

Weixiong Zhang

List of Publications by Year in descending order

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139
papers

7,678
citations

66250

44
h-index

66518

82
g-index

146
all docs

146
docs citations

146
times ranked

11371
citing authors

#	ARTICLE	IF	CITATIONS
1	Graph Triple-Attention Network for Disease-Related LncRNA Prediction. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2022, 26, 2839-2849.	3.9	14
2	Chromosome-scale genome assembly provides insights into speciation of allotetraploid and massive biomass accumulation of elephant grass (<i>Pennisetum purpureum</i> Schum.). <i>Molecular Ecology Resources</i> , 2022, 22, 2363-2378.	2.2	11
3	Response to: Significance and stability of deep learning-based identification of subtypes within major psychiatric disorders. <i>Molecular Psychiatry</i> (2022). <i>Molecular Psychiatry</i> , 2022, 27, 3569-3570.	4.1	2
4	Identifying and validating subtypes within major psychiatric disorders based on frontal-posterior functional imbalance via deep learning. <i>Molecular Psychiatry</i> , 2021, 26, 2991-3002.	4.1	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. <i>Medical Physics</i> , 2021, 48, 227-237.	1.6	18
6	Robust Detection of Link Communities With Summary Description in Social Networks. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2021, 33, 2737-2749.	4.0	23
7	A Survey of Community Detection Approaches: From Statistical Modeling to Deep Learning. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2021, , 1-1.	4.0	118
8	Canonical and Interior Circular RNAs Function as Competing Endogenous RNAs in Psoriatic Skin. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5182.	1.8	8
9	Semi-supervised semantic segmentation of prostate and organs-at-risk on 3D pelvic CT images. <i>Biomedical Physics and Engineering Express</i> , 2021, 7, 065023.	0.6	5
10	GmoDetector: An accurate and efficient GMO identification approach and its applications. <i>Food Research International</i> , 2021, 149, 110662.	2.9	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. <i>Medical Physics</i> , 2021, 48, 7052-7062.	1.6	15
12	Identification of MicroRNAs and Natural Antisense Transcript-Originated Endogenous siRNAs from Small-RNA Sequencing Data. <i>Methods in Molecular Biology</i> , 2021, 2170, 125-131.	0.4	0
13	Inferring Disease-Associated microRNAs in Heterogeneous Networks with Node Attributes. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 17, 1019-1031.	1.9	18
14	Interior circular RNA. <i>RNA Biology</i> , 2020, 17, 87-97.	1.5	22
15	Effects of early cold stress on gene expression in <i>Chlamydomonas reinhardtii</i> . <i>Genomics</i> , 2020, 112, 1128-1138.	1.3	27
16	Modeling with Node Popularities for Autonomous Overlapping Community Detection. <i>ACM Transactions on Intelligent Systems and Technology</i> , 2020, 11, 1-23.	2.9	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. <i>Medical Physics</i> , 2019, 46, 4666-4675.	1.6	69

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19	Application of high-throughput amplicon sequencing-based SSR genotyping in genetic background screening. <i>BMC Genomics</i> , 2019, 20, 444.	1.2	10
20	Autonomous Semantic Community Detection via Adaptively Weighted Low-rank Approximation. <i>ACM Transactions on Multimedia Computing, Communications and Applications</i> , 2019, 15, 1-22.	3.0	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> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4435-4440.	3.3	14
23	A non-negative matrix factorization based method for predicting disease-associated miRNAs in miRNA-disease bilayer network. <i>Bioinformatics</i> , 2018, 34, 267-277.	1.8	48
24	Transcriptional insights into the pyramided resistance to rice bacterial blight. <i>Scientific Reports</i> , 2018, 8, 12358.	1.6	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. <i>Nucleic Acids Research</i> , 2017, 45, e88-e88.	6.5	47
28	Identification of leader and self-organizing communities in complex networks. <i>Scientific Reports</i> , 2017, 7, 704.	1.6	7
29	Detecting and characterizing microRNAs of diverse genomic origins via miRvial. <i>Nucleic Acids Research</i> , 2017, 45, e176-e176.	6.5	6
30	An efficient algorithm for finding all possible input nodes for controlling complex networks. <i>Scientific Reports</i> , 2017, 7, 10677.	1.6	12
31	Comprehensive definition of genome features in <i>Spirodela polyrhiza</i> by high-depth physical mapping and short-read DNA sequencing strategies. <i>Plant Journal</i> , 2017, 89, 617-635.	2.8	115
32	MicroRNA-like RNAs from the same miRNA precursors play a role in cassava chilling responses. <i>Scientific Reports</i> , 2017, 7, 17135.	1.6	9
33	Latitudinal Clines of the Human Vitamin D Receptor and Skin Color Genes. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1251-1266.	0.8	23
34	Large-scale rewiring of innate immunity circuitry and microRNA regulation during initial rice blast infection. <i>Scientific Reports</i> , 2016, 6, 25493.	1.6	27
35	The complete parsimony haplotype inference problem and algorithms based on integer programming, branch-and-bound and Boolean satisfiability. <i>Journal of Discrete Algorithms</i> , 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> . <i>Journal of Integrative Plant Biology</i> , 2016, 58, 426-439.	4.1	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.	1.6	13
38	Expansion and stress responses of AP2/EREBP superfamily in <i>Brachypodium Distachyon</i> . <i>Scientific Reports</i> , 2016, 6, 21623.	1.6	82
39	Identification of hybrid node and link communities in complex networks. <i>Scientific Reports</i> , 2015, 5, 8638.	1.6	36
40	Rice Xa21 primed genes and pathways that are critical for combating bacterial blight infection. <i>Scientific Reports</i> , 2015, 5, 12165.	1.6	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.	1.6	49
42	Human gephyrin is encompassed within giant functional noncoding yin-yang sequences. <i>Nature Communications</i> , 2015, 6, 6534.	5.8	15
43	Ten Simple Rules for Writing Research Papers. <i>PLoS Computational Biology</i> , 2014, 10, e1003453.	1.5	18
44	Allele-Specific Network Reveals Combinatorial Interaction That Transcends Small Effects in Psoriasis GWAS. <i>PLoS Computational Biology</i> , 2014, 10, e1003766.	1.5	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.	6.5	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.	1.9	3
47	Cassava genome from a wild ancestor to cultivated varieties. <i>Nature Communications</i> , 2014, 5, 5110.	5.8	230
48	Endogenous small-noncoding RNAs and their roles in chilling response and stress acclimation in Cassava. <i>BMC Genomics</i> , 2014, 15, 634.	1.2	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.	1.6	47
50	MicroRNAs in normal and psoriatic skin. <i>Physiological Genomics</i> , 2014, 46, 113-122.	1.0	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.	1.1	37
53	DNA methylation polymorphism and stability in Chinese indica hybrid rice. <i>Science China Life Sciences</i> , 2013, 56, 1097-1106.	2.3	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.	2.9	2

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55	Integrative Analysis Using Module-Guided Random Forests Reveals Correlated Genetic Factors Related to Mouse Weight. <i>PLoS Computational Biology</i> , 2013, 9, e1002956.	1.5	24
56	Noncanonical microRNAs and endogenous siRNAs in normal and psoriatic human skin. <i>Human Molecular Genetics</i> , 2013, 22, 737-748.	1.4	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. <i>BMC Genomics</i> , 2013, 14, 738.	1.2	24
58	SeqTar: an effective method for identifying microRNA guided cleavage sites from degradome of polyadenylated transcripts in plants. <i>Nucleic Acids Research</i> , 2012, 40, e28-e28.	6.5	94
59	Genome-wide analysis of plant nat-siRNAs reveals insights into their distribution, biogenesis and function. <i>Genome Biology</i> , 2012, 13, R20.	13.9	120
60	Discovering link communities in complex networks by exploiting link dynamics. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2012, 2012, P10015.	0.9	18
61	Structural features based genome-wide characterization and prediction of nucleosome organization. <i>BMC Bioinformatics</i> , 2012, 13, 49.	1.2	13
62	Noncanonical MicroRNAs and Endogenous siRNAs in Lytic Infection of Murine Gammaherpesvirus. <i>PLoS ONE</i> , 2012, 7, e47863.	1.1	20
63	Identification of MicroRNAs and Natural Antisense Transcript-Originated Endogenous siRNAs from Small-RNA Deep Sequencing Data. <i>Methods in Molecular Biology</i> , 2012, 883, 221-227.	0.4	6
64	Behavioral plasticity in honey bees is associated with differences in brain microRNA transcriptome. <i>Genes, Brain and Behavior</i> , 2012, 11, 660-670.	1.1	87
65	Deep sequencing of small RNAs from human skin reveals major alterations in the psoriasis miRNAome. <i>Human Molecular Genetics</i> , 2011, 20, 4025-4040.	1.4	213
66	Bacteria-responsive microRNAs regulate plant innate immunity by modulating plant hormone networks. <i>Plant Molecular Biology</i> , 2011, 75, 93-105.	2.0	237
67	Deep sequencing of small RNA libraries reveals dynamic regulation of conserved and novel microRNAs and microRNA-stars during silkworm development. <i>BMC Genomics</i> , 2010, 11, 52.	1.2	178
68	Analysis of Alzheimer's disease severity across brain regions by topological analysis of gene co-expression networks. <i>BMC Systems Biology</i> , 2010, 4, 136.	3.0	77
69	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
70	Transcriptome-wide identification of microRNA targets in rice. <i>Plant Journal</i> , 2010, 62, 742-759.	2.8	370
71	siRNAs from miRNA sites mediate DNA methylation of target genes. <i>Nucleic Acids Research</i> , 2010, 38, 6883-6894.	6.5	153
72	Conservation and divergence of microRNAs and their functions in Euphorbiaceous plants. <i>Nucleic Acids Research</i> , 2010, 38, 981-995.	6.5	110

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73	Identification of Novel MicroRNA-Like Molecules Generated from Herpesvirus and Host tRNA Transcripts. <i>Journal of Virology</i> , 2010, 84, 10344-10353.	1.5	79
74	ANIMAL MICRORNA TARGET PREDICTION USING DIVERSE SEQUENCE-SPECIFIC DETERMINANTS. <i>Journal of Bioinformatics and Computational Biology</i> , 2010, 08, 763-788.	0.3	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. <i>Genome Biology</i> , 2010, 11, R81.	13.9	118
78	A SAT Based Effective Algorithm for the Directed Hamiltonian Cycle Problem. <i>Lecture Notes in Computer Science</i> , 2010, , 216-227.	1.0	1
79	Gene Reachability Using Page Ranking on Gene Co-expression Networks. , 2010, , 557-568.		0
80	How frugal is mother nature with haplotypes?. <i>Bioinformatics</i> , 2009, 25, 68-74.	1.8	10
81	Cloning, characterization and expression analysis of porcine microRNAs. <i>BMC Genomics</i> , 2009, 10, 65.	1.2	94
82	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
83	Cloning and characterization of small RNAs from <i>Medicago truncatula</i> reveals four novel legume-specific microRNA families. <i>New Phytologist</i> , 2009, 184, 85-98.	3.5	162
84	Long-distance mutual exclusion for planning. <i>Artificial Intelligence</i> , 2009, 173, 365-391.	3.9	15
85	Genetic Control of Human Brain Transcript Expression in Alzheimer Disease. <i>American Journal of Human Genetics</i> , 2009, 84, 445-458.	2.6	290
86	Integrating Gene Expression and Phenotypic Information to Analyze Alzheimer's Disease. <i>Journal of Alzheimer's Disease</i> , 2009, 16, 73-84.	1.2	10
87	Complete Parsimony Haplotype Inference Problem and Algorithms. <i>Lecture Notes in Computer Science</i> , 2009, , 337-348.	1.0	3
88	Identification of novel and candidate miRNAs in rice by high throughput sequencing. <i>BMC Plant Biology</i> , 2008, 8, 25.	1.6	436
89	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
90	Identification of cold-inducible microRNAs in plants by transcriptome analysis. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2008, 1779, 780-788.	0.9	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.	2.4	107
92	MicroRNA prediction with a novel ranking algorithm based on random walks. <i>Bioinformatics</i> , 2008, 24, i50-i58.	1.8	70
93	Identifying network communities with a high resolution. <i>Physical Review E</i> , 2008, 77, 016104.	0.8	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.	1.1	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.	6.5	24
96	Characterization and Identification of MicroRNA Core Promoters in Four Model Species. <i>PLoS Computational Biology</i> , 2007, 3, e37.	1.5	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.	2.6	37
100	An Iterative Method for Selecting Degenerate Multiplex PCR Primers. <i>Methods in Molecular Biology</i> , 2007, 402, 245-267.	0.4	11
101	A steganalysis-based approach to comprehensive identification and characterization of functional regulatory elements. <i>Genome Biology</i> , 2006, 7, R49.	13.9	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.	3.9	60
104	A bi-dimensional regression tree approach to the modeling of gene expression regulation. <i>Bioinformatics</i> , 2006, 22, 332-340.	1.8	23
105	An Efficient Hybrid Strategy for Temporal Planning. <i>Lecture Notes in Computer Science</i> , 2006, , 273-287.	1.0	3
106	Identification and Evaluation of Functional Modules in Gene Co-expression Networks. <i>Lecture Notes in Computer Science</i> , 2006, , 57-76.	1.0	5
107	MaxSolver: An efficient exact algorithm for (weighted) maximum satisfiability. <i>Artificial Intelligence</i> , 2005, 164, 47-80.	3.9	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.	3.9	177

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109	CAGER: classification analysis of gene expression regulation using multiple information sources. BMC Bioinformatics, 2005, 6, 114.	1.2	6
110	Frontier search. Journal of the ACM, 2005, 52, 715-748.	1.8	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.	1.8	151
112	WordSpy: identifying transcription factor binding motifs by building a dictionary and learning a grammar. Nucleic Acids Research, 2005, 33, W412-W416.	6.5	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.	1.8	213
115	ILM: a web server for predicting RNA secondary structures with pseudoknots. Nucleic Acids Research, 2004, 32, W146-W149.	6.5	32
116	Average-case analysis of best-first search in two representative directed acyclic graphs. Artificial Intelligence, 2004, 155, 183-206.	3.9	8
117	Configuration landscape analysis and backbone guided local search.. Artificial Intelligence, 2004, 158, 1-26.	3.9	64
118	Efficient Strategies for (Weighted) Maximum Satisfiability. Lecture Notes in Computer Science, 2004, , 690-705.	1.0	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.	3.9	3
122	Heuristic search in artificial intelligence. Artificial Intelligence, 2001, 129, 1-4.	3.9	7
123	Phase Transitions and Backbones of 3-SAT and Maximum 3-SAT. Lecture Notes in Computer Science, 2001, , 153-167.	1.0	24
124	The Asymmetric Traveling Salesman Problem: Algorithms, Instance Generators, and Tests. Lecture Notes in Computer Science, 2001, , 32-59.	1.0	72
125	Towards Flexible Teamwork in Persistent Teams: Extended Report. Autonomous Agents and Multi-Agent Systems, 2000, 3, 159-183.	1.3	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.	0.5	6
128	A study of complexity transitions on the asymmetric traveling salesman problem. Artificial Intelligence, 1996, 81, 223-239.	3.9	71
129	Epsilon-transformation: exploiting phase transitions to solve combinatorial optimization problems. Artificial Intelligence, 1996, 81, 297-325.	3.9	15
130	Performance of linear-space search algorithms. Artificial Intelligence, 1995, 79, 241-292.	3.9	59
131	Parallel Heap Operations on an EREW PRAM. Journal of Parallel and Distributed Computing, 1994, 20, 248-255.	2.7	7
132	Building heaps in parallel. Information Processing Letters, 1991, 37, 355-358.	0.4	20
133	Optimal parallel quicksort on EREW PRAM. BIT Numerical Mathematics, 1991, 31, 69-74.	1.0	4
134	A faster optimal algorithm for the measure problem. Parallel Computing, 1991, 17, 683-687.	1.3	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.	1.0	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