms. Artificial Intelligence, 1995, 79, 241-292.	5.8	59
131	Parallel Heap Operations on an EREW PRAM. Journal of Parallel and Distributed Computing, 1994, 20, 248-255.	4.1	7
132	Building heaps in parallel. Information Processing Letters, 1991, 37, 355-358.	0.6	20
133	Optimal parallel quicksort on EREW PRAM. BIT Numerical Mathematics, 1991, 31, 69-74.	2.0	4
134	A faster optimal algorithm for the measure problem. Parallel Computing, 1991, 17, 683-687.	2.1	0
135	Efficient parallel algorithms for some integer problems. , 1991, , .		1
136	Heuristic tree search with nonparametric statistical inference methods. International Journal of Computer Mathematics, 1991, 38, 133-152.	1.8	4
137	Heuristic Tree Search Using Nonparametric Statistical Inference Methods. , 1991, , 205-225.		0
138	Towards flexible teamwork in persistent teams. , 0, , .		66
139	Association-Based Multiple Imputation in Multivariate Datasets: A Summary. , 0, , .		6