Weiping Wang

List of Publications by Year
in descending order

385	7,491	87888	85541
papers	citations	38	71
		h-index	g-index

386	386	386	5965
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	BlockPolish: accurate polishing of long-read assembly via block divide-and-conquer. Briefings in Bioinformatics, 2022, 23, .	6.5	2
2	NPCDR: natural product-based drug combination and its disease-specific molecular regulation. Nucleic Acids Research, 2022, 50, D1324-D1333.	14.5	21
3	Graph-Based Stock Recommendation by Time-Aware Relational Attention Network. ACM Transactions on Knowledge Discovery From Data, 2022, 16, 1-21.	3.5	10
4	Artificial intelligence for prediction of COVID-19 progression using CT imaging and clinical data. European Radiology, 2022, 32, 205-212.	4.5	42
5	A similarity-based deep learning approach for determining the frequencies of drug side effects. Briefings in Bioinformatics, 2022, 23, .	6.5	9
6	Detecting Adversarial Samples for Deep Learning Models: A Comparative Study. IEEE Transactions on Network Science and Engineering, 2022, 9, 231-244.	6.4	8
7	msRepDB: a comprehensive repetitive sequence database of over 80 000 species. Nucleic Acids Research, 2022, 50, D236-D245.	14.5	8
8	SYNBIP: synthetic binding proteins for research, diagnosis and therapy. Nucleic Acids Research, 2022, 50, D560-D570.	14.5	48
9	HyperAttentionDTI: improving drug–protein interaction prediction by sequence-based deep learning with attention mechanism. Bioinformatics, 2022, 38, 655-662.	4.1	55
10	MTGNN: Multi-Task Graph Neural Network based few-shot learning for disease similarity measurement. Methods, 2022, 198, 88-95.	3.8	9
11	An integrated brain-specific network identifies genes associated with neuropathologic and clinical traits of Alzheimer's disease. Briefings in Bioinformatics, 2022, 23, .	6.5	3
12	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.	14.5	11
13	VAMP: A Predictive Approach to Audio/Video Bitrate Adaptation Over Wireless Networks. IEEE Wireless Communications Letters, 2022, 11, 513-517.	5.0	3
14	An Improved Bound and Singleton-Optimal Constructions of Fractional Repetition Codes. IEEE Transactions on Communications, 2022, 70, 749-758.	7.8	0
15	AlzCode: a platform for multiview analysis of genes related to Alzheimer's disease. Bioinformatics, 2022, 38, 2030-2032.	4.1	3
16	An automated COVID-19 triage pipeline using artificial intelligence based on chest radiographs and clinical data. Npj Digital Medicine, 2022, 5, 5.	10.9	22
17	On Some Capacity-Achieving Fractional Repetition Codes. IEEE Transactions on Vehicular Technology, 2022, 71, 3332-3337.	6.3	1
18	Drug repositioning based on multi-view learning with matrix completion. Briefings in Bioinformatics, 2022, 23, .	6.5	9

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19	End-to-End Congestion Control to Provide Deterministic Latency Over Internet. IEEE Communications Letters, 2022, 26, 843-847.	4.1	5
20	A Refined Branching Algorithm for the Maximum Satisfiability Problem. Algorithmica, 2022, 84, 982-1006.	1.3	2
21	PDMDA: predicting deep-level miRNA–disease associations with graph neural networks and sequence features. Bioinformatics, 2022, 38, 2226-2234.	4.1	18
22	TRScore: a 3D RepVGG-based scoring method for ranking protein docking models. Bioinformatics, 2022, 38, 2444-2451.	4.1	6
23	An approximation algorithm for lower-bounded k-median with constant factor. Science China Information Sciences, 2022, 65, 1.	4.3	2
24	MLDRL: Multi-loss disentangled representation learning for predicting esophageal cancer response to neoadjuvant chemoradiotherapy using longitudinal CT images. Medical Image Analysis, 2022, 79, 102423.	11.6	14
25	Chinese clinical named entity recognition via multi-head self-attention based BiLSTM-CRF. Artificial Intelligence in Medicine, 2022, 127, 102282.	6.5	38
26	HDIContact: a novel predictor of residue–residue contacts on hetero-dimer interfaces via sequential information and transfer learning strategy. Briefings in Bioinformatics, 2022, 23, .	6.5	5
27	A Buffer-Based Adaptive Bitrate Approach in Wireless Networks With Iterative Correction. IEEE Wireless Communications Letters, 2022, 11, 1644-1648.	5.0	2
28	Achieving Per-Flow Fairness and High Utilization With Limited Priority Queues in Data Center. IEEE/ACM Transactions on Networking, 2022, 30, 2374-2387.	3.8	4
29	FGL_Droid: An Efficient Android Malware Detection Method Based on Hybrid Analysis. Security and Communication Networks, 2022, 2022, 1-11.	1.5	6
30	High-Rate Constructions of Exact-Repair Regenerating Codes. , 2022, , .		0
31	Graph Searches and Their End Vertices. Algorithmica, 2022, 84, 2642-2666.	1.3	3
32	Copa+: Analysis and Improvement of the Delay-based Congestion Control Algorithm Copa. , 2022, , .		4
33	Identifying and ranking potential cancer drivers using representation learning on attributed network. Methods, 2021, 192, 13-24.	3.8	11
34	Computational drug repositioning based on multi-similarities bilinear matrix factorization. Briefings in Bioinformatics, 2021, 22, .	6.5	49
35	NSDroid: efficient multi-classification of android malware using neighborhood signature in local function call graphs. International Journal of Information Security, 2021, 20, 59-71.	3.4	13
36	Runtime Performances of Randomized Search Heuristics for the Dynamic Weighted Vertex Cover Problem. Algorithmica, 2021, 83, 906-939.	1.3	5

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37	MMHGE: detecting mild cognitive impairment based on multi-atlas multi-view hybrid graph convolutional networks and ensemble learning. Cluster Computing, 2021, 24, 103-113.	5.0	22
38	Phase prediction of Ni-base superalloys via high-throughput experiments and machine learning. Materials Research Letters, 2021, 9, 32-40.	8.7	49
39	Accurate Respiration Monitoring for Mobile Users With Commercial RFID Devices. IEEE Journal on Selected Areas in Communications, 2021, 39, 513-525.	14.0	34
40	Distributed Probabilistic Offloading in Edge Computing for 6G-Enabled Massive Internet of Things. IEEE Internet of Things Journal, 2021, 8, 5298-5308.	8.7	60
41	Heterogeneous graph inference with matrix completion for computational drug repositioning. Bioinformatics, 2021, 36, 5456-5464.	4.1	13
42	A Secure Scheme Based on One-Way Associated Key Management Model in Wireless Sensor Networks. IEEE Internet of Things Journal, 2021, 8, 2920-2930.	8.7	7
43	An Exploit Kits Detection Approach Based on HTTP Message Graph. IEEE Transactions on Information Forensics and Security, 2021, 16, 3387-3400.	6.9	4
44	MultiNanopolish: refined grouping method for reducing redundant calculations in Nanopolish. Bioinformatics, 2021, 37, 2757-2760.	4.1	6
45	SSRE: Cell Type Detection Based on Sparse Subspace Representation and Similarity Enhancement. Genomics, Proteomics and Bioinformatics, 2021, 19, 282-291.	6.9	21
46	An approximation algorithm for k-median with priorities. Science China Information Sciences, 2021, 64, 1.	4.3	6
47	A convolutional neural network and graph convolutional network-based method for predicting the classification of anatomical therapeutic chemicals. Bioinformatics, 2021, 37, 2841-2847.	4.1	18
48	3A.004â€…Internet-based textual big data and road traffic injuries. , 2021, , .		0
49	AAC: Adaptively Adjusting Concurrency by Exploiting Path Diversity in Datacenter Networks. Journal of Network and Systems Management, 2021, 29, 1.	4.9	2
50	Incremental algorithms for the maximum internal spanning tree problem. Science China Information Sciences, 2021, 64, 1.	4.3	1
51	Generalized Predictive Control of the Time Window for Energy Efficient Ethernet With Prediction. IEEE Communications Letters, 2021, 25, 1491-1495.	4.1	0
52	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.	12.3	87
53	NeuralPolish: a novel Nanopore polishing method based on alignment matrix construction and orthogonal Bi-GRU Networks. Bioinformatics, 2021, 37, 3120-3127.	4.1	13
54	Mitigating Packet Reordering for Random Packet Spraying in Data Center Networks. IEEE/ACM Transactions on Networking, 2021, 29, 1183-1196.	3.8	22

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55	Prediction of Egfr Mutation Status in Lung Adenocarcinoma Using Multi-Source Feature Representations. , 2021, , .		6
56	A novel graph attention model for predicting frequencies of drug–side effects from multi-view data. Briefings in Bioinformatics, 2021, 22, .	6.5	21
57	De Novo Prediction of Drug–Target Interactions Using Laplacian Regularized Schatten p-Norm Minimization. Journal of Computational Biology, 2021, 28, 660-673.	1.6	2
58	A Novel Multi-Ensemble Method for Identifying Essential Proteins. Journal of Computational Biology, 2021, 28, 637-649.	1.6	6
59	ORP: An Online Rule Placement Scheme to Optimize the Traffic Overhead for Data Center Networks. IEEE Transactions on Network Science and Engineering, 2021, 8, 2183-2197.	6.4	2
60	A sensitive repeat identification framework based on short and long reads. Nucleic Acids Research, 2021, 49, e100-e100.	14.5	10
61	Modeling and Analysis of Latency Distribution in the 40-100Gbps Dual-Mode Energy Efficient Ethernet. IEEE Transactions on Green Communications and Networking, 2021, 5, 1426-1437.	5.5	0
62	Yap Promotes Noncanonical Wnt Signals From Cardiomyocytes for Heart Regeneration. Circulation Research, 2021, 129, 782-797.	4.5	30
63	Higher-order Interaction Goes Neural: A Substructure Assembling Graph Attention Network for Graph Classification. IEEE Transactions on Knowledge and Data Engineering, 2021, , 1-1.	5.7	11
64	RMC: Reordering Marking and Coding for Fine-Grained Load Balancing in Data Centers. IEEE Transactions on Communications, 2021, 69, 8363-8374.	7.8	4
65	OUP accepted manuscript. Briefings in Bioinformatics, 2021, , .	6.5	1
66	Mitigating Port Starvation for Shallow-buffered Switches in Datacenter Networks. , 2021, , .		3
67	GTCP: Hybrid Congestion Control for Cross-Datacenter Networks. , 2021, , .		5
68	Cutting the Request Completion Time in Key-value Stores with Distributed Adaptive Scheduler. , 2021, , .		1
69	Genome-wide detection of cytosine methylations in plant from Nanopore data using deep learning. Nature Communications, 2021, 12, 5976.	12.8	47
70	Improving circRNA–disease association prediction by sequence and ontology representations with convolutional and recurrent neural networks. Bioinformatics, 2021, 36, 5656-5664.	4.1	21
71	Expandable Fractional Repetition Codes for Distributed Storage Systems. , 2021, , .		0
72	SCOTCluster: Deep Clustering with Optimal Transport for Large-scale Single-cell RNA-seq Data. , 2021, , .		0

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73	IoT-IE: An Information-Entropy-Based Approach to Traffic Anomaly Detection in Internet of Things. Security and Communication Networks, 2021, 2021, 1-13.	1.5	3
74	BEA-SegNet: Body and Edge Aware Network for Medical Image Segmentation. , 2021, , .		3
75	Identifying virus-receptor interactions through matrix completion with similarity fusion. , 2021, , .		1
76	MTFIL-Net: automated Alzheimer's disease detection and MMSE score prediction based on feature interactive learning. , 2021, , .		3
77	MAIN: Multimodal Attention-based Fusion Networks for Diagnosis Prediction. , 2021, , .		2
78	GraphIsoFun: a graph neural network based approach for splice isoform function prediction. , 2021, , .		0
79	ARSC-Net: Adventitious Respiratory Sound Classification Network Using Parallel Paths with Channel-Spatial Attention. , 2021, , .		10
80	EFCA: An Extended Formal Concept Analysis Method for Aspect Extraction in Healthcare Informatics. , 2021, , .		2
81	MultiGuideScan: a multi-processing tool for designing CRISPR guide RNA libraries. Bioinformatics, 2020, 36, 920-921.	4.1	8
82	Protein–protein interaction site prediction through combining local and global features with deep neural networks. Bioinformatics, 2020, 36, 1114-1120.	4.1	157
83	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
84	LSCDroid: Malware Detection Based on Local Sensitive API Invocation Sequences. IEEE Transactions on Reliability, 2020, 69, 174-187.	4.6	20
85	RepAHR: an improved approach for de novo repeat identification by assembly of the high-frequency reads. BMC Bioinformatics, 2020, 21, 463.	2.6	4
86	Sensing-HH: A Deep Hybrid Attention Model for Footwear Recognition. Electronics (Switzerland), 2020, 9, 1552.	3.1	0
87	Attention convolutional neural network for accurate segmentation and quantification of lesions in ischemic stroke disease. Medical Image Analysis, 2020, 65, 101791.	11.6	63
88	Identification of early mild cognitive impairment using multi-modal data and graph convolutional networks. BMC Bioinformatics, 2020, 21, 123.	2.6	17
89	Flow-Aware Adaptive Pacing to Mitigate TCP Incast in Data Center Networks. IEEE/ACM Transactions on Networking, 2020, , 1-14.	3.8	8
90	Predicting unrecognized enhancer-mediated genome topology by an ensemble machine learning model. Genome Research, 2020, 30, 1835-1845.	5.5	12

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91	DeepFrag-k: a fragment-based deep learning approach for protein fold recognition. BMC Bioinformatics, 2020, 21, 203.	2.6	5
92	Information Dissemination for the Adaptive Replica Selection algorithm in Key-Value Stores. , 2020, , .		0
93	AIMAFE: Autism spectrum disorder identification with multi-atlas deep feature representation and ensemble learning. Journal of Neuroscience Methods, 2020, 343, 108840.	2.5	44
94	ClusterMine: A knowledge-integrated clustering approach based on expression profiles of gene sets. Journal of Bioinformatics and Computational Biology, 2020, 18, 2040009.	0.8	3
95	Accurate human activity recognition with multi-task learning. CCF Transactions on Pervasive Computing and Interaction, 2020, 2, 288-298.	2.6	6
96	Pipeline-Based Chunk Scheduling to Improve ABR Performance in DASH System. , 2020, , .		3
97	Rethinking Fast and Friendly Transport in Data Center Networks. IEEE/ACM Transactions on Networking, 2020, 28, 2364-2377.	3.8	21
98	Achieving Fast Convergence and High Efficiency using Differential Explicit Feedback in Data Center. , 2020, , .		2
99	Dynamic kidney paired exchange using modified multiverse optimization. Evolutionary Intelligence, 2020, , 1.	3.6	0
100	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
101	PESM: predicting the essentiality of miRNAs based on gradient boosting machines and sequences. BMC Bioinformatics, 2020, 21, 111.	2.6	10
102	1D electromagnetic response modeling with arbitrary source-receiver geometry based on vector potential and its implementation in MATLAB. Geophysics, 2020, 85, F27-F38.	2.6	7
103	Computational Approaches for Transcriptome Assembly Based on Sequencing Technologies. Current Bioinformatics, 2020, 15, 2-16.	1.5	9
104	Single-Cell Clustering Based on Shared Nearest Neighbor and Graph Partitioning. Interdisciplinary Sciences, Computational Life Sciences, 2020, 12, 117-130.	3.6	21
105	A novel approach based on deep residual learning to predict drug's anatomical therapeutic chemical code. , 2020, , .		4
106	Exploring the dynamics and interplay of human papillomavirus and cervical tumorigenesis by integrating biological data into a mathematical model. BMC Bioinformatics, 2020, 21, 152.	2.6	17
107	Multi-task Based Few-Shot Learning for Disease Similarity Measurement. , 2020, , .		1
108	RPAD: An Unsupervised HTTP Request Parameter Anomaly Detection Method. , 2020, , .		2

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109	WSAD: An Unsupervised Web Session Anomaly Detection Method. , 2020, , .		1
110	Sc-GPE: A Graph Partitioning-Based Cluster Ensemble Method for Single-Cell. Frontiers in Genetics, 2020, 11, 604790.	2.3	11
111	DAVS: Dynamic-Chunk Quality Aware Adaptive Video Streaming using Apprenticeship Learning. , 2020, , .		8
112	On the Optimal Minimum Distance of Fractional Repetition Codes. , 2020, , .		2
113	Joint Learning of Primary and Secondary Labels based on Multi-scale Representation for Alzheimerâ€™s Disease Diagnosis. , 2020, , .		1
114	Achieving High Utilization for Approximate Fair Queueing in Data Center. , 2020, , .		6
115	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.	6.9	9
116	Combining static and dynamic features for real-time moving pedestrian detection. Multimedia Tools and Applications, 2019, 78, 3781-3795.	3.9	19
117	Targeting TRPV1 on cellular plasticity regulated by Ovol 2 and Zeb 1 in hepatocellular carcinoma. Biomedicine and Pharmacotherapy, 2019, 118, 109270.	5.6	16
118	A novel extended Pareto Optimality Consensus model for predicting essential proteins. Journal of Theoretical Biology, 2019, 480, 141-149.	1.7	9
119	Randomized Parameterized Algorithms for the Kidney Exchange Problem. Algorithms, 2019, 12, 50.	2.1	2
120	Drug repositioning based on bounded nuclear norm regularization. Bioinformatics, 2019, 35, i455-i463.	4.1	116
121	An Efficient Authentication Scheme Based on Deployment Knowledge Against Mobile Sink Replication Attack in UWSNs. IEEE Internet of Things Journal, 2019, 6, 9738-9747.	8.7	4
122	PDRCNN: Precise Phishing Detection with Recurrent Convolutional Neural Networks. Security and Communication Networks, 2019, 2019, 1-15.	1.5	50
123	DDT. , 2019, , .		2
124	On Enhancing Network Dynamic Adaptability for Compressive Sensing in WSNs. IEEE Transactions on Communications, 2019, 67, 8450-8459.	7.8	13
125	ReActor: Real-time and Accurate Contactless Gesture Recognition with RFID. , 2019, , .		18
126	A Sequence-Based Novel Approach for Quality Evaluation of Third-Generation Sequencing Reads. Genes, 2019, 10, 44.	2.4	3

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127	A Novel Core–Attachment–Based Method to Identify Dynamic Protein Complexes Based on Gene Expression Profiles and PPI Networks. Proteomics, 2019, 19, e1800129.	2.2	9
128	Task-Aware TCP in Data Center Networks. IEEE/ACM Transactions on Networking, 2019, 27, 389-404.	3.8	20
129	A Hybrid Clustering Algorithm for Identifying Cell Types from Single-Cell RNA-Seq Data. Genes, 2019, 10, 98.	2.4	14
130	An improved algorithm for the $(n, 3)$-MaxSAT problem: asking branchings to satisfy the clauses. Journal of Combinatorial Optimization, 2019, , 1.	1.3	1
131	Identifying Interactions Between Kinases and Substrates Based on Protein–Protein Interaction Network. Journal of Computational Biology, 2019, 26, 836-845.	1.6	5
132	DeepSignal: detecting DNA methylation state from Nanopore sequencing reads using deep-learning. Bioinformatics, 2019, 35, 4586-4595.	4.1	158
133	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
134	Nothing Blocks Me: Precise and Real-Time LOS/NLOS Path Recognition in RFID Systems. IEEE Internet of Things Journal, 2019, 6, 5814-5824.	8.7	19
135	Automatic ICD code assignment of Chinese clinical notes based on multilayer attention BiRNN. Journal of Biomedical Informatics, 2019, 91, 103114.	4.3	47
136	Project-driven information talents training mode in opening environment. , 2019, , .		1
137	de novo repeat detection based on the third generation sequencing reads. , 2019, , .		1
138	Tentative diagnosis prediction via deep understanding of patient narratives. , 2019, , .		3
139	Prediction of Microbe-Drug Associations Based on KATZ Measure. , 2019, , .		14
140	Classification of Schizophrenia by Iterative Random Forest Feature Selection Based on DNA Methylation Array Data. , 2019, , .		1
141	VDetector: Detecting Vulnerability Based on Inter-Component Data Flows in Android Applications. , 2019, , .		0
142	Identifying driver genes involving gene dysregulated expression, tissue-specific expression and gene-gene network. BMC Medical Genomics, 2019, 12, 168.	1.5	11
143	IILLS: predicting virus-receptor interactions based on similarity and semi-supervised learning. BMC Bioinformatics, 2019, 20, 651.	2.6	8
144	Multi-level Glioma Segmentation using 3D U-Net Combined Attention Mechanism with Atrous Convolution. , 2019, , .		16

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145	An attention-based neural network basecaller for Oxford Nanopore sequencing data. , 2019, , .		8
146	Drug and disease similarity calculation platform for drug repositioning. , 2019, , .		2
147	AttentionDTA: prediction of drug–target binding affinity using attention model. , 2019, , .		48
148	D3GRN: a data driven dynamic network construction method to infer gene regulatory networks. BMC Genomics, 2019, 20, 929.	2.8	6
149	AG: Adaptive Switching Granularity for Load Balancing with Asymmetric Topology in Data Center Network. , 2019, , .		12
150	On the Optimal Reconstruction Degree of Fractional Repetition Codes. , 2019, , .		0
151	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
152	CSA: a web service for the complete process of ChIP-Seq analysis. BMC Bioinformatics, 2019, 20, 515.	2.6	2
153	DDIGIP: predicting drug-drug interactions based on Gaussian interaction profile kernels. BMC Bioinformatics, 2019, 20, 538.	2.6	24
154	Overlap matrix completion for predicting drug-associated indications. PLoS Computational Biology, 2019, 15, e1007541.	3.2	35
155	SCOP: a novel scaffolding algorithm based on contig classification and optimization. Bioinformatics, 2019, 35, 1142-1150.	4.1	13
156	Improved PTAS for the constrained k-means problem. Journal of Combinatorial Optimization, 2019, 37, 1091-1110.	1.3	11
157	BiXGBoost: a scalable, flexible boosting-based method for reconstructing gene regulatory networks. Bioinformatics, 2019, 35, 1893-1900.	4.1	59
158	Control principles for complex biological networks. Briefings in Bioinformatics, 2019, 20, 2253-2266.	6.5	46
159	Against Signed Graph Deanonymization Attacks on Social Networks. International Journal of Parallel Programming, 2019, 47, 725-739.	1.5	8
160	Adjusting Packet Size to Mitigate TCP Incast in Data Center Networks with COTS Switches. IEEE Transactions on Cloud Computing, 2019, , 1-1.	4.4	23
161	Evaluation of Pathway Activation for a Single Sample Toward Inflammatory Bowel Disease Classification. Frontiers in Genetics, 2019, 10, 1401.	2.3	9
162	MAC: Merging Assemblies by Using Adjacency Algebraic Model and Classification. Frontiers in Genetics, 2019, 10, 1396.	2.3	10

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163	Schizophrenia Identification Using Multi-View Graph Measures of Functional Brain Networks. Frontiers in Bioengineering and Biotechnology, 2019, 7, 479.	4.1	27
164	Resolution and Domination: An Improved Exact MaxSAT Algorithm. , 2019, , .		3
165	Overlap matrix completion for predicting drug-associated indications. , 2019, 15, e1007541.		0
166	Overlap matrix completion for predicting drug-associated indications. , 2019, 15, e1007541.		0
167	Overlap matrix completion for predicting drug-associated indications. , 2019, 15, e1007541.		0
168	Overlap matrix completion for predicting drug-associated indications. , 2019, 15, e1007541.		0
169	Resisting re-identification mining on social graph data. World Wide Web, 2018, 21, 1759-1771.	4.0	10
170	CytoCtrlAnalyser: a Cytoscape app for biomolecular network controllability analysis. Bioinformatics, 2018, 34, 1428-1430.	4.1	17
171	Computational drug repositioning using low-rank matrix approximation and randomized algorithms. Bioinformatics, 2018, 34, 1904-1912.	4.1	183
172	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
173	DyNetViewer: a Cytoscape app for dynamic network construction, analysis and visualization. Bioinformatics, 2018, 34, 1597-1599.	4.1	27
174	Prediction of lncRNAâ€"disease associations based on inductive matrix completion. Bioinformatics, 2018, 34, 3357-3364.	4.1	227
175	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
176	A (<inline-formula> <tex-math notation="LaTeX">${M}$ </tex-math>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 232 Td (< in Unattended Sensor Networks. IEEE Wireless Communications Letters, 2018, 7, 250-253.	5.0	6
177	Disease Inference with Symptom Extraction and Bidirectional Recurrent Neural Network. , 2018, , .		7
178	BioRank: A Similarity Assessment Method for Single Cell Clustering. , 2018, , .		1
179	K-mer Counting: memory-efficient strategy, parallel computing and field of application for Bioinformatics. , 2018, , .		2
180	QDAPS: Queueing Delay Aware Packet Spraying for Load Balancing in Data Center. , 2018, , .		10

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181	An interpretable boosting model to predict side effects of analgesics for osteoarthritis. BMC Systems Biology, 2018, 12, 105.	3.0	35
182	Efficient Association Rules Hiding Using Genetic Algorithms. Symmetry, 2018, 10, 576.	2.2	7
183	CAPS: Coding-based Adaptive Packet Spraying to Reduce Flow Completion Time in Data Center. , 2018, , .		16
184	DWNN-RLS: regularized least squares method for predicting circRNA-disease associations. BMC Bioinformatics, 2018, 19, 520.	2.6	68
185	The purpose driven privacy preservation for accelerometer-based activity recognition. World Wide Web, 2018, 21, 1773-1785.	4.0	3
186	A Novel Indoor Localization Algorithm for Efficient Mobility Management in Wireless Networks. Wireless Communications and Mobile Computing, 2018, 2018, 1-12.	1.2	6
187	Designing Fast and Friendly TCP to Fit High Speed Data Center Networks. , 2018, , .		7
188	ConnectedAlign: a PPI network alignment method for identifying conserved protein complexes across multiple species. BMC Bioinformatics, 2018, 19, 286.	2.6	4
189	Multiwinner Voting with Restricted Admissible Sets: Complexity and Strategyproofness. , 2018, , .		10
190	LDAP: a web server for lncRNA-disease association prediction. Bioinformatics, 2017, 33, 458-460.	4.1	182
191	A Secure Scheme for Heterogeneous Sensor Networks. IEEE Wireless Communications Letters, 2017, , 1-1.	5.0	7
192	PECC: Correcting contigs based on paired-end read distribution. Computational Biology and Chemistry, 2017, 69, 178-184.	2.3	17
193	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
194	Flow-Aware Adaptive Pacing to Mitigate TCP Incast in Data Center Networks. , 2017, , .		5
195	Task-aware TCP in Data Center Networks. , 2017, , .		0
196	A High Throughput Reader Scheduling Algorithm for Large RFID Systems in Smart Environments. , 2017, , .		0
197	BOSS: a novel scaffolding algorithm based on an optimized scaffold graph. Bioinformatics, 2017, 33, 169-176.	4.1	33
198	Performance Analysis and Improvement of Replica Selection Algorithms for Key-Value Stores. , 2017, , .		8

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199	TC-CCS: A cooperative caching strategy in mobile transparent computing system. , 2017, , .		1
200	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
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202	An interpretable model for predicting side effects of analgesics for osteoarthritis. , 2017, , .		0
203	Guest Editors Introduction to the Special Section on ISBRA 2014. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 314-315.	3.0	0
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