

Jianxing Wang

List of Publications by Year in descending order

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588
papers

13,699
citations

30070

54
h-index

43889

91
g-index

599
all docs

599
docs citations

599
times ranked

9139
citing authors

#	ARTICLE	IF	CITATIONS
1	CytoNCA: A cytoscape plugin for centrality analysis and evaluation of protein interaction networks. <i>BioSystems</i> , 2015, 127, 67-72.	2.0	813
2	Drug repositioning based on comprehensive similarity measures and Bi-Random walk algorithm. <i>Bioinformatics</i> , 2016, 32, 2664-2671.	4.1	311
3	Identification of Essential Proteins Based on Edge Clustering Coefficient. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 1070-1080.	3.0	254
4	A survey of MRI-based brain tumor segmentation methods. <i>Tsinghua Science and Technology</i> , 2014, 19, 578-595.	6.1	252
5	Prediction of lncRNA-disease associations based on inductive matrix completion. <i>Bioinformatics</i> , 2018, 34, 3357-3364.	4.1	227
6	A new essential protein discovery method based on the integration of protein-protein interaction and gene expression data. <i>BMC Systems Biology</i> , 2012, 6, 15.	3.0	211
7	Modifying the DPPlus algorithm for identifying protein complexes based on new topological structures. <i>BMC Bioinformatics</i> , 2008, 9, 398.	2.6	209
8	WiFinger. , 2016, , .		184
9	Computational drug repositioning using low-rank matrix approximation and randomized algorithms. <i>Bioinformatics</i> , 2018, 34, 1904-1912.	4.1	183
10	LDAP: a web server for lncRNA-disease association prediction. <i>Bioinformatics</i> , 2017, 33, 458-460.	4.1	182
11	A Fast Hierarchical Clustering Algorithm for Functional Modules Discovery in Protein Interaction Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 607-620.	3.0	171
12	Efficient assembly of nanopore reads via highly accurate and intact error correction. <i>Nature Communications</i> , 2021, 12, 60.	12.8	166
13	Classification of autism spectrum disorder by combining brain connectivity and deep neural network classifier. <i>Neurocomputing</i> , 2019, 324, 63-68.	5.9	161
14	Predicting Essential Proteins Based on Weighted Degree Centrality. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 407-418.	3.0	160
15	DeepSignal: detecting DNA methylation state from Nanopore sequencing reads using deep-learning. <i>Bioinformatics</i> , 2019, 35, 4586-4595.	4.1	158
16	Protein-protein interaction site prediction through combining local and global features with deep neural networks. <i>Bioinformatics</i> , 2020, 36, 1114-1120.	4.1	157
17	A survey on U-shaped networks in medical image segmentations. <i>Neurocomputing</i> , 2020, 409, 244-258.	5.9	157
18	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

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19	Minimizing Movement for Target Coverage and Network Connectivity in Mobile Sensor Networks. IEEE Transactions on Parallel and Distributed Systems, 2015, 26, 1971-1983.	5.6	149
20	Classification of Alzheimer's Disease Using Whole Brain Hierarchical Network. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 624-632.	3.0	142
21	Construction and application of dynamic protein interaction network based on time course gene expression data. Proteomics, 2013, 13, 301-312.	2.2	141
22	Iteration method for predicting essential proteins based on orthology and protein-protein interaction networks. BMC Systems Biology, 2012, 6, 87.	3.0	128
23	Towards the identification of protein complexes and functional modules by integrating PPI network and gene expression data. BMC Bioinformatics, 2012, 13, 109.	2.6	122
24	Predicting MicroRNA-Disease Associations Based on Improved MicroRNA and Disease Similarities. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1774-1782.	3.0	116
25	Drug repositioning based on bounded nuclear norm regularization. Bioinformatics, 2019, 35, i455-i463.	4.1	116
26	SinNLRR: a robust subspace clustering method for cell type detection by non-negative and low-rank representation. Bioinformatics, 2019, 35, 3642-3650.	4.1	112
27	Biomedical data and computational models for drug repositioning: a comprehensive review. Briefings in Bioinformatics, 2021, 22, 1604-1619.	6.5	110
28	Recent advances in clustering methods for protein interaction networks. BMC Genomics, 2010, 11, S10.	2.8	104
29	A comparison of the functional modules identified from time course and static PPI network data. BMC Bioinformatics, 2011, 12, 339.	2.6	103
30	ClusterViz: A Cytoscape APP for Cluster Analysis of Biological Network. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 815-822.	3.0	103
31	CytoCluster: A Cytoscape Plugin for Cluster Analysis and Visualization of Biological Networks. International Journal of Molecular Sciences, 2017, 18, 1880.	4.1	90
32	Complex Brain Network Analysis and Its Applications to Brain Disorders: A Survey. Complexity, 2017, 1-27.	1.6	90
33	Effective identification of essential proteins based on priori knowledge, network topology and gene expressions. Methods, 2014, 67, 325-333.	3.8	89
34	Dynamic protein interaction network construction and applications. Proteomics, 2014, 14, 338-352.	2.2	88
35	A Topology Potential-Based Method for Identifying Essential Proteins from PPI Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 372-383.	3.0	88
36	Predicting drug-target interaction using positive-unlabeled learning. Neurocomputing, 2016, 206, 50-57.	5.9	83

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37	Automatic ICD-9 coding via deep transfer learning. <i>Neurocomputing</i> , 2019, 324, 43-50.	5.9	79
38	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
39	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
40	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
41	DWNN-RLS: regularized least squares method for predicting circRNA-disease associations. <i>BMC Bioinformatics</i> , 2018, 19, 520.	2.6	68
42	DeepDSC: A Deep Learning Method to Predict Drug Sensitivity of Cancer Cell Lines. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 575-582.	3.0	67
43	Identifying essential proteins from active PPI networks constructed with dynamic gene expression. <i>BMC Genomics</i> , 2015, 16, S1.	2.8	66
44	Predicting essential proteins based on subcellular localization, orthology and PPI networks. <i>BMC Bioinformatics</i> , 2016, 17, 279.	2.6	66
45	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
46	Computational approaches for prioritizing candidate disease genes based on PPI networks. <i>Tsinghua Science and Technology</i> , 2015, 20, 500-512.	6.1	64
47	Protein-protein interactions: detection, reliability assessment and applications. <i>Briefings in Bioinformatics</i> , 2017, 18, bbw066.	6.5	64
48	Deeper local search for parameterized and approximation algorithms for maximum internal spanning tree. <i>Information and Computation</i> , 2017, 252, 187-200.	0.7	63
49	Attention convolutional neural network for accurate segmentation and quantification of lesions in ischemic stroke disease. <i>Medical Image Analysis</i> , 2020, 65, 101791.	11.6	63
50	Integration of breast cancer gene signatures based on graph centrality. <i>BMC Systems Biology</i> , 2011, 5, S10.	3.0	62
51	A Fully Automated Multimodal MRI-Based Multi-Task Learning for Glioma Segmentation and IDH Genotyping. <i>IEEE Transactions on Medical Imaging</i> , 2022, 41, 1520-1532.	8.9	62
52	Accurate Range-Free Localization for Anisotropic Wireless Sensor Networks. <i>ACM Transactions on Sensor Networks</i> , 2015, 11, 1-28.	3.6	61
53	Prediction of Essential Proteins Based on Overlapping Essential Modules. <i>IEEE Transactions on Nanobioscience</i> , 2014, 13, 415-424.	3.3	60
54	Computational approaches to predicting essential proteins: A survey. <i>Proteomics - Clinical Applications</i> , 2013, 7, 181-192.	1.6	59

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55	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
56	BiXGBoost: a scalable, flexible boosting-based method for reconstructing gene regulatory networks. <i>Bioinformatics</i> , 2019, 35, 1893-1900.	4.1	59
57	Multi-Receptive-Field CNN for Semantic Segmentation of Medical Images. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2020, 24, 3215-3225.	6.3	58
58	ILDMSF: Inferring Associations Between Long Non-Coding RNA and Disease Based on Multi-Similarity Fusion. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 1106-1112.	3.0	57
59	Improving Alzheimer's Disease Classification by Combining Multiple Measures. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1649-1659.	3.0	56
60	HyperAttentionDTI: improving drug-protein interaction prediction by sequence-based deep learning with attention mechanism. <i>Bioinformatics</i> , 2022, 38, 655-662.	4.1	55
61	Prediction of essential proteins based on gene expression programming. <i>BMC Genomics</i> , 2013, 14, S7.	2.8	54
62	H-PoP and H-PoPG: heuristic partitioning algorithms for single individual haplotyping of polyploids. <i>Bioinformatics</i> , 2016, 32, 3735-3744.	4.1	54
63	A secure data collection scheme based on compressive sensing in wireless sensor networks. <i>Ad Hoc Networks</i> , 2018, 70, 73-84.	5.5	54
64	An improved kernelization for ϵ -packing. <i>Information Processing Letters</i> , 2010, 110, 188-192.	0.6	53
65	Deep convolutional neural network for automatically segmenting acute ischemic stroke lesion in multi-modality MRI. <i>Neural Computing and Applications</i> , 2020, 32, 6545-6558.	5.6	53
66	Planar graph vertex partition for linear problem kernels. <i>Journal of Computer and System Sciences</i> , 2013, 79, 609-621.	1.2	52
67	Alzheimer's Disease Classification Based on Individual Hierarchical Networks Constructed With 3-D Texture Features. <i>IEEE Transactions on Nanobioscience</i> , 2017, 16, 428-437.	3.3	51
68	Multi-functional secure data aggregation schemes for WSNs. <i>Ad Hoc Networks</i> , 2018, 69, 86-99.	5.5	51
69	United neighborhood closeness centrality and orthology for predicting essential proteins. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 17, 1-1.	3.0	50
70	Transittability of complex networks and its applications to regulatory biomolecular networks. <i>Scientific Reports</i> , 2014, 4, 4819.	3.3	49
71	Identification of Protein Complexes Using Weighted PageRank-Nibble Algorithm and Core-Attachment Structure. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 179-192.	3.0	49
72	Rechecking the Centrality-Lethality Rule in the Scope of Protein Subcellular Localization Interaction Networks. <i>PLoS ONE</i> , 2015, 10, e0130743.	2.5	47

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73	Automatic ICD code assignment of Chinese clinical notes based on multilayer attention BiRNN. Journal of Biomedical Informatics, 2019, 91, 103114.	4.3	47
74	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
75	LDICDL: LncRNA-Disease Association Identification Based on Collaborative Deep Learning. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 1715-1723.	3.0	47
76	Genome-wide detection of cytosine methylations in plant from Nanopore data using deep learning. Nature Communications, 2021, 12, 5976.	12.8	47
77	An Efficient Algorithm for Constructing Maximum lifetime Tree for Data Gathering Without Aggregation in Wireless Sensor Networks. , 2010, , .		46
78	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
79	Performance Enhancement of Multipath TCP for Wireless Communications With Multiple Radio Interfaces. IEEE Transactions on Communications, 2016, 64, 3456-3466.	7.8	45
80	Transparent Computing: A Promising Network Computing Paradigm. Computing in Science and Engineering, 2017, 19, 7-20.	1.2	45
81	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
82	AIMAFE: Autism spectrum disorder identification with multi-atlas deep feature representation and ensemble learning. Journal of Neuroscience Methods, 2020, 343, 108840.	2.5	44
83	Improving protein function prediction using domain and protein complexes in PPI networks. BMC Systems Biology, 2014, 8, 35.	3.0	43
84	A fast and high performance multiple data integration algorithm for identifying human disease genes. BMC Medical Genomics, 2015, 8, S2.	1.5	43
85	Deep Matrix Factorization Improves Prediction of Human CircRNA-Disease Associations. IEEE Journal of Biomedical and Health Informatics, 2021, 25, 891-899.	6.3	43
86	A Fast Agglomerate Algorithm for Mining Functional Modules in Protein Interaction Networks. , 2008, , .		40
87	An optimization of virtual machine selection and placement by using memory content similarity for server consolidation in cloud. Future Generation Computer Systems, 2018, 84, 98-107.	7.5	40
88	Load-balancing routing in software defined networks with multiple controllers. Computer Networks, 2018, 141, 82-91.	5.1	40
89	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
90	Defending collaborative false data injection attacks in wireless sensor networks. Information Sciences, 2014, 254, 39-53.	6.9	39

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91	Biological network motif detection and evaluation. BMC Systems Biology, 2011, 5, S5.	3.0	38
92	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
93	DMFLDA: A Deep Learning Framework for Predicting lncRNAâ€™Disease Associations. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2353-2363.	3.0	38
94	Complexity and parameterized algorithms for Cograph Editing. Theoretical Computer Science, 2012, 461, 45-54.	0.9	37
95	IDENTIFICATION OF ESSENTIAL PROTEINS FROM WEIGHTED PROTEINâ€™PROTEIN INTERACTION NETWORKS. Journal of Bioinformatics and Computational Biology, 2013, 11, 1341002.	0.8	37
96	Improved ASD classification using dynamic functional connectivity and multi-task feature selection. Pattern Recognition Letters, 2020, 138, 82-87.	4.2	37
97	Identifying the overlapping complexes in protein interaction networks. International Journal of Data Mining and Bioinformatics, 2010, 4, 91.	0.1	36
98	Identifying disease genes by integrating multiple data sources. BMC Medical Genomics, 2014, 7, S2.	1.5	36
99	CAPS: Coding-Based Adaptive Packet Spraying to Reduce Flow Completion Time in Data Center. IEEE/ACM Transactions on Networking, 2019, 27, 2338-2353.	3.8	36
100	Essential protein discovery based on a combination of modularity and conservatism. Methods, 2016, 110, 54-63.	3.8	35
101	HybridDock: A Hybrid Proteinâ€™Ligand Docking Protocol Integrating Protein- and Ligand-Based Approaches. Journal of Chemical Information and Modeling, 2016, 56, 1078-1087.	5.4	35
102	An interpretable boosting model to predict side effects of analgesics for osteoarthritis. BMC Systems Biology, 2018, 12, 105.	3.0	35
103	Overlap matrix completion for predicting drug-associated indications. PLoS Computational Biology, 2019, 15, e1007541.	3.2	35
104	Drug-Target Interaction Prediction Using Multi-Head Self-Attention and Graph Attention Network. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 2208-2218.	3.0	35
105	Identification of Hierarchical and Overlapping Functional Modules in PPI Networks. IEEE Transactions on Nanobioscience, 2012, 11, 386-393.	3.3	33
106	Disease gene identification by using graph kernels and Markov random fields. Science China Life Sciences, 2014, 57, 1054-1063.	4.9	33
107	A feature selection method for prediction essential protein. Tsinghua Science and Technology, 2015, 20, 491-499.	6.1	33
108	BOSS: a novel scaffolding algorithm based on an optimized scaffold graph. Bioinformatics, 2017, 33, 169-176.	4.1	33

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109	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
110	Essential Proteins Discovery from Weighted Protein Interaction Networks. Lecture Notes in Computer Science, 2010, , 89-100.	1.3	33
111	Predicting Human lncRNA-Disease Associations Based on Geometric Matrix Completion. IEEE Journal of Biomedical and Health Informatics, 2020, 24, 2420-2429.	6.3	32
112	Integrating Omics Data With a Multiplex Network-Based Approach for the Identification of Cancer Subtypes. IEEE Transactions on Nanobioscience, 2016, 15, 335-342.	3.3	31
113	High-Risk Prediction of Cardiovascular Diseases via Attention-Based Deep Neural Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1093-1105.	3.0	31
114	A Framework for Integrating Multiple Biological Networks to Predict MicroRNA-Disease Associations. IEEE Transactions on Nanobioscience, 2017, 16, 100-107.	3.3	30
115	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
116	Prediction of Essential Proteins by Integration of PPI Network Topology and Protein Complexes Information. Lecture Notes in Computer Science, 2011, , 12-24.	1.3	30
117	Reducing transport latency for short flows with multipath TCP. Journal of Network and Computer Applications, 2018, 108, 20-36.	9.1	29
118	Constructing Disease Similarity Networks Based on Disease Module Theory. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 906-915.	3.0	29
119	A New Method for Predicting Protein Functions From Dynamic Weighted Interactome Networks. IEEE Transactions on Nanobioscience, 2016, 15, 131-139.	3.3	28
120	An improved linear kernel for complementary maximal strip recovery: Simpler and smaller. Theoretical Computer Science, 2019, 786, 55-66.	0.9	28
121	Efficient multi-kernel DCNN with pixel dropout for stroke MRI segmentation. Neurocomputing, 2019, 350, 117-127.	5.9	28
122	A discrete-time Geo/G/1 retrial queue with preferred and impatient customers. Applied Mathematical Modelling, 2013, 37, 2552-2561.	4.2	27
123	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
124	On Threshold-Free Error Detection for Industrial Wireless Sensor Networks. IEEE Transactions on Industrial Informatics, 2018, 14, 2199-2209.	11.3	27
125	DyNetViewer: a Cytoscape app for dynamic network construction, analysis and visualization. Bioinformatics, 2018, 34, 1597-1599.	4.1	27
126	Social profile-based multicast routing scheme for delay-tolerant networks. , 2013, , .		26

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127	Parameterized complexity of Max-lifetime Target Coverage in wireless sensor networks. Theoretical Computer Science, 2014, 518, 32-41.	0.9	26
128	Energy-efficient active tag searching in large scale RFID systems. Information Sciences, 2015, 317, 143-156.	6.9	26
129	Design of a stabilizing AQM controller for large-delay networks based on internal model control. Computer Communications, 2008, 31, 1911-1918.	5.1	25
130	<i>hFâ€measure</i> : A new measurement for evaluating clusters in proteinâ€protein interaction networks. Proteomics, 2013, 13, 291-300.	2.2	25
131	EPGA: <i>de novo</i> assembly using the distributions of reads and insert size. Bioinformatics, 2015, 31, 825-833.	4.1	25
132	Controllability and Its Applications to Biological Networks. Journal of Computer Science and Technology, 2019, 34, 16-34.	1.5	25
133	A New Method for Identifying Essential Proteins Based on Edge Clustering Coefficient. Lecture Notes in Computer Science, 2011, , 87-98.	1.3	25
134	An AODV-based anycast protocol in mobile ad hoc network. , 0, , .		24
135	Essential Protein Discovery Based on Network Motif and Gene Ontology. , 2011, , .		24
136	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
137	DDIGIP: predicting drug-drug interactions based on Gaussian interaction profile kernels. BMC Bioinformatics, 2019, 20, 538.	2.6	24
138	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
139	Deep convolutional neural network for accurate segmentation and quantification of white matter hyperintensities. Neurocomputing, 2020, 384, 231-242.	5.9	24
140	An Effective Convolutional Neural Network for Classifying Red Blood Cells in Malaria Diseases. Interdisciplinary Sciences, Computational Life Sciences, 2020, 12, 217-225.	3.6	24
141	Prediction of disease genes using tissue-specified gene-gene network. BMC Systems Biology, 2014, 8, S3.	3.0	23
142	Discovering essential proteins based on PPI network and protein complex. International Journal of Data Mining and Bioinformatics, 2015, 12, 24.	0.1	23
143	Randomized parameterized algorithms for P_2 -Packing and Co-Path Packing problems. Journal of Combinatorial Optimization, 2015, 29, 125-140.	1.3	23
144	Sprites: detection of deletions from sequencing data by re-aligning split reads. Bioinformatics, 2016, 32, 1788-1796.	4.1	23

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145	MMM: classification of schizophrenia using multi-modality multi-atlas feature representation and multi-kernel learning. <i>Multimedia Tools and Applications</i> , 2018, 77, 29651-29667.	3.9	23
146	Multimodal Disentangled Variational Autoencoder With Game Theoretic Interpretability for Glioma Grading. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2022, 26, 673-684.	6.3	23
147	Identifying protein complexes from interaction networks based on clique percolation and distance restriction. <i>BMC Genomics</i> , 2010, 11, S10.	2.8	22
148	A fast and accurate algorithm for single individual haplotyping. <i>BMC Systems Biology</i> , 2012, 6, S8.	3.0	22
149	Identifying Dynamic Protein Complexes Based on Gene Expression Profiles and PPI Networks. <i>BioMed Research International</i> , 2014, 2014, 1-10.	1.9	22
150	Synthesizing Existing CSMA and TDMA Based MAC Protocols for VANETs. <i>Sensors</i> , 2017, 17, 338.	3.8	22
151	MMHGE: detecting mild cognitive impairment based on multi-atlas multi-view hybrid graph convolutional networks and ensemble learning. <i>Cluster Computing</i> , 2021, 24, 103-113.	5.0	22
152	Mitigating Packet Reordering for Random Packet Spraying in Data Center Networks. <i>IEEE/ACM Transactions on Networking</i> , 2021, 29, 1183-1196.	3.8	22
153	Prioritizing Disease Genes by Using Search Engine Algorithm. <i>Current Bioinformatics</i> , 2016, 11, 195-202.	1.5	22
154	An automated COVID-19 triage pipeline using artificial intelligence based on chest radiographs and clinical data. <i>Npj Digital Medicine</i> , 2022, 5, 5.	10.9	22
155	Identifying protein complexes based on density and modularity in protein-protein interaction network. <i>BMC Systems Biology</i> , 2013, 7, S12.	3.0	21
156	A hybrid algorithm based on binary chemical reaction optimization and tabu search for feature selection of high-dimensional biomedical data. <i>Tsinghua Science and Technology</i> , 2018, 23, 733-743.	6.1	21
157	Rethinking Fast and Friendly Transport in Data Center Networks. <i>IEEE/ACM Transactions on Networking</i> , 2020, 28, 2364-2377.	3.8	21
158	MCHMDA: Predicting Microbe-Disease Associations Based on Similarities and Low-Rank Matrix Completion. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 611-620.	3.0	21
159	SSRE: Cell Type Detection Based on Sparse Subspace Representation and Similarity Enhancement. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 282-291.	6.9	21
160	Analysis of Single-Cell RNA-seq Data by Clustering Approaches. <i>Current Bioinformatics</i> , 2019, 14, 314-322.	1.5	21
161	Improving circRNA-disease association prediction by sequence and ontology representations with convolutional and recurrent neural networks. <i>Bioinformatics</i> , 2021, 36, 5656-5664.	4.1	21
162	A model of higher accuracy for the individual haplotyping problem based on weighted SNP fragments and genotype with errors. <i>Bioinformatics</i> , 2008, 24, i105-i113.	4.1	20

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163	Adaptive explicit congestion control based on bandwidth estimation for high bandwidth-delay product networks. <i>Computer Communications</i> , 2013, 36, 1235-1244.	5.1	20
164	Prioritization of orphan disease-causing genes using topological feature and GO similarity between proteins in interaction networks. <i>Science China Life Sciences</i> , 2014, 57, 1064-1071.	4.9	20
165	Searching High-Order SNP Combinations for Complex Diseases Based on Energy Distribution Difference. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 695-704.	3.0	20
166	ARS: Cross-layer adaptive request scheduling to mitigate TCP incast in data center networks. , 2016, , .		20
167	ISEA: Iterative Seed-Extension Algorithm for De Novo Assembly Using Paired-End Information and Insert Size Distribution. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 916-925.	3.0	20
168	Task-Aware TCP in Data Center Networks. <i>IEEE/ACM Transactions on Networking</i> , 2019, 27, 389-404.	3.8	20
169	Receiver-driven fair congestion control for TCP outcast in data center networks. <i>Journal of Network and Computer Applications</i> , 2019, 131, 75-88.	9.1	20
170	Page-sharing-based virtual machine packing with multi-resource constraints to reduce network traffic in migration for clouds. <i>Future Generation Computer Systems</i> , 2019, 96, 462-471.	7.5	20
171	Prediction of Glioma Grade using Intratumoral and Peritumoral Radiomic Features from Multiparametric MRI Images. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, PP, 1-1.	3.0	20
172	A robust proportional controller for AQM based on optimized second-order system model. <i>Computer Communications</i> , 2008, 31, 2468-2477.	5.1	19
173	A cross-layer TCP for providing fairness in wireless mesh networks. <i>International Journal of Communication Systems</i> , 2011, 24, 1611-1626.	2.5	19
174	Improved deterministic algorithms for weighted matching and packing problems. <i>Theoretical Computer Science</i> , 2011, 412, 2503-2512.	0.9	19
175	EPGA2: memory-efficient <i>de novo</i> assembler. <i>Bioinformatics</i> , 2015, 31, 3988-3990.	4.1	19
176	Combining static and dynamic features for real-time moving pedestrian detection. <i>Multimedia Tools and Applications</i> , 2019, 78, 3781-3795.	3.9	19
177	Nothing Blocks Me: Precise and Real-Time LOS/NLOS Path Recognition in RFID Systems. <i>IEEE Internet of Things Journal</i> , 2019, 6, 5814-5824.	8.7	19
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586	Overlap matrix completion for predicting drug-associated indications. , 2019, 15, e1007541.		0
587	Overlap matrix completion for predicting drug-associated indications. , 2019, 15, e1007541.		0
588	Overlap matrix completion for predicting drug-associated indications. , 2019, 15, e1007541.		0