Weiping Wang

List of Publications by Year
in descending order

385 papers	7,491 citations	87723 38 h-index	85405 71 g-index
386 all docs	386 docs citations	386 times ranked	5965 citing authors

#	Article	IF	Citations
1	CytoNCA: A cytoscape plugin for centrality analysis and evaluation of protein interaction networks. BioSystems, 2015, 127, 67-72.	0.9	813
2	Drug repositioning based on comprehensive similarity measures and Bi-Random walk algorithm. Bioinformatics, 2016, 32, 2664-2671.	1.8	311
3	Identification of Essential Proteins Based on Edge Clustering Coefficient. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1070-1080.	1.9	254
4	Prediction of lncRNAâ€"disease associations based on inductive matrix completion. Bioinformatics, 2018, 34, 3357-3364.	1.8	227
5	Computational drug repositioning using low-rank matrix approximation and randomized algorithms. Bioinformatics, 2018, 34, 1904-1912.	1.8	183
6	LDAP: a web server for lncRNA-disease association prediction. Bioinformatics, 2017, 33, 458-460.	1.8	182
7	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.	1.9	171
8	DeepSignal: detecting DNA methylation state from Nanopore sequencing reads using deep-learning. Bioinformatics, 2019, 35, 4586-4595.	1.8	158
9	Proteinâ€"protein interaction site prediction through combining local and global features with deep neural networks. Bioinformatics, 2020, 36, 1114-1120.	1.8	157
10	Minimizing Movement for Target Coverage and Network Connectivity in Mobile Sensor Networks. IEEE Transactions on Parallel and Distributed Systems, 2015, 26, 1971-1983.	4.0	149
11	Construction and application of dynamic protein interaction network based on time course gene expression data. Proteomics, 2013, 13, 301-312.	1.3	141
12	Drug repositioning based on bounded nuclear norm regularization. Bioinformatics, 2019, 35, i455-i463.	1.8	116
13	SinNLRR: a robust subspace clustering method for cell type detection by non-negative and low-rank representation. Bioinformatics, 2019, 35, 3642-3650.	1.8	112
14	Recent advances in clustering methods for protein interaction networks. BMC Genomics, 2010, 11, S10.	1.2	104
15	CytoCluster: A Cytoscape Plugin for Cluster Analysis and Visualization of Biological Networks. International Journal of Molecular Sciences, 2017, 18, 1880.	1.8	90
16	Complex Brain Network Analysis and Its Applications to Brain Disorders: A Survey. Complexity, 2017, 2017, 1-27.	0.9	90
17	Effective identification of essential proteins based on priori knowledge, network topology and gene expressions. Methods, 2014, 67, 325-333.	1.9	89
18	Dynamic protein interaction network construction and applications. Proteomics, 2014, 14, 338-352.	1.3	88

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19	Prognostication of patients with COVID-19 using artificial intelligence based on chest x-rays and clinical data: a retrospective study. The Lancet Digital Health, 2021, 3, e286-e294.	5.9	87
20	DWNN-RLS: regularized least squares method for predicting circRNA-disease associations. BMC Bioinformatics, 2018, 19, 520.	1.2	68
21	Predicting essential proteins based on subcellular localization, orthology and PPI networks. BMC Bioinformatics, 2016, 17, 279.	1.2	66
22	Attention convolutional neural network for accurate segmentation and quantification of lesions in ischemic stroke disease. Medical Image Analysis, 2020, 65, 101791.	7.0	63
23	Integration of breast cancer gene signatures based on graph centrality. BMC Systems Biology, 2011, 5, S10.	3.0	62
24	Distributed Probabilistic Offloading in Edge Computing for 6G-Enabled Massive Internet of Things. IEEE Internet of Things Journal, 2021, 8, 5298-5308.	5.5	60
25	Computational approaches to predicting essential proteins: A survey. Proteomics - Clinical Applications, 2013, 7, 181-192.	0.8	59
26	BiXGBoost: a scalable, flexible boosting-based method for reconstructing gene regulatory networks. Bioinformatics, 2019, 35, 1893-1900.	1.8	59
27	HyperAttentionDTI: improving drug–protein interaction prediction by sequence-based deep learning with attention mechanism. Bioinformatics, 2022, 38, 655-662.	1.8	55
28	H-PoP and H-PoPG: heuristic partitioning algorithms for single individual haplotyping of polyploids. Bioinformatics, 2016, 32, 3735-3744.	1.8	54
29	Deep convolutional neural network for automatically segmenting acute ischemic stroke lesion in multi-modality MRI. Neural Computing and Applications, 2020, 32, 6545-6558.	3.2	53
30	PDRCNN: Precise Phishing Detection with Recurrent Convolutional Neural Networks. Security and Communication Networks, 2019, 2019, 1-15.	1.0	50
31	Transittability of complex networks and its applications to regulatory biomolecular networks. Scientific Reports, 2014, 4, 4819.	1.6	49
32	Computational drug repositioning based on multi-similarities bilinear matrix factorization. Briefings in Bioinformatics, 2021, 22, .	3.2	49
33	Phase prediction of Ni-base superalloys via high-throughput experiments and machine learning. Materials Research Letters, 2021, 9, 32-40.	4.1	49
34	AttentionDTA: prediction of drug–target binding affinity using attention model. , 2019, , .		48
35	SYNBIP: synthetic binding proteins for research, diagnosis and therapy. Nucleic Acids Research, 2022, 50, D560-D570.	6.5	48
36	Rechecking the Centrality-Lethality Rule in the Scope of Protein Subcellular Localization Interaction Networks. PLoS ONE, 2015, 10, e0130743.	1.1	47

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37	Automatic ICD code assignment of Chinese clinical notes based on multilayer attention BiRNN. Journal of Biomedical Informatics, 2019, 91, 103114.	2.5	47
38	Genome-wide detection of cytosine methylations in plant from Nanopore data using deep learning. Nature Communications, 2021, 12, 5976.	5.8	47
39	An Efficient Algorithm for Constructing Maximum lifetime Tree for Data Gathering Without Aggregation in Wireless Sensor Networks. , 2010, , .		46
40	Identifying essential proteins based on sub-network partition and prioritization by integrating subcellular localization information. Journal of Theoretical Biology, 2018, 447, 65-73.	0.8	46
41	Control principles for complex biological networks. Briefings in Bioinformatics, 2019, 20, 2253-2266.	3.2	46
42	Performance Enhancement of Multipath TCP for Wireless Communications With Multiple Radio Interfaces. IEEE Transactions on Communications, 2016, 64, 3456-3466.	4.9	45
43	AIMAFE: Autism spectrum disorder identification with multi-atlas deep feature representation and ensemble learning. Journal of Neuroscience Methods, 2020, 343, 108840.	1.3	44
44	Improving protein function prediction using domain and protein complexes in PPI networks. BMC Systems Biology, 2014, 8, 35.	3.0	43
45	Artificial intelligence for prediction of COVID-19 progression using CT imaging and clinical data. European Radiology, 2022, 32, 205-212.	2.3	42
46	A Fast Agglomerate Algorithm for Mining Functional Modules in Protein Interaction Networks. , 2008, , .		40
47	Chinese clinical named entity recognition via multi-head self-attention based BiLSTM-CRF. Artificial Intelligence in Medicine, 2022, 127, 102282.	3.8	38
48	CAPS: Coding-Based Adaptive Packet Spraying to Reduce Flow Completion Time in Data Center. IEEE/ACM Transactions on Networking, 2019, 27, 2338-2353.	2.6	36
49	Essential protein discovery based on a combination of modularity and conservatism. Methods, 2016, 110, 54-63.	1.9	35
50	HybridDock: A Hybrid Protein–Ligand Docking Protocol Integrating Protein- and Ligand-Based Approaches. Journal of Chemical Information and Modeling, 2016, 56, 1078-1087.	2.5	35
51	An interpretable boosting model to predict side effects of analgesics for osteoarthritis. BMC Systems Biology, 2018, 12, 105.	3.0	35
52	Overlap matrix completion for predicting drug-associated indications. PLoS Computational Biology, 2019, 15, e1007541.	1.5	35
53	Accurate Respiration Monitoring for Mobile Users With Commercial RFID Devices. IEEE Journal on Selected Areas in Communications, 2021, 39, 513-525.	9.7	34
54	BOSS: a novel scaffolding algorithm based on an optimized scaffold graph. Bioinformatics, 2017, 33, 169-176.	1.8	33

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55	Yap Promotes Noncanonical Wnt Signals From Cardiomyocytes for Heart Regeneration. Circulation Research, 2021, 129, 782-797.	2.0	30
56	A novel method of predicting microRNA-disease associations based on microRNA, disease, gene and environment factor networks. Methods, 2017, 124, 69-77.	1.9	27
57	DyNetViewer: a Cytoscape app for dynamic network construction, analysis and visualization. Bioinformatics, 2018, 34, 1597-1599.	1.8	27
58	Schizophrenia Identification Using Multi-View Graph Measures of Functional Brain Networks. Frontiers in Bioengineering and Biotechnology, 2019, 7, 479.	2.0	27
59	Social profile-based multicast routing scheme for delay-tolerant networks. , 2013, , .		26
60	EPGA: <i>de novo</i> assembly using the distributions of reads and insert size. Bioinformatics, 2015, 31, 825-833.	1.8	25
61	An AODV-based anycast protocol in mobile ad hoc network. , 0, , .		24
62	Essential Protein Discovery Based on Network Motif and Gene Ontology. , 2011, , .		24
63	Tuning the Aggressive TCP Behavior for Highly Concurrent HTTP Connections in Intra-Datacenter. IEEE/ACM Transactions on Networking, 2017, 25, 3808-3822.	2.6	24
64	DDIGIP: predicting drug-drug interactions based on Gaussian interaction profile kernels. BMC Bioinformatics, 2019, 20, 538.	1.2	24
65	An Effective Convolutional Neural Network for Classifying Red Blood Cells in Malaria Diseases. Interdisciplinary Sciences, Computational Life Sciences, 2020, 12, 217-225.	2.2	24
66	Randomized parameterized algorithms for $$P_2$$ P 2 -Packing and Co-Path Packing problems. Journal of Combinatorial Optimization, 2015, 29, 125-140.	0.8	23
67	Sprites: detection of deletions from sequencing data by re-aligning split reads. Bioinformatics, 2016, 32, 1788-1796.	1.8	23
68	MMM: classification of schizophrenia using multi-modality multi-atlas feature representation and multi-kernel learning. Multimedia Tools and Applications, 2018, 77, 29651-29667.	2.6	23
69	Adjusting Packet Size to Mitigate TCP Incast in Data Center Networks with COTS Switches. IEEE Transactions on Cloud Computing, 2019, , 1-1.	3.1	23
70	Identifying protein complexes from interaction networks based on clique percolation and distance restriction. BMC Genomics, 2010, 11, S10.	1.2	22
71	Identifying Dynamic Protein Complexes Based on Gene Expression Profiles and PPI Networks. BioMed Research International, 2014, 2014, 1-10.	0.9	22
72	Synthesizing Existing CSMA and TDMA Based MAC Protocols for VANETs. Sensors, 2017, 17, 338.	2.1	22

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73	MMHGE: detecting mild cognitive impairment based on multi-atlas multi-view hybrid graph convolutional networks and ensemble learning. Cluster Computing, 2021, 24, 103-113.	3.5	22
74	Mitigating Packet Reordering for Random Packet Spraying in Data Center Networks. IEEE/ACM Transactions on Networking, 2021, 29, 1183-1196.	2.6	22
75	An automated COVID-19 triage pipeline using artificial intelligence based on chest radiographs and clinical data. Npj Digital Medicine, 2022, 5, 5.	5.7	22
76	Rethinking Fast and Friendly Transport in Data Center Networks. IEEE/ACM Transactions on Networking, 2020, 28, 2364-2377.	2.6	21
77	Single-Cell Clustering Based on Shared Nearest Neighbor and Graph Partitioning. Interdisciplinary Sciences, Computational Life Sciences, 2020, 12, 117-130.	2.2	21
78	NPCDR: natural product-based drug combination and its disease-specific molecular regulation. Nucleic Acids Research, 2022, 50, D1324-D1333.	6.5	21
79	SSRE: Cell Type Detection Based on Sparse Subspace Representation and Similarity Enhancement. Genomics, Proteomics and Bioinformatics, 2021, 19, 282-291.	3.0	21
80	A novel graph attention model for predicting frequencies of drug–side effects from multi-view data. Briefings in Bioinformatics, 2021, 22, .	3.2	21
81	Improving circRNA–disease association prediction by sequence and ontology representations with convolutional and recurrent neural networks. Bioinformatics, 2021, 36, 5656-5664.	1.8	21
82	SVM Learning from Imbalanced Data by GA Sampling for Protein Domain Prediction. , 2008, , .		20
83	ARS: Cross-layer adaptive request scheduling to mitigate TCP incast in data center networks. , 2016, , .		20
84	Task-Aware TCP in Data Center Networks. IEEE/ACM Transactions on Networking, 2019, 27, 389-404.	2.6	20
85	LSCDroid: Malware Detection Based on Local Sensitive API Invocation Sequences. IEEE Transactions on Reliability, 2020, 69, 174-187.	3.5	20
86	EPGA2: memory-efficient <i>de novo</i> assembler. Bioinformatics, 2015, 31, 3988-3990.	1.8	19
87	Combining static and dynamic features for real-time moving pedestrian detection. Multimedia Tools and Applications, 2019, 78, 3781-3795.	2.6	19
88	Nothing Blocks Me: Precise and Real-Time LOS/NLOS Path Recognition in RFID Systems. IEEE Internet of Things Journal, 2019, 6, 5814-5824.	5.5	19
89	An Improved (and Practical) Parameterized Algorithm for the Individual Haplotyping Problem MFR with Mate-Pairs. Algorithmica, 2008, 52, 250-266.	1.0	18
90	Vehicle Density Based Forwarding Protocol for Safety Message Broadcast in VANET. Scientific World Journal, The, 2014, 2014, 1-9.	0.8	18

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91	ReActor: Real-time and Accurate Contactless Gesture Recognition with RFID. , 2019, , .		18
92	A convolutional neural network and graph convolutional network-based method for predicting the classification of anatomical therapeutic chemicals. Bioinformatics, 2021, 37, 2841-2847.	1.8	18
93	PDMDA: predicting deep-level miRNAâ€"disease associations with graph neural networks and sequence features. Bioinformatics, 2022, 38, 2226-2234.	1.8	18
94	PECC: Correcting contigs based on paired-end read distribution. Computational Biology and Chemistry, 2017, 69, 178-184.	1.1	17
95	CytoCtrlAnalyser: a Cytoscape app for biomolecular network controllability analysis. Bioinformatics, 2018, 34, 1428-1430.	1.8	17
96	Identification of early mild cognitive impairment using multi-modal data and graph convolutional networks. BMC Bioinformatics, 2020, 21, 123.	1.2	17
97	Exploring the dynamics and interplay of human papillomavirus and cervical tumorigenesis by integrating biological data into a mathematical model. BMC Bioinformatics, 2020, 21, 152.	1.2	17
98	A Novel Verification Scheme for Fine-Grained Top-k Queries in Two-Tiered Sensor Networks. Wireless Personal Communications, 2014, 75, 1809-1826.	1.8	16
99	An efficient method to identify essential proteins for different species by integrating protein subcellular localization information. , 2015, , .		16
100	Tag size profiling in multiple reader RFID systems. , 2017, , .		16
101	CAPS: Coding-based Adaptive Packet Spraying to Reduce Flow Completion Time in Data Center. , 2018, , .		16
102	Targeting TRPV1 on cellular plasticity regulated by Ovol 2 and Zeb 1 in hepatocellular carcinoma. Biomedicine and Pharmacotherapy, 2019, 118, 109270.	2.5	16
103	Multi-level Glioma Segmentation using 3D U-Net Combined Attention Mechanism with Atrous Convolution. , 2019, , .		16
104	Identifying Protein Complexes From Interactome Based on Essential Proteins and Local Fitness Method. IEEE Transactions on Nanobioscience, 2012, 11, 324-335.	2.2	15
105	De novo assembly methods for next generation sequencing data. Tsinghua Science and Technology, 2013, 18, 500-514.	4.1	15
106	Adaptive-Acceleration Data Center TCP. IEEE Transactions on Computers, 2014, , 1-1.	2.4	15
107	Minimum steering node set of complex networks and its applications to biomolecular networks. IET Systems Biology, 2016, 10, 116-123.	0.8	15
108	A-DSR: A DSR-based anycast protocol for IPv6 flow in mobile ad hoc networks. , 2003, , .		14

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109	A Broadcasting Retransmission Approach Based on Random Linear Network Coding. , 2008, , .		14
110	FLEXc: protein flexibility prediction using context-based statistics, predicted structural features, and sequence information. BMC Bioinformatics, 2016, 17, 281.	1.2	14
111	Identification of protein complexes from multi-relationship protein interaction networks. Human Genomics, 2016, 10, 17.	1.4	14
112	A Hybrid Clustering Algorithm for Identifying Cell Types from Single-Cell RNA-Seq Data. Genes, 2019, 10, 98.	1.0	14
113	Prediction of Microbe-Drug Associations Based on KATZ Measure. , 2019, , .		14
114	MLDRL: Multi-loss disentangled representation learning for predicting esophageal cancer response to neoadjuvant chemoradiotherapy using longitudinal CT images. Medical Image Analysis, 2022, 79, 102423.	7.0	14
115	Minimizing Movement for Target Coverage in Mobile Sensor Networks. , 2012, , .		13
116	A buffer management algorithm for improving up/down transmission congestion protocol fairness in IEEE 802.11 wireless local area networks. International Journal of Communication Systems, 2014, 27, 2228-2240.	1.6	13
117	Packet Slicing for Highly Concurrent TCPs in Data Center Networks with COTS Switches. , 2015, , .		13
118	On Enhancing Network Dynamic Adaptability for Compressive Sensing in WSNs. IEEE Transactions on Communications, 2019, 67, 8450-8459.	4.9	13
119	SCOP: a novel scaffolding algorithm based on contig classification and optimization. Bioinformatics, 2019, 35, 1142-1150.	1.8	13
120	NSDroid: efficient multi-classification of android malware using neighborhood signature in local function call graphs. International Journal of Information Security, 2021, 20, 59-71.	2.3	13
121	Heterogeneous graph inference with matrix completion for computational drug repositioning. Bioinformatics, 2021, 36, 5456-5464.	1.8	13
122	NeuralPolish: a novel Nanopore polishing method based on alignment matrix construction and orthogonal Bi-GRU Networks. Bioinformatics, 2021, 37, 3120-3127.	1.8	13
123	An Energy-Efficient DSR Routing Protocol Based on Mobility Prediction. , 0, , .		12
124	Predicting microRNA-disease associations by integrating multiple biological information. , 2015, , .		12
125	Approximating Maximum Agreement Forest on Multiple Binary Trees. Algorithmica, 2016, 76, 867-889.	1.0	12
126	AG: Adaptive Switching Granularity for Load Balancing with Asymmetric Topology in Data Center Network. , 2019, , .		12

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127	Predicting unrecognized enhancer-mediated genome topology by an ensemble machine learning model. Genome Research, 2020, 30, 1835-1845.	2.4	12
128	A simple linear time approximation algorithm for multi-processor job scheduling on four processors. Journal of Combinatorial Optimization, 2006, 13, 33-45.	0.8	11
129	A Practical Exact Algorithm for the Individual Haplotyping Problem MEC/GI. Algorithmica, 2010, 56, 283-296.	1.0	11
130	C-DEVA: Detection, evaluation, visualization and annotation of clusters from biological networks. BioSystems, 2016, 150, 78-86.	0.9	11
131	Identifying driver genes involving gene dysregulated expression, tissue-specific expression and gene-gene network. BMC Medical Genomics, 2019, 12, 168.	0.7	11
132	Improved PTAS for the constrained k-means problem. Journal of Combinatorial Optimization, 2019, 37, 1091-1110.	0.8	11
133	Identifying and ranking potential cancer drivers using representation learning on attributed network. Methods, 2021, 192, 13-24.	1.9	11
134	Higher-order Interaction Goes Neural: A Substructure Assembling Graph Attention Network for Graph Classification. IEEE Transactions on Knowledge and Data Engineering, 2021, , 1-1.	4.0	11
135	A Method to Evaluate Genome-Wide Methylation in Archival Formalin-Fixed, Paraffin-Embedded Ovarian Epithelial Cells. PLoS ONE, 2014, 9, e104481.	1.1	11
136	Sc-GPE: A Graph Partitioning-Based Cluster Ensemble Method for Single-Cell. Frontiers in Genetics, 2020, 11, 604790.	1.1	11
137	TissueNexus: a database of human tissue functional gene networks built with a large compendium of curated RNA-seq data. Nucleic Acids Research, 2022, 50, D710-D718.	6.5	11
138	A Buffer Management Scheme Based on Message Transmission Status in Delay Tolerant Networks. , 2011, , .		10
139	A Novel Algorithm for Detecting Protein Complexes with the Breadth First Search. BioMed Research International, 2014, 2014, 1-8.	0.9	10
140	Resisting re-identification mining on social graph data. World Wide Web, 2018, 21, 1759-1771.	2.7	10
141	QDAPS: Queueing Delay Aware Packet Spraying for Load Balancing in Data Center. , 2018, , .		10
142	PESM: predicting the essentiality of miRNAs based on gradient boosting machines and sequences. BMC Bioinformatics, 2020, 21, 111.	1.2	10
143	MAC: Merging Assemblies by Using Adjacency Algebraic Model and Classification. Frontiers in Genetics, 2019, 10, 1396.	1.1	10
144	Graph-Based Stock Recommendation by Time-Aware Relational Attention Network. ACM Transactions on Knowledge Discovery From Data, 2022, 16, 1-21.	2.5	10

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145	A sensitive repeat identification framework based on short and long reads. Nucleic Acids Research, 2021, 49, e100-e100.	6.5	10
146	Multiwinner Voting with Restricted Admissible Sets: Complexity and Strategyproofness. , 2018, , .		10
147	ARSC-Net: Adventitious Respiratory Sound Classification Network Using Parallel Paths with Channel-Spatial Attention. , 2021, , .		10
148	Identifying essential proteins via integration of protein interaction and gene expression data. , 2012, , .		9
149	A Continuous Secure Scheme in Static Heterogeneous Sensor Networks. IEEE Communications Letters, 2013, 17, 1868-1871.	2.5	9
150	BridgeTaint: A Bi-Directional Dynamic Taint Tracking Method for JavaScript Bridges in Android Hybrid Applications. IEEE Transactions on Information Forensics and Security, 2019, 14, 677-692.	4.5	9
151	A novel extended Pareto Optimality Consensus model for predicting essential proteins. Journal of Theoretical Biology, 2019, 480, 141-149.	0.8	9
152	A Novel Coreâ€Attachmentâ€"Based Method to Identify Dynamic Protein Complexes Based on Gene Expression Profiles and PPI Networks. Proteomics, 2019, 19, e1800129.	1.3	9
153	Evaluation of Pathway Activation for a Single Sample Toward Inflammatory Bowel Disease Classification. Frontiers in Genetics, 2019, 10, 1401.	1.1	9
154	Computational Approaches for Transcriptome Assembly Based on Sequencing Technologies. Current Bioinformatics, 2020, 15, 2-16.	0.7	9
155	A similarity-based deep learning approach for determining the frequencies of drug side effects. Briefings in Bioinformatics, 2022, 23, .	3.2	9
156	MTGNN: Multi-Task Graph Neural Network based few-shot learning for disease similarity measurement. Methods, 2022, 198, 88-95.	1.9	9
157	Drug repositioning based on multi-view learning with matrix completion. Briefings in Bioinformatics, 2022, 23, .	3.2	9
158	A Delay-Constrained and Maximum Lifetime Data Gathering Algorithm for Wireless Sensor Networks. , 2009, , .		8
159	Active Protein Interaction Network and Its Application on Protein Complex Detection. , 2011, , .		8
160	An effective method for refining predicted protein complexes based on protein activity and the mechanism of protein complex formation. BMC Systems Biology, 2013, 7, 28.	3.0	8
161	On the Minimum Link-Length Rectilinear Spanning Path Problem: Complexity and Algorithms. IEEE Transactions on Computers, 2014, 63, 3092-3100.	2.4	8
162	Detecting conserved protein complexes using a dividing-and-matching algorithm and unequally lenient criteria for network comparison. Algorithms for Molecular Biology, 2015, 10, 21.	0.3	8

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163	ProSim: A Method for Prioritizing Disease Genes Based on Protein Proximity and Disease Similarity. BioMed Research International, 2015, 2015, 1-11.	0.9	8
164	A two-step logistic regression algorithm for identifying individual-cancer-related genes. , 2015, , .		8
165	Performance Analysis and Improvement of Replica Selection Algorithms for Key-Value Stores. , 2017, , .		8
166	Computational Methods to Predict Protein Functions from Protein-Protein Interaction Networks. Current Protein and Peptide Science, 2017, 18, 1120-1131.	0.7	8
167	MultiGuideScan: a multi-processing tool for designing CRISPR guide RNA libraries. Bioinformatics, 2020, 36, 920-921.	1.8	8
168	IILLS: predicting virus-receptor interactions based on similarity and semi-supervised learning. BMC Bioinformatics, 2019, 20, 651.	1.2	8
169	An attention-based neural network basecaller for Oxford Nanopore sequencing data. , 2019, , .		8
170	Against Signed Graph Deanonymization Attacks on Social Networks. International Journal of Parallel Programming, 2019, 47, 725-739.	1.1	8
171	Flow-Aware Adaptive Pacing to Mitigate TCP Incast in Data Center Networks. IEEE/ACM Transactions on Networking, 2020, , 1-14.	2.6	8
172	Detecting Adversarial Samples for Deep Learning Models: A Comparative Study. IEEE Transactions on Network Science and Engineering, 2022, 9, 231-244.	4.1	8
173	msRepDB: a comprehensive repetitive sequence database of over 80 000 species. Nucleic Acids Research, 2022, 50, D236-D245.	6.5	8
174	DAVS: Dynamic-Chunk Quality Aware Adaptive Video Streaming using Apprenticeship Learning. , 2020, , .		8
175	Design and Implementation of Compression Algorithm Comparator for Digital Image Processing Based on Component. , 2008, , .		7
176	GO Semantic Similarity Based Analysis for Huaman Protein Interactions. , 2009, , .		7
177	Base Station Scheduler Scheme of IEEE 802.16 Mesh Mode. , 2009, , .		7
178	A logistic regression based algorithm for identifying human disease genes. , 2014, , .		7
179	A new approach to designing firewall based on multidimensional matrix. Concurrency Computation Practice and Experience, 2015, 27, 3075-3088.	1.4	7
180	Double-layer clustering method to predict protein complexes based on power-law distribution and protein sublocalization. Journal of Theoretical Biology, 2016, 395, 186-193.	0.8	7

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181	Improved approximation algorithm for maximum agreement forest of two rooted binary phylogenetic trees. Journal of Combinatorial Optimization, 2016, 32, 111-143.	0.8	7
182	A Secure Scheme for Heterogeneous Sensor Networks. IEEE Wireless Communications Letters, 2017, , 1-1.	3.2	7
183	Disease Inference with Symptom Extraction and Bidirectional Recurrent Neural Network. , 2018, , .		7
184	Efficient Association Rules Hiding Using Genetic Algorithms. Symmetry, 2018, 10, 576.	1.1	7
185	Designing Fast and Friendly TCP to Fit High Speed Data Center Networks. , 2018, , .		7
186	1D electromagnetic response modeling with arbitrary source-receiver geometry based on vector potential and its implementation in MATLAB. Geophysics, 2020, 85, F27-F38.	1.4	7
187	A Secure Scheme Based on One-Way Associated Key Management Model in Wireless Sensor Networks. IEEE Internet of Things Journal, 2021, 8, 2920-2930.	5.5	7
188	Boosting VoIP Capacity via Service Differentiation in IEEE 802.11e EDCA Networks. International Journal of Distributed Sensor Networks, 2015, 11, 235648.	1.3	7
189	QoS routing with mobility prediction in MANET. , 0, , .		6
190	SHM: Scalable and Backbone Topology-Aware Hybrid Multicast. , 2007, , .		6
191	An Improved TCP with Cross-layer Congestion Notification over Wired/Wireless Hybrid Networks. , 2008, , .		6
192	An energy-balanced clustering protocol based on dominating set for data gathering in wireless sensor networks. , 2012, , .		6
193	A (<inline-formula> <tex-math notation="LaTeX">${M}$ </tex-math>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 2 in Unattended Sensor Networks. IEEE Wireless Communications Letters, 2018, 7, 250-253.	3.2	6
194	A Novel Indoor Localization Algorithm for Efficient Mobility Management in Wireless Networks. Wireless Communications and Mobile Computing, 2018, 2018, 1-12.	0.8	6
195	D3GRN: a data driven dynamic network construction method to infer gene regulatory networks. BMC Genomics, 2019, 20, 929.	1.2	6
196	Accurate human activity recognition with multi-task learning. CCF Transactions on Pervasive Computing and Interaction, 2020, 2, 288-298.	1.7	6
197	MultiNanopolish: refined grouping method for reducing redundant calculations in Nanopolish. Bioinformatics, 2021, 37, 2757-2760.	1.8	6
198	An approximation algorithm for k-median with priorities. Science China Information Sciences, 2021, 64, 1.	2.7	6

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199	Prediction of Egfr Mutation Status in Lung Adenocarcinoma Using Multi-Source Feature Representations. , 2021, , .		6
200	A Novel Multi-Ensemble Method for Identifying Essential Proteins. Journal of Computational Biology, 2021, 28, 637-649.	0.8	6
201	Achieving High Utilization for Approximate Fair Queueing in Data Center. , 2020, , .		6
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