

# Yi Pan

## List of Publications by Year in descending order

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477  
papers

14,535  
citations

20817

60  
h-index

34986

98  
g-index

526  
all docs

526  
docs citations

526  
times ranked

11455  
citing authors

#	ARTICLE	IF	CITATIONS
1	CytoNCA: A cytoscape plugin for centrality analysis and evaluation of protein interaction networks. BioSystems, 2015, 127, 67-72.	2.0	813
2	Genome-wide association studies dissect the genetic networks underlying agronomical traits in soybean. Genome Biology, 2017, 18, 161.	8.8	363
3	Drug repositioning based on comprehensive similarity measures and Bi-Random walk algorithm. Bioinformatics, 2016, 32, 2664-2671.	4.1	311
4	Effects of lactic acid bacteria and molasses additives on the microbial community and fermentation quality of soybean silage. Bioresource Technology, 2017, 238, 706-715.	9.6	288
5	Identification of Essential Proteins Based on Edge Clustering Coefficient. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1070-1080.	3.0	254
6	A study of the routing and spectrum allocation in spectrum-sliced Elastic Optical Path networks. , 2011,,.		252
7	A survey of MRI-based brain tumor segmentation methods. Tsinghua Science and Technology, 2014, 19, 578-595.	6.1	252
8	Prediction of lncRNA-disease associations based on inductive matrix completion. Bioinformatics, 2018, 34, 3357-3364.	4.1	227
9	b-SPECS+: Batch Verification for Secure Pseudonymous Authentication in VANET. IEEE Transactions on Information Forensics and Security, 2013, 8, 1860-1875.	6.9	214
10	A new essential protein discovery method based on the integration of protein-protein interaction and gene expression data. BMC Systems Biology, 2012, 6, 15.	3.0	211
11	Platelet-Secreted MicroRNA-223 Promotes Endothelial Cell Apoptosis Induced by Advanced Glycation End Products via Targeting the Insulin-like Growth Factor 1 Receptor. Journal of Immunology, 2014, 192, 437-446.	0.8	207
12	Applications of deep learning to MRI images: A survey. Big Data Mining and Analytics, 2018, 1, 1-18.	8.9	195
13	An Efficient Watermarking Method Based on Significant Difference of Wavelet Coefficient Quantization. IEEE Transactions on Multimedia, 2008, 10, 746-757.	7.2	185
14	LDAP: a web server for lncRNA-disease association prediction. Bioinformatics, 2017, 33, 458-460.	4.1	182
15	Generative Adversarial Networks. ACM Computing Surveys, 2022, 54, 1-38.	23.0	180
16	A Fast Hierarchical Clustering Algorithm for Functional Modules Discovery in Protein Interaction Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 607-620.	3.0	171
17	Classification of autism spectrum disorder by combining brain connectivity and deep neural network classifier. Neurocomputing, 2019, 324, 63-68.	5.9	161
18	Predicting Essential Proteins Based on Weighted Degree Centrality. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 407-418.	3.0	160

#	ARTICLE	IF	CITATIONS
19	Assessing the fermentation quality and microbial community of the mixed silage of forage soybean with crop corn or sorghum. <i>Bioresource Technology</i> , 2018, 265, 563-567.	9.6	158
20	A local average connectivity-based method for identifying essential proteins from the network level. <i>Computational Biology and Chemistry</i> , 2011, 35, 143-150.	2.3	152
21	MicroRNA-223 delivered by platelet-derived microvesicles promotes lung cancer cell invasion via targeting tumor suppressor EPB41L3. <i>Molecular Cancer</i> , 2015, 14, 58.	19.2	145
22	Classification of Alzheimer's Disease Using Whole Brain Hierarchical Network. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 624-632.	3.0	142
23	Construction and application of dynamic protein interaction network based on time course gene expression data. <i>Proteomics</i> , 2013, 13, 301-312.	2.2	141
24	Iteration method for predicting essential proteins based on orthology and protein-protein interaction networks. <i>BMC Systems Biology</i> , 2012, 6, 87.	3.0	128
25	Deep Learning Based Drug Screening for Novel Coronavirus 2019-nCov. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2020, 12, 368-376.	3.6	127
26	Towards the identification of protein complexes and functional modules by integrating PPI network and gene expression data. <i>BMC Bioinformatics</i> , 2012, 13, 109.	2.6	122
27	Predicting MicroRNA-Disease Associations Based on Improved MicroRNA and Disease Similarities. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1774-1782.	3.0	116
28	SinNLRR: a robust subspace clustering method for cell type detection by non-negative and low-rank representation. <i>Bioinformatics</i> , 2019, 35, 3642-3650.	4.1	112
29	LncCCAT1 Promotes Breast Cancer Stem Cell Function through Activating WNT/ $\beta$ 2-catenin Signaling. <i>Theranostics</i> , 2019, 9, 7384-7402.	10.0	109
30	A blind watermarking method using maximum wavelet coefficient quantization. <i>Expert Systems With Applications</i> , 2009, 36, 11509-11516.	7.6	107
31	Recent advances in clustering methods for protein interaction networks. <i>BMC Genomics</i> , 2010, 11, S10.	2.8	104
32	A comparison of the functional modules identified from time course and static PPI network data. <i>BMC Bioinformatics</i> , 2011, 12, 339.	2.6	103
33	ClusterViz: A Cytoscape APP for Cluster Analysis of Biological Network. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 815-822.	3.0	103
34	Stochastic Load Balancing for Virtual Resource Management in Datacenters. <i>IEEE Transactions on Cloud Computing</i> , 2020, 8, 459-472.	4.4	91
35	Nonclassical Protein Secretion by <i>Bacillus subtilis</i> in the Stationary Phase Is Not Due to Cell Lysis. <i>Journal of Bacteriology</i> , 2011, 193, 5607-5615.	2.2	90
36	Complex Brain Network Analysis and Its Applications to Brain Disorders: A Survey. <i>Complexity</i> , 2017, 2017, 1-27.	1.6	90

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37	Effective identification of essential proteins based on priori knowledge, network topology and gene expressions. <i>Methods</i> , 2014, 67, 325-333.	3.8	89
38	A Topology Potential-Based Method for Identifying Essential Proteins from PPI Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 372-383.	3.0	88
39	Analysis of dynamic location management for PCS networks. <i>IEEE Transactions on Vehicular Technology</i> , 2002, 51, 1109-1119.	6.3	85
40	Predicting drug-target interaction using positive-unlabeled learning. <i>Neurocomputing</i> , 2016, 206, 50-57.	5.9	83
41	Variational Few-Shot Learning for Microservice-Oriented Intrusion Detection in Distributed Industrial IoT. <i>IEEE Transactions on Industrial Informatics</i> , 2022, 18, 5087-5095.	11.3	82
42	Up-regulation of miR-210 induced by a hypoxic microenvironment promotes breast cancer stem cell metastasis, proliferation, and self-renewal by targeting E-cadherin. <i>FASEB Journal</i> , 2018, 32, 6965-6981.	0.5	81
43	Improved K-Means Clustering Algorithm for Exploring Local Protein Sequence Motifs Representing Common Structural Property. <i>IEEE Transactions on Nanobioscience</i> , 2005, 4, 255-265.	3.3	80
44	Automatic ICD-9 coding via deep transfer learning. <i>Neurocomputing</i> , 2019, 324, 43-50.	5.9	79
45	Improved Protein Secondary Structure Prediction Using Support Vector Machine With a New Encoding Scheme and an Advanced Tertiary Classifier. <i>IEEE Transactions on Nanobioscience</i> , 2004, 3, 265-271.	3.3	78
46	Automated ICD-9 Coding via A Deep Learning Approach. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1193-1202.	3.0	78
47	Detecting Protein Complexes Based on Uncertain Graph Model. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 486-497.	3.0	77
48	Artificial intelligence in cancer target identification and drug discovery. <i>Signal Transduction and Targeted Therapy</i> , 2022, 7, 156.	17.1	77
49	A Parallel Matrix-Based Method for Computing Approximations in Incomplete Information Systems. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2015, 27, 326-339.	5.7	76
50	Copyright Protection for E-Government Document Images. <i>IEEE MultiMedia</i> , 2012, 19, 62-73.	1.7	75
51	UDoNC: An Algorithm for Identifying Essential Proteins Based on Protein Domains and Protein-Protein Interaction Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 276-288.	3.0	75
52	Block5GIntell: Blockchain for AI-Enabled 5G Networks. <i>IEEE Access</i> , 2020, 8, 145918-145935.	4.2	74
53	Towards Elastic and Fine-Granular Bandwidth Allocation in Spectrum-Sliced Optical Networks. <i>Journal of Optical Communications and Networking</i> , 2012, 4, 906.	4.8	71
54	Parallel granular neural networks for fast credit card fraud detection. , 0, , .		70

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55	A novel dynamic network data replication scheme based on historical access record and proactive deletion. <i>Journal of Supercomputing</i> , 2012, 62, 227-250.	3.6	70
56	Cloud computing for detecting high-order genome-wide epistatic interaction via dynamic clustering. <i>BMC Bioinformatics</i> , 2014, 15, 102.	2.6	70
57	A comparison of parallel large-scale knowledge acquisition using rough set theory on different MapReduce runtime systems. <i>International Journal of Approximate Reasoning</i> , 2014, 55, 896-907.	3.3	67
58	Identifying essential proteins from active PPI networks constructed with dynamic gene expression. <i>BMC Genomics</i> , 2015, 16, S1.	2.8	66
59	Predicting essential proteins based on subcellular localization, orthology and PPI networks. <i>BMC Bioinformatics</i> , 2016, 17, 279.	2.6	66
60	An Efficient and Compacted DAG-Based Blockchain Protocol for Industrial Internet of Things. <i>IEEE Transactions on Industrial Informatics</i> , 2020, 16, 4134-4145.	11.3	66
61	A deep learning framework for identifying essential proteins by integrating multiple types of biological information. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 18, 1-1.	3.0	65
62	Proteinâ€protein interactions: detection, reliability assessment and applications. <i>Briefings in Bioinformatics</i> , 2017, 18, bbw066.	6.5	64
63	Integration of breast cancer gene signatures based on graph centrality. <i>BMC Systems Biology</i> , 2011, 5, S10.	3.0	62
64	BlockDeepNet: A Blockchain-Based Secure Deep Learning for IoT Network. <i>Sustainability</i> , 2019, 11, 3974.	3.2	62
65	Gradient amplification: An efficient way to train deep neural networks. <i>Big Data Mining and Analytics</i> , 2020, 3, 196-207.	8.9	62
66	Adaptive computation offloading and resource allocation strategy in a mobile edge computing environment. <i>Information Sciences</i> , 2020, 537, 116-131.	6.9	62
67	Periodic-Aware Intelligent Prediction Model for Information Diffusion in Social Networks. <i>IEEE Transactions on Network Science and Engineering</i> , 2021, 8, 894-904.	6.4	62
68	Edge Computing for the Internet of Things. <i>IEEE Network</i> , 2018, 32, 6-7.	6.9	61
69	Prediction of Essential Proteins Based on Overlapping Essential Modules. <i>IEEE Transactions on Nanobioscience</i> , 2014, 13, 415-424.	3.3	60
70	miR-29a contributes to breast cancer cells epithelialâ€mesenchymal transition, migration, and invasion via down-regulating histone H4K20 trimethylation through directly targeting SUV420H2. <i>Cell Death and Disease</i> , 2019, 10, 176.	6.3	60
71	DNRLMF-MDA:Predicting microRNA-Disease Associations Based on Similarities of microRNAs and Diseases. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 233-243.	3.0	59
72	BiXGBoost: a scalable, flexible boosting-based method for reconstructing gene regulatory networks. <i>Bioinformatics</i> , 2019, 35, 1893-1900.	4.1	59

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73	Practical Deadlock-Free Fault-Tolerant Routing in Meshes Based on the Planar Network Fault Model. IEEE Transactions on Computers, 2009, 58, 620-633.	3.4	58
74	A novel ensemble deep learning model for stock prediction based on stock prices and news. International Journal of Data Science and Analytics, 2022, 13, 139-149.	4.1	57
75	A Modified Ant Colony Optimization Algorithm for Network Coding Resource Minimization. IEEE Transactions on Evolutionary Computation, 2016, 20, 325-342.	10.0	56
76	Improving Alzheimer's Disease Classification by Combining Multiple Measures. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1649-1659.	3.0	56
77	Slug-upregulated miR-221 promotes breast cancer progression through suppressing E-cadherin expression. Scientific Reports, 2016, 6, 25798.	3.3	55
78	Prediction of essential proteins based on gene expression programming. BMC Genomics, 2013, 14, S7.	2.8	54
79	A Self-tuning Failure Detection Scheme for Cloud Computing Service. , 2012, , .		53
80	Deep convolutional neural network for automatically segmenting acute ischemic stroke lesion in multi-modality MRI. Neural Computing and Applications, 2020, 32, 6545-6558.	5.6	53
81	A Decentralized and Trusted Edge Computing Platform for Internet of Things. IEEE Internet of Things Journal, 2020, 7, 3910-3922.	8.7	52
82	Secure D2D Communication for 5G IoT Network Based on Lightweight Cryptography. Applied Sciences (Switzerland), 2020, 10, 217.	2.5	52
83	Alzheimer's Disease Classification Based on Individual Hierarchical Networks Constructed With 3-D Texture Features. IEEE Transactions on Nanobioscience, 2017, 16, 428-437.	3.3	51
84	United neighborhood closeness centrality and orthology for predicting essential proteins. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 17, 1-1.	3.0	50
85	microRNA-200b and microRNA-200c promote colorectal cancer cell proliferation via targeting the reversion-inducing cysteine-rich protein with Kazal motifs. RNA Biology, 2015, 12, 276-289.	3.1	49
86	Rechecking the Centrality-Lethality Rule in the Scope of Protein Subcellular Localization Interaction Networks. PLoS ONE, 2015, 10, e0130743.	2.5	47
87	Computational Drug Repositioning with Random Walk on a Heterogeneous Network. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1890-1900.	3.0	47
88	Identifying essential proteins based on sub-network partition and prioritization by integrating subcellular localization information. Journal of Theoretical Biology, 2018, 447, 65-73.	1.7	46
89	Constructing Load-Balanced Data Aggregation Trees in Probabilistic Wireless Sensor Networks. IEEE Transactions on Parallel and Distributed Systems, 2014, 25, 1681-1690.	5.6	45
90	A review of infant cry analysis and classification. Eurasip Journal on Audio, Speech, and Music Processing, 2021, 2021, .	2.1	45

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91	Gain-bandwidth characteristics of thin avalanche photodiodes. IEEE Transactions on Electron Devices, 2002, 49, 770-781.	3.0	44
92	Efficient parallel boolean matrix based algorithms for computing composite rough set approximations. Information Sciences, 2016, 329, 287-302.	6.9	44
93	Construction of Refined Protein Interaction Network for Predicting Essential Proteins. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1386-1397.	3.0	44
94	Rule Generation for Protein Secondary Structure Prediction With Support Vector Machines and Decision Tree. IEEE Transactions on Nanobioscience, 2006, 5, 46-53.	3.3	43
95	Clustering support vector machines for protein local structure prediction. Expert Systems With Applications, 2007, 32, 518-526.	7.6	43
96	Diagnosis of COVID-19 Pneumonia via a Novel Deep Learning Architecture. Journal of Computer Science and Technology, 2022, 37, 330-343.	1.5	43
97	Approximation algorithms for load-balanced virtual backbone construction in wireless sensor networks. Theoretical Computer Science, 2013, 507, 2-16.	0.9	42
98	Machine Learning-Based Network Sub-Slicing Framework in a Sustainable 5G Environment. Sustainability, 2020, 12, 6250.	3.2	42
99	A novel virtual screening procedure identifies Pralatrexate as inhibitor of SARS-CoV-2 RdRp and it reduces viral replication in vitro. PLoS Computational Biology, 2020, 16, e1008489.	3.2	42
100	Equivalent permutation capabilities between time-division optical Omega networks and non-optical extra-stage Omega networks. IEEE/ACM Transactions on Networking, 2001, 9, 518-524.	3.8	41
101	Methylation-mediated silencing of miR-133a-3p promotes breast cancer cell migration and stemness via miR-133a-3p/MAML1/DNMT3A positive feedback loop. Journal of Experimental and Clinical Cancer Research, 2019, 38, 429.	8.6	41
102	A More Realistic Thinning Scheme for Call Admission Control in Multimedia Wireless Networks. IEEE Transactions on Computers, 2008, 57, 1143-1147.	3.4	40
103	DeepEP: a deep learning framework for identifying essential proteins. BMC Bioinformatics, 2019, 20, 506.	2.6	40
104	Enhancing the feature representation of multi-modal MRI data by combining multi-view information for MCI classification. Neurocomputing, 2020, 400, 322-332.	5.9	40
105	Modeling and Cost Analysis of Movement-Based Location Management for PCS Networks With HLR/VLR Architecture, General Location Area and Cell Residence Time Distributions. IEEE Transactions on Vehicular Technology, 2008, 57, 3815-3831.	6.3	39
106	Architecture, mobility management, and quality of service for integrated 3G and WLAN networks. Wireless Communications and Mobile Computing, 2005, 5, 805-823.	1.2	38
107	Differentiation, QoS guarantee, and optimization for real-time traffic over one-hop ad hoc networks. IEEE Transactions on Parallel and Distributed Systems, 2005, 16, 538-549.	5.6	38
108	Biological network motif detection and evaluation. BMC Systems Biology, 2011, 5, S5.	3.0	38

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109	Classification of Schizophrenia Based on Individual Hierarchical Brain Networks Constructed From Structural MRI Images. IEEE Transactions on Nanobioscience, 2017, 16, 600-608.	3.3	38
110	A comprehensive survey on computational methods of non-coding RNA and disease association prediction. Briefings in Bioinformatics, 2021, 22, .	6.5	38
111	IDENTIFICATION OF ESSENTIAL PROTEINS FROM WEIGHTED PROTEIN-PROTEIN INTERACTION NETWORKS. Journal of Bioinformatics and Computational Biology, 2013, 11, 1341002.	0.8	37
112	FAST NEAREST NEIGHBOR ALGORITHMS ON A LINEAR ARRAY WITH A RECONFIGURABLE PIPELINED BUS SYSTEM. International Journal of Parallel, Emergent and Distributed Systems, 1998, 13, 1-25.	0.4	36
113	HybridDock: A Hybrid Protein-Ligand Docking Protocol Integrating Protein- and Ligand-Based Approaches. Journal of Chemical Information and Modeling, 2016, 56, 1078-1087.	5.4	35
114	An interpretable boosting model to predict side effects of analgesics for osteoarthritis. BMC Systems Biology, 2018, 12, 105.	3.0	35
115	Title is missing!. Journal of Supercomputing, 2000, 15, 163-181.	3.6	33
116	BRWMDA:Predicting microbe-disease associations based on similarities and bi-random walk on disease and microbe networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 17, 1-1.	3.0	33
117	Association predictions of genomics, proteomics, transcriptomics, microbiome, metabolomics, pathomics, radiomics, drug, symptoms, environment factor, and disease networks: A comprehensive approach. Medicinal Research Reviews, 2022, 42, 441-461.	10.5	33
118	Essential Proteins Discovery from Weighted Protein Interaction Networks. Lecture Notes in Computer Science, 2010, , 89-100.	1.3	33
119	A parallel computing method based on zeroing neural networks for time-varying complex-valued matrix Moore-Penrose inversion. Information Sciences, 2020, 524, 216-228.	6.9	33
120	CircRNA-disease associations prediction based on metapath2vec++ and matrix factorization. Big Data Mining and Analytics, 2020, 3, 280-291.	8.9	33
121	KGANCA: predicting circRNA-disease associations based on knowledge graph attention network. Briefings in Bioinformatics, 2022, 23, .	6.5	33
122	Introduction: Recent Developments in Parallel and Distributed Data Mining. Genetic Resources and Crop Evolution, 2002, 49, 491-501.	1.6	32
123	Blockchain-enabled Secure Framework for Energy-Efficient Smart Parking in Sustainable City Environment. Sustainable Cities and Society, 2022, 76, 103364.	10.4	32
124	Novel Hybrid Hierarchical-K-means Clustering Method (H-K-means) for Microarray Analysis. , 0, , .		31
125	A Framework for Integrating Multiple Biological Networks to Predict MicroRNA-Disease Associations. IEEE Transactions on Nanobioscience, 2017, 16, 100-107.	3.3	30
126	Smart Contract-Based Pool Hopping Attack Prevention for Blockchain Networks. Symmetry, 2019, 11, 941.	2.2	30



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127	Predicting Drug-Drug Interactions Based on Integrated Similarity and Semi-Supervised Learning. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 168-179.	3.0	30
128	Delay-Bounded and Energy-Efficient Composite Event Monitoring in Heterogeneous Wireless Sensor Networks. IEEE Transactions on Parallel and Distributed Systems, 2010, 21, 1373-1385.	5.6	29
129	Reducing transport latency for short flows with multipath TCP. Journal of Network and Computer Applications, 2018, 108, 20-36.	9.1	29
130	Constructing Disease Similarity Networks Based on Disease Module Theory. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 906-915.	3.0	29
131	A New Method for Predicting Protein Functions From Dynamic Weighted Interactome Networks. IEEE Transactions on Nanobioscience, 2016, 15, 131-139.	3.3	28
132	Optimally Scaling Permutation Routing on Reconfigurable Linear Arrays with Optical Buses. Journal of Parallel and Distributed Computing, 2000, 60, 1125-1136.	4.1	27
133	A novel method of predicting microRNA-disease associations based on microRNA, disease, gene and environment factor networks. Methods, 2017, 124, 69-77.	3.8	27
134	An Iterative Locally Auto-Weighted Least Squares Method for Microarray Missing Value Estimation. IEEE Transactions on Nanobioscience, 2017, 16, 21-33.	3.3	27
135	DyNetViewer: a Cytoscape app for dynamic network construction, analysis and visualization. Bioinformatics, 2018, 34, 1597-1599.	4.1	27
136	CF-CloudOrch: container fog node-based cloud orchestration for IoT networks. Journal of Supercomputing, 2018, 74, 7024-7045.	3.6	27
137	Symbolic Communication Set Generation for Irregular Parallel Applications. Journal of Supercomputing, 2003, 25, 199-214.	3.6	26
138	Performance evaluation of a hierarchical cellular system with mobile velocity-based bidirectional call-overflow scheme. IEEE Transactions on Parallel and Distributed Systems, 2003, 14, 72-83.	5.6	26
139	Load-balanced CDS construction in wireless sensor networks via genetic algorithm. International Journal of Sensor Networks, 2012, 11, 166.	0.4	26
140	Parallel rough set based knowledge acquisition using MapReduce from big data. , 2012, , .		26
141	Editorial Special Issue on “AI-Driven Informatics, Sensing, Imaging and Big Data Analytics for Fighting the COVID-19 Pandemic”, IEEE Journal of Biomedical and Health Informatics, 2020, 24, 2731-2732.	6.3	26
142	TW-Co-MFC: Two-level weighted collaborative fuzzy clustering based on maximum entropy for multi-view data. Tsinghua Science and Technology, 2021, 26, 185-198.	6.1	26
143	<i>h</i> -measure: A new measurement for evaluating clusters in protein-protein interaction networks. Proteomics, 2013, 13, 291-300.	2.2	25
144	EPGA: <i>de novo</i> assembly using the distributions of reads and insert size. Bioinformatics, 2015, 31, 825-833.	4.1	25

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145	A reliable neighbor-based method for identifying essential proteins by integrating gene expressions, orthology, and subcellular localization information. Tsinghua Science and Technology, 2016, 21, 668-677.	6.1	25
146	Convolutional networks with cross-layer neurons for image recognition. Information Sciences, 2018, 433-434, 241-254.	6.9	25
147	Protease Nexin I is a feedback regulator of EGF/PKC/MAPK/EGR1 signaling in breast cancer cells metastasis and stemness. Cell Death and Disease, 2019, 10, 649.	6.3	25
148	Deep Fuzzy Neural Networks for Biomarker Selection for Accurate Cancer Detection. IEEE Transactions on Fuzzy Systems, 2020, 28, 3219-3228.	9.8	25
149	A New Method for Identifying Essential Proteins Based on Edge Clustering Coefficient. Lecture Notes in Computer Science, 2011, , 87-98.	1.3	25
150	A Novel Multistage Network Architecture with Multicast and Broadcast Capability. Journal of Supercomputing, 2006, 35, 277-300.	3.6	24
151	Essential Protein Discovery Based on Network Motif and Gene Ontology. , 2011, , .		24
152	Tuning the Aggressive TCP Behavior for Highly Concurrent HTTP Connections in Intra-Datacenter. IEEE/ACM Transactions on Networking, 2017, 25, 3808-3822.	3.8	24
153	DDIGIP: predicting drug-drug interactions based on Gaussian interaction profile kernels. BMC Bioinformatics, 2019, 20, 538.	2.6	24
154	Identification of Protein Complexes by Using a Spatial and Temporal Active Protein Interaction Network. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 817-827.	3.0	24
155	BloVT: Blockchain-Based Secure Storage Architecture for Intelligent Internet of Vehicular Things. IEEE Consumer Electronics Magazine, 2022, 11, 75-82.	2.3	24
156	Sprites: detection of deletions from sequencing data by re-aligning split reads. Bioinformatics, 2016, 32, 1788-1796.	4.1	23
157	MMM: classification of schizophrenia using multi-modality multi-atlas feature representation and multi-kernel learning. Multimedia Tools and Applications, 2018, 77, 29651-29667.	3.9	23
158	Blockchain-Based Cyber Threat Intelligence System Architecture for Sustainable Computing. Sustainability, 2020, 12, 6401.	3.2	23
159	CircR2Disease v2.0: An Updated Web Server for Experimentally Validated circRNA“Disease Associations and Its Application. Genomics, Proteomics and Bioinformatics, 2022, 20, 435-445.	6.9	23
160	A Stacking Ensemble Deep Learning Model for Bitcoin Price Prediction Using Twitter Comments on Bitcoin. Mathematics, 2022, 10, 1307.	2.2	23
161	Efficient fault-tolerant routing in multihop optical WDM networks. IEEE Transactions on Parallel and Distributed Systems, 1999, 10, 1012-1025.	5.6	22
162	Identifying protein complexes from interaction networks based on clique percolation and distance restriction. BMC Genomics, 2010, 11, S10.	2.8	22

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163	Identifying Dynamic Protein Complexes Based on Gene Expression Profiles and PPI Networks. BioMed Research International, 2014, 2014, 1-10.	1.9	22
164	A deep learning method for lincRNA detection using auto-encoder algorithm. BMC Bioinformatics, 2017, 18, 511.	2.6	22
165	Rethinking Fast and Friendly Transport in Data Center Networks. IEEE/ACM Transactions on Networking, 2020, 28, 2364-2377.	3.8	21
166	A Deep Learning Framework for Gene Ontology Annotations With Sequence- and Network-Based Information. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2208-2217.	3.0	21
167	MCHMDA: Predicting Microbe-Disease Associations Based on Similarities and Low-Rank Matrix Completion. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 611-620.	3.0	21
168	Reaction-diffusion modeling of malware propagation in mobile wireless sensor networks. Science China Information Sciences, 2013, 56, 1-18.	4.3	20
169	Prioritization of orphan disease-causing genes using topological feature and GO similarity between proteins in interaction networks. Science China Life Sciences, 2014, 57, 1064-1071.	4.9	20
170	Searching High-Order SNP Combinations for Complex Diseases Based on Energy Distribution Difference. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 695-704.	3.0	20
171	ISEA: Iterative Seed-Extension Algorithm for De Novo Assembly Using Paired-End Information and Insert Size Distribution. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 916-925.	3.0	20
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