

# Yi Pan

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3720084/publications.pdf>

Version: 2024-02-01

477  
papers

14,535  
citations

23879

60  
h-index

39744

98  
g-index

526  
all docs

526  
docs citations

526  
times ranked

12699  
citing authors

#	ARTICLE	IF	CITATIONS
1	Energy-efficient resource allocation in blockchain-based Cybertwin-driven 6G. <i>Journal of Ambient Intelligence and Humanized Computing</i> , 2024, 15, 103-114.	3.3	0
2	A Refined 3-in-1 Fused Protein Similarity Measure: Application in Threshold-Free Hub Detection. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 192-206.	1.9	5
3	Predicting Drug-Drug Interactions Based on Integrated Similarity and Semi-Supervised Learning. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 168-179.	1.9	30
4	Edge-Based Video Surveillance With Graph-Assisted Reinforcement Learning in Smart Construction. <i>IEEE Internet of Things Journal</i> , 2022, 9, 9249-9265.	5.5	9
5	RTT-Based Rogue UAV Detection in IoV Networks. <i>IEEE Internet of Things Journal</i> , 2022, 9, 5909-5919.	5.5	2
6	Cryptanalysis of a Honeyword System in the IoT Platform. <i>IEEE Internet of Things Journal</i> , 2022, 9, 2614-2626.	5.5	3
7	Generative Adversarial Networks. <i>ACM Computing Surveys</i> , 2022, 54, 1-38.	16.1	180
8	Association predictions of genomics, proteomics, transcriptomics, microbiome, metabolomics, pathomics, radiomics, drug, symptoms, environment factor, and disease networks: A comprehensive approach. <i>Medicinal Research Reviews</i> , 2022, 42, 441-461.	5.0	33
9	A novel ensemble deep learning model for stock prediction based on stock prices and news. <i>International Journal of Data Science and Analytics</i> , 2022, 13, 139-149.	2.4	57
10	Blockchain-enabled Secure Framework for Energy-Efficient Smart Parking in Sustainable City Environment. <i>Sustainable Cities and Society</i> , 2022, 76, 103364.	5.1	32
11	Variational Few-Shot Learning for Microservice-Oriented Intrusion Detection in Distributed Industrial IoT. <i>IEEE Transactions on Industrial Informatics</i> , 2022, 18, 5087-5095.	7.2	82
12	Predicting Microbe-Disease Association Based on Multiple Similarities and LINE Algorithm. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 2399-2408.	1.9	8
13	BloVt: Blockchain-Based Secure Storage Architecture for Intelligent Internet of Vehicular Things. <i>IEEE Consumer Electronics Magazine</i> , 2022, 11, 75-82.	2.3	24
14	Diagnosis of COVID-19 Pneumonia via a Novel Deep Learning Architecture. <i>Journal of Computer Science and Technology</i> , 2022, 37, 330-343.	0.9	43
15	MMCo-Clus: An Evolutionary Co-clustering Algorithm for Gene Selection. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2022, 34, 4371-4384.	4.0	5
16	KGANcDA: predicting circRNA-disease associations based on knowledge graph attention network. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	33
17	Predicting CircRNA disease associations using novel node classification and link prediction models on Graph Convolutional Networks. <i>Methods</i> , 2022, 198, 32-44.	1.9	13
18	CircR2Disease v2.0: An Updated Web Server for Experimentally Validated circRNA-Disease Associations and Its Application. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 435-445.	3.0	23

#	ARTICLE	IF	CITATIONS
19	Blockchain-Based Distributed Information Hiding Framework for Data Privacy Preserving in Medical Supply Chain Systems. <i>Sensors</i> , 2022, 22, 1371.	2.1	20
20	Predicting Microbe-Disease Association Based on Heterogeneous Network and Global Graph Feature Learning. <i>Chinese Journal of Electronics</i> , 2022, 31, 345-353.	0.7	8
21	A Stacking Ensemble Deep Learning Model for Bitcoin Price Prediction Using Twitter Comments on Bitcoin. <i>Mathematics</i> , 2022, 10, 1307.	1.1	23
22	Drug Repositioning with GraphSAGE and Clustering Constraints Based on Drug and Disease Networks. <i>Frontiers in Pharmacology</i> , 2022, 13, .	1.6	6
23	Artificial intelligence in cancer target identification and drug discovery. <i>Signal Transduction and Targeted Therapy</i> , 2022, 7, 156.	7.1	77
24	Validation of Deep Learning-Based DFCNN in Extremely Large-Scale Virtual Screening and Application in Trypsin I Protease Inhibitor Discovery. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, .	1.6	4
25	SGFNNs: Signed Graph Filtering-based Neural Networks for Predicting Drug-Drug Interactions. <i>Journal of Computational Biology</i> , 2022, 29, 1104-1116.	0.8	0
26	Identification of Autism spectrum disorder based on a novel feature selection method and Variational Autoencoder. <i>Computers in Biology and Medicine</i> , 2022, 148, 105854.	3.9	9
27	A comprehensive survey on computational methods of non-coding RNA and disease association prediction. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	38
28	A Deep Learning Framework for Gene Ontology Annotations With Sequence- and Network-Based Information. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 2208-2217.	1.9	21
29	An Ensemble Method to Reconstruct Gene Regulatory Networks Based on Multivariate Adaptive Regression Splines. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 347-354.	1.9	17
30	TW-Co-MFC: Two-level weighted collaborative fuzzy clustering based on maximum entropy for multi-view data. <i>Tsinghua Science and Technology</i> , 2021, 26, 185-198.	4.1	26
31	A Gene Rank Based Approach for Single Cell Similarity Assessment and Clustering. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 431-442.	1.9	12
32	Deletion Detection Method Using the Distribution of Insert Size and a Precise Alignment Strategy. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 1070-1081.	1.9	0
33	A Novel Drug Repositioning Approach Based on Collaborative Metric Learning. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 463-471.	1.9	11
34	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.	1.9	21
35	Inferring Metabolite-disease Association Using Graph Convolutional Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, PP, 1-1.	1.9	4
36	Prediction of disease-associated circRNAs via circRNA-disease pair graph and weighted nuclear norm minimization. <i>Knowledge-Based Systems</i> , 2021, 214, 106694.	4.0	14

#	ARTICLE	IF	CITATIONS
37	A review of infant cry analysis and classification. Eurasip Journal on Audio, Speech, and Music Processing, 2021, 2021, .	1.3	45
38	Predicting CircRNA-Disease Associations Based on Improved Weighted Biased Meta-Structure. Journal of Computer Science and Technology, 2021, 36, 288-298.	0.9	9
39	On Designing a Lesser Obtrusive Authentication Protocol to Prevent Machine-Learning-Based Threats in Internet of Things. IEEE Internet of Things Journal, 2021, 8, 3255-3267.	5.5	6
40	Periodic-Aware Intelligent Prediction Model for Information Diffusion in Social Networks. IEEE Transactions on Network Science and Engineering, 2021, 8, 894-904.	4.1	62
41	Infant Cry Classification with Graph Convolutional Networks. , 2021, , .		9
42	Editorial: Computational Genomics and Molecular Medicine for Emerging COVID-19. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1227-1229.	1.9	1
43	CoronaPep: An Anti-Coronavirus Peptide Generation Tool. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1299-1304.	1.9	5
44	Slashing Communication Traffic in Federated Learning by Transmitting Clustered Model Updates. IEEE Journal on Selected Areas in Communications, 2021, 39, 2572-2589.	9.7	18
45	Treatment initiation prediction by EHR mapped PPD tensor based convolutional neural networks boosting algorithm. Journal of Biomedical Informatics, 2021, 120, 103840.	2.5	5
46	OTS Scheme Based Secure Architecture for Energy-Efficient IoT in Edge Infrastructure. Computers, Materials and Continua, 2021, 66, 2905-2922.	1.5	11
47	Infant Vocal Tract Development Analysis and Diagnosis by Cry Signals with CNN Age Classification. , 2021, , .		0
48	An Integrated Deep Learning and Molecular Dynamics Simulation-Based Screening Pipeline Identifies Inhibitors of a New Cancer Drug Target TIPE2. Frontiers in Pharmacology, 2021, 12, 772296.	1.6	13
49	Epigenetic interaction between UTX and DNMT1 regulates diet-induced myogenic remodeling in brown fat. Nature Communications, 2021, 12, 6838.	5.8	11
50	Multi-View Feature Aggregation for predicting microbe-disease association. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	1.9	5
51	GapReduce: A Gap Filling Algorithm Based on Partitioned Read Sets. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 877-886.	1.9	11
52	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.	1.9	24
53	Constructing Disease Similarity Networks Based on Disease Module Theory. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 906-915.	1.9	29
54	MEC: Misassembly Error Correction in Contigs based on Distribution of Paired-End Reads and Statistics of GC-contents. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 847-857.	1.9	17

#	ARTICLE	IF	CITATIONS
55	miRTRS: A Recommendation Algorithm for Predicting miRNA Targets. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 1032-1041.	1.9	10
56	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
57	An Efficient Trimming Algorithm based on Multi-Feature Fusion Scoring Model for NGS Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 728-738.	1.9	14
58	Improving de novo Assembly Based on Read Classification. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 177-188.	1.9	19
59	PTCP: A priority-based transport control protocol for timeout mitigation in commodity data center. Future Generation Computer Systems, 2020, 102, 619-632.	4.9	5
60	An Efficient and Compacted DAG-Based Blockchain Protocol for Industrial Internet of Things. IEEE Transactions on Industrial Informatics, 2020, 16, 4134-4145.	7.2	66
61	A Decentralized and Trusted Edge Computing Platform for Internet of Things. IEEE Internet of Things Journal, 2020, 7, 3910-3922.	5.5	52
62	Deep Fuzzy Neural Networks for Biomarker Selection for Accurate Cancer Detection. IEEE Transactions on Fuzzy Systems, 2020, 28, 3219-3228.	6.5	25
63	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.	3.9	26
64	Prioritizing CircRNA-Disease Associations With Convolutional Neural Network Based on Multiple Similarity Feature Fusion. Frontiers in Genetics, 2020, 11, 540751.	1.1	17
65	An efficient pipeline processing scheme for programming Protocol-independent Packet Processors. Journal of Network and Computer Applications, 2020, 171, 102806.	5.8	6
66	On Understanding the Impact of RTT in the Mobile Network for Detecting the Rogue UAVs. IEEE Transactions on Cognitive Communications and Networking, 2020, 6, 1218-1229.	4.9	3
67	Gradient amplification: An efficient way to train deep neural networks. Big Data Mining and Analytics, 2020, 3, 196-207.	7.5	62
68	Block5GIntell: Blockchain for AI-Enabled 5G Networks. IEEE Access, 2020, 8, 145918-145935.	2.6	74
69	Blockchain-Based Cyber Threat Intelligence System Architecture for Sustainable Computing. Sustainability, 2020, 12, 6401.	1.6	23
70	Rethinking Fast and Friendly Transport in Data Center Networks. IEEE/ACM Transactions on Networking, 2020, 28, 2364-2377.	2.6	21
71	Special Issue Editorial: Intelligent Data Analysis for Sustainable Computing. IEEE Transactions on Sustainable Computing, 2020, 5, 304-307.	2.2	0
72	A consensus multi-view multi-objective gene selection approach for improved sample classification. BMC Bioinformatics, 2020, 21, 386.	1.2	3

#	ARTICLE	IF	CITATIONS
73	Machine Learning-Based Network Sub-Slicing Framework in a Sustainable 5G Environment. Sustainability, 2020, 12, 6250.	1.6	42
74	Data integrity attack detection in smart grid: a deep learning approach. International Journal of Security and Networks, 2020, 15, 15.	0.1	8
75	IEEE Access Special Section Editorial: Scalable Deep Learning for Big Data. IEEE Access, 2020, 8, 216617-216622.	2.6	1
76	A Study on the Digital Forensic Investigation Method of Clever Malware in IoT Devices. IEEE Access, 2020, 8, 224487-224499.	2.6	6
77	Deep Learning Based Drug Screening for Novel Coronavirus 2019-nCov. Interdisciplinary Sciences, Computational Life Sciences, 2020, 12, 368-376.	2.2	127
78	Adaptive computation offloading and resource allocation strategy in a mobile edge computing environment. Information Sciences, 2020, 537, 116-131.	4.0	62
79	Mutation of YL Results in a Yellow Leaf with Chloroplast RNA Editing Defect in Soybean. International Journal of Molecular Sciences, 2020, 21, 4275.	1.8	12
80	Secure D2D Communication for 5G IoT Network Based on Lightweight Cryptography. Applied Sciences (Switzerland), 2020, 10, 217.	1.3	52
81	Enhancing the feature representation of multi-modal MRI data by combining multi-view information for MCI classification. Neurocomputing, 2020, 400, 322-332.	3.5	40
82	Stochastic Load Balancing for Virtual Resource Management in Datacenters. IEEE Transactions on Cloud Computing, 2020, 8, 459-472.	3.1	91
83	Infant Sound Classification on Multi-stage CNNs with Hybrid Features and Prior Knowledge. Lecture Notes in Computer Science, 2020, , 3-16.	1.0	7
84	A parallel computing method based on zeroing neural networks for time-varying complex-valued matrix Moore-Penrose inversion. Information Sciences, 2020, 524, 216-228.	4.0	33
85	Prediction of Glioma Grade using Intratumoral and Peritumoral Radiomic Features from Multiparametric MRI Images. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, PP, 1-1.	1.9	20
86	Multi-view feature selection for identifying gene markers: a diversified biological data driven approach. BMC Bioinformatics, 2020, 21, 483.	1.2	3
87	Analysis of heterogeneous genomic samples using image normalization and machine learning. BMC Genomics, 2020, 21, 405.	1.2	4
88	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.	1.5	42
89	CircRNA-disease associations prediction based on metapath2vec++ and matrix factorization. Big Data Mining and Analytics, 2020, 3, 280-291.	7.5	33
90	Online Tutoring Through a Cloud-Based Virtual Tutoring Center. Lecture Notes in Computer Science, 2020, , 270-277.	1.0	0

#	ARTICLE	IF	CITATIONS
91	Graph Convolution Networks Using Message Passing and Multi-Source Similarity Features for Predicting circRNA-Disease Association. , 2020, , .		5
92	A multi-view approach for predicting microbedisease associations by fusing the linear and nonlinear features. , 2020, , .		2
93	Joint Learning of Primary and Secondary Labels based on Multi-scale Representation for Alzheimerâ€™s Disease Diagnosis. , 2020, , .		1
94	Title is missing!. , 2020, 16, e1008489.		0
95	Title is missing!. , 2020, 16, e1008489.		0
96	Title is missing!. , 2020, 16, e1008489.		0
97	Title is missing!. , 2020, 16, e1008489.		0
98	Automatic ICD-9 coding via deep transfer learning. Neurocomputing, 2019, 324, 43-50.	3.5	79
99	Big Data Transmission in Industrial IoT Systems With Small Capacitor Supplying Energy. IEEE Transactions on Industrial Informatics, 2019, 15, 2360-2371.	7.2	14
100	A Novel Scaffolding Algorithm Based on Contig Error Correction and Path Extension. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 764-773.	1.9	8
101	Classification of autism spectrum disorder by combining brain connectivity and deep neural network classifier. Neurocomputing, 2019, 324, 63-68.	3.5	161
102	DNRLMF-MDA:Predicting microRNA-Disease Associations Based on Similarities of microRNAs and Diseases. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 233-243.	1.9	59
103	A parallel team formation approach using crowd intelligence from social network. Computers in Human Behavior, 2019, 101, 429-434.	5.1	8
104	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
105	A novel extended Pareto Optimality Consensus model for predicting essential proteins. Journal of Theoretical Biology, 2019, 480, 141-149.	0.8	9
106	Smart Contract-Based Pool Hopping Attack Prevention for Blockchain Networks. Symmetry, 2019, 11, 941.	1.1	30
107	BlockDeepNet: A Blockchain-Based Secure Deep Learning for IoT Network. Sustainability, 2019, 11, 3974.	1.6	62
108	EPGA-SC : A framework for de novo assembly of single-cell sequencing reads. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 18, 1-1.	1.9	3

#	ARTICLE	IF	CITATIONS
109	LncCCAT1 Promotes Breast Cancer Stem Cell Function through Activating WNT/ $\beta$ 2-catenin Signaling. Theranostics, 2019, 9, 7384-7402.	4.6	109
110	On Overcoming the Identified Limitations of a Usable PIN Entry Method. IEEE Access, 2019, 7, 124366-124378.	2.6	5
111	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.	3.5	41
112	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.	2.7	25
113	A deep learning framework for identifying essential proteins by integrating multiple types of biological information. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 18, 1-1.	1.9	65
114	Guest Editorial Special Issue on Advanced Computational Technologies in Mobile Edge Computing for the Internet of Things. IEEE Internet of Things Journal, 2019, 6, 4742-4743.	5.5	1
115	IDNDDI: An Integrated Drug Similarity Network Method for Predicting Drug-Drug Interactions. Lecture Notes in Computer Science, 2019, , 89-99.	1.0	6
116	Automated Hub-Protein Detection via a New Fused Similarity Measure-Based Multi-objective Clustering Framework. Lecture Notes in Computer Science, 2019, , 138-145.	1.0	2
117	Page-sharing-based virtual machine packing with multi-resource constraints to reduce network traffic in migration for clouds. Future Generation Computer Systems, 2019, 96, 462-471.	4.9	20
118	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
119	Reconstruction of Hidden Representation for Robust Feature Extraction. ACM Transactions on Intelligent Systems and Technology, 2019, 10, 1-24.	2.9	8
120	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.	1.9	33
121	miR-29a contributes to breast cancer cells epithelial $\rightarrow$ mesenchymal transition, migration, and invasion via down-regulating histone H4K20 trimethylation through directly targeting SUV420H2. Cell Death and Disease, 2019, 10, 176.	2.7	60
122	Using Transfer Learning, SVM, and Ensemble Classification to Classify Baby Cries Based on Their Spectrogram Images. , 2019, , .		18
123	Multi-level Glioma Segmentation using 3D U-Net Combined Attention Mechanism with Atrous Convolution. , 2019, , .		16
124	Deep Learning for Asphyxiated Infant Cry Classification Based on Acoustic Features and Weighted Prosodic Features. , 2019, , .		15
125	CSA: a web service for the complete process of ChIP-Seq analysis. BMC Bioinformatics, 2019, 20, 515.	1.2	2
126	DDIGIP: predicting drug-drug interactions based on Gaussian interaction profile kernels. BMC Bioinformatics, 2019, 20, 538.	1.2	24



#	ARTICLE	IF	CITATIONS
127	DeepEP: a deep learning framework for identifying essential proteins. BMC Bioinformatics, 2019, 20, 506.	1.2	40
128	Fast Deep Learning Training through Intelligently Freezing Layers. , 2019, , .		13
129	SCOP: a novel scaffolding algorithm based on contig classification and optimization. Bioinformatics, 2019, 35, 1142-1150.	1.8	13
130	BiXGBoost: a scalable, flexible boosting-based method for reconstructing gene regulatory networks. Bioinformatics, 2019, 35, 1893-1900.	1.8	59
131	Multi-view learning for benign epilepsy with centrotemporal spikes. IET Computer Vision, 2019, 13, 109-116.	1.3	0
132	Automated ICD-9 Coding via A Deep Learning Approach. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1193-1202.	1.9	78
133	Computational Drug Repositioning with Random Walk on a Heterogeneous Network. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1890-1900.	1.9	47
134	Construction of Refined Protein Interaction Network for Predicting Essential Proteins. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1386-1397.	1.9	44
135	MAC: Merging Assemblies by Using Adjacency Algebraic Model and Classification. Frontiers in Genetics, 2019, 10, 1396.	1.1	10
136	Edge Computing for the Internet of Things. IEEE Network, 2018, 32, 6-7.	4.9	61
137	A fine-grained rule partition algorithm in cloud data centers. Journal of Network and Computer Applications, 2018, 113, 14-25.	5.8	5
138	Applications of deep learning to MRI images: A survey. Big Data Mining and Analytics, 2018, 1, 1-18.	7.5	195
139	Reducing transport latency for short flows with multipath TCP. Journal of Network and Computer Applications, 2018, 108, 20-36.	5.8	29
140	Convolutional networks with cross-layer neurons for image recognition. Information Sciences, 2018, 433-434, 241-254.	4.0	25
141	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
142	DyNetViewer: a Cytoscape app for dynamic network construction, analysis and visualization. Bioinformatics, 2018, 34, 1597-1599.	1.8	27
143	Prediction of lncRNA-disease associations based on inductive matrix completion. Bioinformatics, 2018, 34, 3357-3364.	1.8	227
144	Automatic translation from Java to Spark. Concurrency Computation Practice and Experience, 2018, 30, e4459.	1.4	1

#	ARTICLE	IF	CITATIONS
145	Identifying essential proteins based on sub-network partition and prioritization by integrating subcellular localization information. <i>Journal of Theoretical Biology</i> , 2018, 447, 65-73.	0.8	46
146	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.	1.9	116
147	Classification of Alzheimer's Disease Using Whole Brain Hierarchical Network. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 624-632.	1.9	142
148	Improving Alzheimer's Disease Classification by Combining Multiple Measures. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1649-1659.	1.9	56
149	An Optimized Method for Bayesian Connectivity Change Point Model. <i>Journal of Computational Biology</i> , 2018, 25, 337-347.	0.8	3
150	Collaborative Learning in Cloud-based Virtual Computer Labs. , 2018, , .		10
151	A Deep Learning Framework for Identifying Essential Proteins Based on Protein-Protein Interaction Network and Gene Expression Data. , 2018, , .		12
152	United neighborhood closeness centrality and orthology for predicting essential proteins. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 17, 1-1.	1.9	50
153	BioRank: A Similarity Assessment Method for Single Cell Clustering. , 2018, , .		1
154	An interpretable boosting model to predict side effects of analgesics for osteoarthritis. <i>BMC Systems Biology</i> , 2018, 12, 105.	3.0	35
155	An Undergraduate Curriculum Model for Intelligence Science and Technology. , 2018, , .		1
156	Advanced computer science and applications for soft computing of converged IT environments. <i>Soft Computing</i> , 2018, 22, 6617-6619.	2.1	0
157	Upâ€regulation of miRâ€210 induced by a hypoxic microenvironment promotes breast cancer stem cell metastasis, proliferation, and selfâ€renewal by targeting Eâ€cadherin. <i>FASEB Journal</i> , 2018, 32, 6965-6981.	0.2	81
158	CF-CloudOrch: container fog node-based cloud orchestration for IoT networks. <i>Journal of Supercomputing</i> , 2018, 74, 7024-7045.	2.4	27
159	Designing Fast and Friendly TCP to Fit High Speed Data Center Networks. , 2018, , .		7
160	An algorithm to estimate enemy's location in WarGame based on pheromone. , 2018, , .		1
161	Fast induced sorting suffixes on a multicore machine. <i>Journal of Supercomputing</i> , 2018, 74, 3468-3485.	2.4	13
162	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.	4.8	158

#	ARTICLE	IF	CITATIONS
163	Advances in intelligence and internet of things for human-centric computing. <i>Soft Computing</i> , 2018, 22, 4165-4167.	2.1	1
164	Protein-protein interactions: detection, reliability assessment and applications. <i>Briefings in Bioinformatics</i> , 2017, 18, bbw066.	3.2	64
165	LDAP: a web server for lncRNA-disease association prediction. <i>Bioinformatics</i> , 2017, 33, 458-460.	1.8	182
166	Searching Genome-Wide Multi-Locus Associations for Multiple Diseases Based on Bayesian Inference. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 600-610.	1.9	14
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.	1.9	20
168	FSQCN: Fast and simple quantized congestion notification in data center ethernet. <i>Journal of Network and Computer Applications</i> , 2017, 83, 53-62.	5.8	12
169	PECC: Correcting contigs based on paired-end read distribution. <i>Computational Biology and Chemistry</i> , 2017, 69, 178-184.	1.1	17
170	Effects of lactic acid bacteria and molasses additives on the microbial community and fermentation quality of soybean silage. <i>Bioresource Technology</i> , 2017, 238, 706-715.	4.8	288
171	A novel method of predicting microRNA-disease associations based on microRNA, disease, gene and environment factor networks. <i>Methods</i> , 2017, 124, 69-77.	1.9	27
172	GaussianCpG: a Gaussian model for detection of CpG island in human genome sequences. <i>BMC Genomics</i> , 2017, 18, 392.	1.2	13
173	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.	2.2	51
174	A Framework for Integrating Multiple Biological Networks to Predict MicroRNA-Disease Associations. <i>IEEE Transactions on Nanobioscience</i> , 2017, 16, 100-107.	2.2	30
175	An Iterative Locally Auto-Weighted Least Squares Method for Microarray Missing Value Estimation. <i>IEEE Transactions on Nanobioscience</i> , 2017, 16, 21-33.	2.2	27
176	Classification of Schizophrenia Based on Individual Hierarchical Brain Networks Constructed From Structural MRI Images. <i>IEEE Transactions on Nanobioscience</i> , 2017, 16, 600-608.	2.2	38
177	Protein Inference from the Integration of Tandem MS Data and Interactome Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 1399-1409.	1.9	3
178	A Parallel Pairwise Alignment with Pruning for Large Genomic Sequences. , 2017, , .		0
179	Tuning the Aggressive TCP Behavior for Highly Concurrent HTTP Connections in Intra-Datacenter. <i>IEEE/ACM Transactions on Networking</i> , 2017, 25, 3808-3822.	2.6	24
180	Guest Editors Introduction to the Special Section on ISBRA 2014. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 314-315.	1.9	0

#	ARTICLE	IF	CITATIONS
181	MEC: Misassembly error correction in contigs using a combination of paired-end reads and GC-contents. , 2017, , .		2
182	SDTRLS: Predicting Drug-Target Interactions for Complex Diseases Based on Chemical Substructures. Complexity, 2017, 2017, 1-10.	0.9	15
183	Complex Brain Network Analysis and Its Applications to Brain Disorders: A Survey. Complexity, 2017, 2017, 1-27.	0.9	90
184	Genome-wide association studies dissect the genetic networks underlying agronomical traits in soybean. Genome Biology, 2017, 18, 161.	3.8	363
185	VAlIBS: a visual aligner for bisulfite sequences. BMC Bioinformatics, 2017, 18, 410.	1.2	2
186	A deep learning method for lincRNA detection using auto-encoder algorithm. BMC Bioinformatics, 2017, 18, 511.	1.2	22
187	Evaluating the Impact of Encoding Schemes on Deep Auto-Encoders for DNA Annotation. Lecture Notes in Computer Science, 2017, , 390-395.	1.0	2
188	Detecting Change Points in fMRI Data via Bayesian Inference and Genetic Algorithm Model. Lecture Notes in Computer Science, 2017, , 314-324.	1.0	2
189	LSLS: A Novel Scaffolding Method Based on Path Extension. Lecture Notes in Computer Science, 2017, , 428-438.	1.0	1
190	Multiple Biological Sequence Alignment: Scoring Functions, Algorithms and Applications. , 2016, , .		9
191	Bayesian Inference for Functional Dynamics Exploring in fMRI Data. Computational and Mathematical Methods in Medicine, 2016, 2016, 1-9.	0.7	4
192	A User-Customized Virtual Network Platform for NaaS Cloud. Scientific Programming, 2016, 2016, 1-6.	0.5	0
193	Construction of the spatial and temporal active protein interaction network for identifying protein complexes. , 2016, , .		5
194	Predicting essential proteins based on subcellular localization, orthology and PPI networks. BMC Bioinformatics, 2016, 17, 279.	1.2	66
195	A deep learning method for lincRNA identification using auto-encoder algorithm. , 2016, , .		0
196	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.	4.1	25
197	Predicting microRNA-environmental factor interactions based on bi-random walk and multi-label learning. , 2016, , .		3
198	Predicting microRNA-disease associations by walking on four biological networks. , 2016, , .		1

#	ARTICLE	IF	CITATIONS
199	J2M: a Java to MapReduce translator for cloud computing. Journal of Supercomputing, 2016, 72, 1928-1945.	2.4	7
200	Predicting MicroRNA-Disease Associations by Random Walking on Multiple Networks. Lecture Notes in Computer Science, 2016, , 127-135.	1.0	2
201	Identifying Essential Proteins by Purifying Protein Interaction Networks. Lecture Notes in Computer Science, 2016, , 106-116.	1.0	1
202	Signalign: An Ontology of DNA as Signal for Comparative Gene Structure Prediction Using Information-Coding-and-Processing Techniques. IEEE Transactions on Nanobioscience, 2016, 15, 119-130.	2.2	8
203	Drug repositioning based on comprehensive similarity measures and Bi-Random walk algorithm. Bioinformatics, 2016, 32, 2664-2671.	1.8	311
204	Tuning the Aggressive TCP Behavior for Highly Concurrent HTTP Connections in Data Center. , 2016, , .		3
205	C-DEVA: Detection, evaluation, visualization and annotation of clusters from biological networks. BioSystems, 2016, 150, 78-86.	0.9	11
206	Slug-upregulated miR-221 promotes breast cancer progression through suppressing E-cadherin expression. Scientific Reports, 2016, 6, 25798.	1.6	55
207	Underwater acoustic sensor networks. International Journal of Distributed Sensor Networks, 2016, 12, 155014771666549.	1.3	4
208	A Cloud-Assisted Application over Apache Spark for Investigating Epigenetic Markers on DNA Genome Sequences. , 2016, , .		1
209	A Novel Deep Learning Network Architecture with Cross-Layer Neurons. , 2016, , .		0
210	Circulating human cytomegalovirus-encoded HCMV-miR-US4-1 as an indicator for predicting the efficacy of IFN $\beta$ treatment in chronic hepatitis B patients. Scientific Reports, 2016, 6, 23007.	1.6	18
211	Identification of protein complexes from multi-relationship protein interaction networks. Human Genomics, 2016, 10, 17.	1.4	14
212	Predicting drug-target interaction using positive-unlabeled learning. Neurocomputing, 2016, 206, 50-57.	3.5	83
213	A hybrid discrete particle swarm optimization-genetic algorithm for multi-task scheduling problem in service oriented manufacturing systems. Journal of Central South University, 2016, 23, 421-429.	1.2	10
214	Sprites: detection of deletions from sequencing data by re-aligning split reads. Bioinformatics, 2016, 32, 1788-1796.	1.8	23
215	A New Method for Predicting Protein Functions From Dynamic Weighted Interactome Networks. IEEE Transactions on Nanobioscience, 2016, 15, 131-139.	2.2	28
216	Adaptive marking threshold method for delay-sensitive TCP in data center network. Journal of Network and Computer Applications, 2016, 61, 222-234.	5.8	13

#	ARTICLE	IF	CITATIONS
217	Efficient parallel boolean matrix based algorithms for computing composite rough set approximations. <i>Information Sciences</i> , 2016, 329, 287-302.	4.0	44
218	A Modified Ant Colony Optimization Algorithm for Network Coding Resource Minimization. <i>IEEE Transactions on Evolutionary Computation</i> , 2016, 20, 325-342.	7.5	56
219	HybridDock: A Hybrid Protein-Ligand Docking Protocol Integrating Protein- and Ligand-Based Approaches. <i>Journal of Chemical Information and Modeling</i> , 2016, 56, 1078-1087.	2.5	35
220	Predicting drug-target interaction based on sequence and structure information. <i>IFAC-PapersOnLine</i> , 2015, 48, 12-16.	0.5	9
221	Re-alignment of the unmapped reads with base quality score. <i>BMC Bioinformatics</i> , 2015, 16, S8.	1.2	14
222	Identifying essential proteins from active PPI networks constructed with dynamic gene expression. <i>BMC Genomics</i> , 2015, 16, S1.	1.2	66
223	Rechecking the Centrality-Lethality Rule in the Scope of Protein Subcellular Localization Interaction Networks. <i>PLoS ONE</i> , 2015, 10, e0130743.	1.1	47
224	Ubiquitous Systems towards Green, Sustainable, and Secured Smart Environment. <i>Scientific World Journal, The</i> , 2015, 2015, 1-3.	0.8	1
225	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.	1.9	20
226	GaussianCpG: A Gaussian model for detection of human CpG island. , 2015, , .		2
227	An efficient method to identify essential proteins for different species by integrating protein subcellular localization information. , 2015, , .		16
228	Predicting microRNA-disease associations by integrating multiple biological information. , 2015, , .		12
229	Dynamic Bayesian brain network partition and connectivity change point detection. , 2015, , .		0
230	Dynamic ensemble selection with local expertise consistency. , 2015, , .		1
231	DIME: A Novel Framework for De Novo Metagenomic Sequence Assembly. <i>Journal of Computational Biology</i> , 2015, 22, 159-177.	0.8	15
232	MicroRNA-223 delivered by platelet-derived microvesicles promotes lung cancer cell invasion via targeting tumor suppressor EPB41L3. <i>Molecular Cancer</i> , 2015, 14, 58.	7.9	145
233	ClusterViz: A Cytoscape APP for Cluster Analysis of Biological Network. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 815-822.	1.9	103
234	microRNA-200b and microRNA-200c promote colorectal cancer cell proliferation via targeting the reversion-inducing cysteine-rich protein with Kazal motifs. <i>RNA Biology</i> , 2015, 12, 276-289.	1.5	49

#	ARTICLE	IF	CITATIONS
235	UDoNC: An Algorithm for Identifying Essential Proteins Based on Protein Domains and Protein-Protein Interaction Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 276-288.	1.9	75
236	A Topology Potential-Based Method for Identifying Essential Proteins from PPI Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 372-383.	1.9	88
237	Guest Editorial: Introduction to the Special Issue on the 10th International Symposium on Bioinformatics Research and Applications (ISBRA 2014). IEEE Transactions on Nanobioscience, 2015, 14, 154-156.	2.2	0
238	EPGA2: memory-efficient <i>de novo</i> assembler. Bioinformatics, 2015, 31, 3988-3990.	1.8	19
239	A Parallel Matrix-Based Method for Computing Approximations in Incomplete Information Systems. IEEE Transactions on Knowledge and Data Engineering, 2015, 27, 326-339.	4.0	76
240	CytoNCA: A cytoscape plugin for centrality analysis and evaluation of protein interaction networks. BioSystems, 2015, 127, 67-72.	0.9	813
241	EPGA: <i>de novo</i> assembly using the distributions of reads and insert size. Bioinformatics, 2015, 31, 825-833.	1.8	25
242	DNA AS X: An Information-Coding-Based Model to Improve the Sensitivity in Comparative Gene Analysis. Lecture Notes in Computer Science, 2015, , 366-377.	1.0	7
243	DAM: A Bayesian Method for Detecting Genome-wide Associations on Multiple Diseases. Lecture Notes in Computer Science, 2015, , 96-107.	1.0	6
244	Boosting VoIP Capacity via Service Differentiation in IEEE 802.11e EDCA Networks. International Journal of Distributed Sensor Networks, 2015, 11, 235648.	1.3	7
245	Improving Performance of QoS Applications for Wireless Networks. International Journal of Distributed Sensor Networks, 2015, 2015, 1-12.	1.3	1
246	Predicting Protein Functions Based on Dynamic Protein Interaction Networks. Lecture Notes in Computer Science, 2015, , 390-401.	1.0	1
247	Identifying Dynamic Protein Complexes Based on Gene Expression Profiles and PPI Networks. BioMed Research International, 2014, 2014, 1-10.	0.9	22
248	Adaptive-Acceleration Data Center TCP. IEEE Transactions on Computers, 2014, , 1-1.	2.4	15
249	A Novel Algorithm for Detecting Protein Complexes with the Breadth First Search. BioMed Research International, 2014, 2014, 1-8.	0.9	10
250	Prediction of Essential Proteins Based on Overlapping Essential Modules. IEEE Transactions on Nanobioscience, 2014, 13, 415-424.	2.2	60
251	Identification of Essential Proteins by Using Complexes and Interaction Network. Lecture Notes in Computer Science, 2014, , 255-265.	1.0	6
252	Adaptive dual cluster heads collaborative target tracking in wireless sensor networks. International Journal of Sensor Networks, 2014, 15, 11.	0.2	9

#	ARTICLE	IF	CITATIONS
253	Genome-Wide Interaction-Based Association of human diseases - A survey. <i>Tsinghua Science and Technology</i> , 2014, 19, 596-616.	4.1	12
254	A survey of MRI-based brain tumor segmentation methods. <i>Tsinghua Science and Technology</i> , 2014, 19, 578-595.	4.1	252
255	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.	2.3	20
256	Greedy construction of load-balanced virtual backbones in wireless sensor networks. <i>Wireless Communications and Mobile Computing</i> , 2014, 14, 673-688.	0.8	14
257	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.	1.9	67
258	Constructing Load-Balanced Data Aggregation Trees in Probabilistic Wireless Sensor Networks. <i>IEEE Transactions on Parallel and Distributed Systems</i> , 2014, 25, 1681-1690.	4.0	45
259	Dynamic formation control for autonomous underwater vehicles. <i>Journal of Central South University</i> , 2014, 21, 113-123.	1.2	9
260	Effective identification of essential proteins based on priori knowledge, network topology and gene expressions. <i>Methods</i> , 2014, 67, 325-333.	1.9	89
261	Platelet-Secreted MicroRNA-223 Promotes Endothelial Cell Apoptosis Induced by Advanced Glycation End Products via Targeting the Insulin-like Growth Factor 1 Receptor. <i>Journal of Immunology</i> , 2014, 192, 437-446.	0.4	207
262	Detecting Protein Complexes Based on Uncertain Graph Model. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 486-497.	1.9	77
263	Predicting Essential Proteins Based on Weighted Degree Centrality. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 407-418.	1.9	160
264	Cloud computing for detecting high-order genome-wide epistatic interaction via dynamic clustering. <i>BMC Bioinformatics</i> , 2014, 15, 102.	1.2	70
265	Multi-level clustering support vector machine trees for improved protein local structure prediction. <i>International Journal of Data Mining and Bioinformatics</i> , 2014, 9, 172.	0.1	0
266	A distributed middleware for self-configurable wireless sensor networks. <i>International Journal of Sensor Networks</i> , 2014, 16, 1.	0.2	3
267	Predicting Protein Functions by Using Unbalanced Bi-Random Walk Algorithm on Protein-Protein Interaction Network and Functional Interrelationship Network. <i>Current Protein and Peptide Science</i> , 2014, 15, 529-539.	0.7	10
268	Continuous data aggregation and capacity in probabilistic wireless sensor networks. <i>Journal of Parallel and Distributed Computing</i> , 2013, 73, 729-745.	2.7	16
269	An effective method for refining predicted protein complexes based on protein activity and the mechanism of protein complex formation. <i>BMC Systems Biology</i> , 2013, 7, 28.	3.0	8
270	A Knowledge-Based Multiple-Sequence Alignment Algorithm. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 884-896.	1.9	8



#	ARTICLE	IF	CITATIONS
271	H2T: A Simple Hadoop-to-Twister Translator for Cloud Computing. , 2013, , .		1
272	Approximation algorithms for load-balanced virtual backbone construction in wireless sensor networks. Theoretical Computer Science, 2013, 507, 2-16.	0.5	42
273	Prediction of essential proteins based on gene expression programming. BMC Genomics, 2013, 14, S7.	1.2	54
274	Reaction-diffusion modeling of malware propagation in mobile wireless sensor networks. Science China Information Sciences, 2013, 56, 1-18.	2.7	20
275	b-SPECS+: Batch Verification for Secure Pseudonymous Authentication in VANET. IEEE Transactions on Information Forensics and Security, 2013, 8, 1860-1875.	4.5	214
276	A new method for predicting essential proteins based on topology potential. , 2013, , .		3
277	PLAR: Parallel Large-Scale Attribute Reduction on Cloud Systems. , 2013, , .		9
278	Identifying essential proteins based on protein domains in protein-protein interaction networks. , 2013, , .		3
279	Construction and application of dynamic protein interaction network based on time course gene expression data. Proteomics, 2013, 13, 301-312.	1.3	141
280	<i>hFâ€measure</i> : A new measurement for evaluating clusters in proteinâ€protein interaction networks. Proteomics, 2013, 13, 291-300.	1.3	25
281	Clustering based on multiple biological information: approach for predicting protein complexes. IET Systems Biology, 2013, 7, 223-230.	0.8	12
282	M2M: A simple Matlab-to-MapReduce translator for cloud computing. Tsinghua Science and Technology, 2013, 18, 1-9.	4.1	19
283	A novel algorithm for mining protein complex from the weighted network. , 2013, , .		0
284	Large-scale restricted boltzmann machines on single GPU. , 2013, , .		6
285	IDENTIFICATION OF ESSENTIAL PROTEINS FROM WEIGHTED PROTEINâ€PROTEIN INTERACTION NETWORKS. Journal of Bioinformatics and Computational Biology, 2013, 11, 1341002.	0.3	37
286	Guest Editorial: Special issue on bioinformatics and computational biology. Tsinghua Science and Technology, 2013, 18, 429-430.	4.1	0
287	A Parallel Implementation of Computing Composite Rough Set Approximations on GPUs. Lecture Notes in Computer Science, 2013, , 240-250.	1.0	4
288	Construction of Uncertain Protein-Protein Interaction Networks and Its Applications. Lecture Notes in Computer Science, 2013, , 286-297.	1.0	0

#	ARTICLE	IF	CITATIONS
289	Identifying essential proteins via integration of protein interaction and gene expression data. , 2012, , .		9
290	Real-World Relevant Learning with Android Smartphones. , 2012, , .		5
291	Constructing a load-balanced virtual backbone in Wireless Sensor Networks. , 2012, , .		10
292	Load-balanced CDS construction in wireless sensor networks via genetic algorithm. International Journal of Sensor Networks, 2012, 11, 166.	0.2	26
293	Guest editorial: Special issue on bioinformatics and computational biology. Tsinghua Science and Technology, 2012, 17, 607-608.	4.1	0
294	PDSEC Introduction. , 2012, , .		0
295	Copyright Protection for E-Government Document Images. IEEE MultiMedia, 2012, 19, 62-73.	1.5	75
296	A novel dynamic network data replication scheme based on historical access record and proactive deletion. Journal of Supercomputing, 2012, 62, 227-250.	2.4	70
297	Mis-classified instance learning and recovery in classification. , 2012, , .		0
298	Predicting protein complexes via the integration of multiple biological information. , 2012, , .		2
299	Identifying Protein Complexes From Interactome Based on Essential Proteins and Local Fitness Method. IEEE Transactions on Nanobioscience, 2012, 11, 324-335.	2.2	15
300	An Efficient Run Time Control Flow Errors Detection by DCT Technique. , 2012, , .		0
301	Towards the identification of protein complexes and functional modules by integrating PPI network and gene expression data. BMC Bioinformatics, 2012, 13, 109.	1.2	122
302	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
303	Iteration method for predicting essential proteins based on orthology and protein-protein interaction networks. BMC Systems Biology, 2012, 6, 87.	3.0	128
304	Towards Elastic and Fine-Granular Bandwidth Allocation in Spectrum-Sliced Optical Networks. Journal of Optical Communications and Networking, 2012, 4, 906.	3.3	71
305	Identification of Essential Proteins Based on Edge Clustering Coefficient. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1070-1080.	1.9	254
306	Symmetry Compression Method for Discovering Network Motifs. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1776-1789.	1.9	14

#	ARTICLE	IF	CITATIONS
307	A Self-tuning Failure Detection Scheme for Cloud Computing Service. , 2012, , .		53
308	Parallel rough set based knowledge acquisition using MapReduce from big data. , 2012, , .		26
309	Load-Balanced Virtual Backbone Construction for Wireless Sensor Networks. Lecture Notes in Computer Science, 2012, , 1-12.	1.0	6
310	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
311	Active Protein Interaction Network and Its Application on Protein Complex Detection. , 2011, , .		8
312	Identification of Breast Cancer Gene Signature in Protein Interaction Network Using Graph Centrality. , 2011, , .		0
313	A New Measurement for Evaluating Clusters in Protein Interaction Networks. , 2011, , .		1
314	A comparison of the functional modules identified from time course and static PPI network data. BMC Bioinformatics, 2011, 12, 339.	1.2	103
315	A study of the routing and spectrum allocation in spectrum-sliced Elastic Optical Path networks. , 2011, , .		252
316	Essential Protein Discovery Based on Network Motif and Gene Ontology. , 2011, , .		24
317	An Improved Scoring Method for Protein Residue Conservation and Multiple Sequence Alignment. IEEE Transactions on Nanobioscience, 2011, 10, 275-285.	2.2	9
318	Multiple sequence alignment based on dynamic weighted guidance tree. International Journal of Bioinformatics Research and Applications, 2011, 7, 168.	0.1	11
319	Reliable and energy efficient target coverage for wireless sensor networks. Tsinghua Science and Technology, 2011, 16, 464-474.	4.1	13
320	Genetic-algorithm-based construction of Load-Balanced CDSs in Wireless Sensor Networks. , 2011, , .		15
321	Integration of breast cancer gene signatures based on graph centrality. BMC Systems Biology, 2011, 5, S10.	3.0	62
322	Biological network motif detection and evaluation. BMC Systems Biology, 2011, 5, S5.	3.0	38
323	Parallel progressive multiple sequence alignment on reconfigurable meshes. BMC Genomics, 2011, 12, S4.	1.2	11
324	Self-stabilizing flocking of a group of mobile robots with memory corruption. Wireless Communications and Mobile Computing, 2011, 11, 1061-1072.	0.8	0

#	ARTICLE	IF	CITATIONS
325	Effective monitoring and control of centralized schemes in third generation router based WiMAX mesh network. <i>Wireless Communications and Mobile Computing</i> , 2011, 11, 1117-1126.	0.8	0
326	Sparse nonnegative matrix factorization for protein sequence motif discovery. <i>Expert Systems With Applications</i> , 2011, 38, 13198-13207.	4.4	16
327	A local average connectivity-based method for identifying essential proteins from the network level. <i>Computational Biology and Chemistry</i> , 2011, 35, 143-150.	1.1	152
328	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.	1.0	90
329	A New Method for Identifying Essential Proteins Based on Edge Clustering Coefficient. <i>Lecture Notes in Computer Science</i> , 2011, , 87-98.	1.0	25
330	A Genetic Algorithm for Constructing a Reliable MCDS in Probabilistic Wireless Networks. <i>Lecture Notes in Computer Science</i> , 2011, , 96-107.	1.0	14
331	Impact of the Busy-Line Effect on the Interservice Time Distribution and Modeling of Portable Movements in PCS Networks. <i>IEEE Transactions on Vehicular Technology</i> , 2010, 59, 950-961.	3.9	3
332	Identifying protein complexes from interaction networks based on clique percolation and distance restriction. <i>BMC Genomics</i> , 2010, 11, S10.	1.2	22
333	Recent advances in clustering methods for protein interaction networks. <i>BMC Genomics</i> , 2010, 11, S10.	1.2	104
334	A hybrid swarm intelligence algorithm for the travelling salesman problem. <i>Expert Systems</i> , 2010, 27, 166-179.	2.9	15
335	A Reliable Energy Efficient Algorithm for Target Coverage in Wireless Sensor Networks. , 2010, , .		11
336	Delay-Bounded and Energy-Efficient Composite Event Monitoring in Heterogeneous Wireless Sensor Networks. <i>IEEE Transactions on Parallel and Distributed Systems</i> , 2010, 21, 1373-1385.	4.0	29
337	Essential Proteins Discovery from Weighted Protein Interaction Networks. <i>Lecture Notes in Computer Science</i> , 2010, , 89-100.	1.0	33
338	Hierarchical Organization of Functional Modules in Weighted Protein Interaction Networks Using Clustering Coefficient. <i>Lecture Notes in Computer Science</i> , 2009, , 75-86.	1.0	14
339	IPBGA: a hybrid P2P based grid architecture by using information pool protocol. <i>Journal of Supercomputing</i> , 2009, 49, 159-189.	2.4	3
340	Incomplete crossed hypercubes. <i>Journal of Supercomputing</i> , 2009, 49, 318-333.	2.4	5
341	A blind watermarking method using maximum wavelet coefficient quantization. <i>Expert Systems With Applications</i> , 2009, 36, 11509-11516.	4.4	107
342	Construction of Anti-Collusion Codes Based on Cover-Free Families. , 2009, , .		7

#	ARTICLE	IF	CITATIONS
343	A novel Graph-based Selection Wrapper for learning enhancement in a semi-supervised manner. , 2009, , .		0
344	Tri-Cluster-Tri-Scheme-Training: Exploiting Unlabeled Data for Transmembrane Segments Prediction. , 2009, , .		0
345	Practical Deadlock-Free Fault-Tolerant Routing in Meshes Based on the Planar Network Fault Model. IEEE Transactions on Computers, 2009, 58, 620-633.	2.4	58
346	Guest Editors' Introduction to the Special Section on Bioinformatics Research and Applications. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2009, 6, 178-179.	1.9	0
347	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.	3.9	39
348	An Efficient Watermarking Method Based on Significant Difference of Wavelet Coefficient Quantization. IEEE Transactions on Multimedia, 2008, 10, 746-757.	5.2	185
349	A More Realistic Thinning Scheme for Call Admission Control in Multimedia Wireless Networks. IEEE Transactions on Computers, 2008, 57, 1143-1147.	2.4	40
350	Deadlock-Free Fully Adaptive Routing in Tori Based on a New Virtual Network Partitioning Scheme. , 2008, , .		1
351	Protein Sequence Motif Super-Rule-Tree (SRT) Structure Constructed by Hybrid Hierarchical K-Means Clustering Algorithm. , 2008, , .		4
352	Distributed Sequence Alignment Applications for the Public Computing Architecture. IEEE Transactions on Nanobioscience, 2008, 7, 35-43.	2.2	9
353	Scientific computing on public computing platforms &#x2014; practices and experiences. Parallel and Distributed Processing Symposium (IPDPS), Proceedings of the International Conference on, 2008, , .	1.0	0
354	Detecting pop&#x2014;up advertisement browser windows using support vector machines. Journal of the Chinese Institute of Engineers, Transactions of the Chinese Institute of Engineers, Series A/Chung-kuo Kung Ch'eng Hsueh K'an, 2008, 31, 1189-1198.	0.6	3
355	Efficient Super Granular SVM Feature Elimination (Super GSVM-FE) model for protein sequence motif information extraction. International Journal of Functional Informatics and Personalised Medicine, 2008, 1, 8.	0.4	8
356	Deadlock-Free Adaptive Routing in Meshes Based on Cost-Effective Deadlock Avoidance Schemes. Parallel Processing (ICPP), Proceedings of the International Symposium, 2007, , .	0.0	15
357	Parallel Contour Matching and 3D Partial Retrieval in Bio-Image Database. , 2007, , .		0
358	Multiclass Fuzzy Clustering Support Vector Machines for Protein Local Structure Prediction. , 2007, , .		2
359	A Reliable Metric for Quantifying Multiple Sequence Alignment. , 2007, , .		3
360	Guest Editors' Introduction to the Special Section on Bioinformatics Research and Applications. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2007, 4, 513-514.	1.9	0

#	ARTICLE	IF	CITATIONS
361	Understanding the Prediction of Transmembrane Proteins by Support Vector Machine using Association Rule Mining. , 2007, , .		0
362	To Be or Not to Be: Predicting Soluble SecAs as Membrane Proteins. IEEE Transactions on Nanobioscience, 2007, 6, 168-179.	2.2	18
363	An Incremental Algorithm for Mining Default Definite Decision Rules from Incomplete Decision Tables. , 2007, , .		2
364	Protein Structure Prediction and Its Understanding Based on Machine Learning Methods. , 2007, , .		2
365	Parallel protein secondary structure prediction schemes using Pthread and OpenMP over hyper-threading technology. Journal of Supercomputing, 2007, 41, 1-16.	2.4	11
366	Analyzing the performance of optical multistage interconnection networks with limited crosstalk. Cluster Computing, 2007, 10, 241-250.	3.5	15
367	Clustering support vector machines for protein local structure prediction. Expert Systems With Applications, 2007, 32, 518-526.	4.4	43
368	An Incremental Algorithm for Mining Default Definite Decision Rules from Incomplete Decision Tables. , 2007, , .		1
369	FIK Model: Novel Efficient Granular Computing Model for Protein Sequence Motifs and Structure Information Discovery. , 2006, , .		18
370	Knowledge Dependency Relationships in Incomplete Information System Based on Tolerance Relations. , 2006, , .		0
371	ISE02-5: Analysis of Large-Scale Hybrid Peer-to-Peer Network Topology. IEEE Global Telecommunications Conference (GLOBECOM), 2006, , .	0.0	5
372	Rule Generation for Protein Secondary Structure Prediction With Support Vector Machines and Decision Tree. IEEE Transactions on Nanobioscience, 2006, 5, 46-53.	2.2	43
373	Study of Cache-Enhanced Dynamic Movement-Based Location Management Schemes for 3G Cellular Networks. , 2006, , 627-641.		0
374	A Novel Multistage Network Architecture with Multicast and Broadcast Capability. Journal of Supercomputing, 2006, 35, 277-300.	2.4	24
375	Access Control of Data in Integrated Voice/Video/Data Wireless CDMA Systems. , 2006, , .		0
376	Protein Structure Prediction and Interpretation with Support Vector Machines and Decision Trees. , 2005, , .		0
377	Proportional degradation services in wireless/mobile adaptive multimedia networks. Wireless Communications and Mobile Computing, 2005, 5, 219-243.	0.8	13
378	Architecture, mobility management, and quality of service for integrated 3G and WLAN networks. Wireless Communications and Mobile Computing, 2005, 5, 805-823.	0.8	38

#	ARTICLE	IF	CITATIONS
379	ROUTING IN OPTICAL MULTISTAGE NETWORKS WITH LIMITED CROSSTALK USING ANT COLONY OPTIMIZATION. International Journal of Foundations of Computer Science, 2005, 16, 301-320.	0.8	4
380	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.	4.0	38
381	Vulnerabilities and security enhancements for the IEEE 802.11 WLANs. , 2005, , .		8
382	Improved K-Means Clustering Algorithm for Exploring Local Protein Sequence Motifs Representing Common Structural Property. IEEE Transactions on Nanobioscience, 2005, 4, 255-265.	2.2	80
383	A RELIABLE AND ENERGY-EFFICIENT ROUTING PROTOCOL FOR WIRELESS SENSOR NETWORKS. , 2005, , .		7
384	DISCOVERY OF LOCAL PROTEIN SEQUENCE MOTIFS USING IMPROVED K-MEANS CLUSTERING TECHNIQUE. , 2005, , .		1
385	On Optimizing Energy Consumption for Mobile Handsets. IEEE Transactions on Vehicular Technology, 2004, 53, 1927-1941.	3.9	12
386	A Fast Efficient Parallel Hough Transform Algorithm on LARPBS. Journal of Supercomputing, 2004, 29, 185-195.	2.4	11
387	Parallel bandwidth characteristics calculations for thin avalanche photodiodes on a SGI Origin 2000 supercomputer. Concurrency Computation Practice and Experience, 2004, 16, 1207-1225.	1.4	4
388	Improved Protein Secondary Structure Prediction Using Support Vector Machine With a New Encoding Scheme and an Advanced Tertiary Classifier. IEEE Transactions on Nanobioscience, 2004, 3, 265-271.	2.2	78
389	Symbolic Communication Set Generation for Irregular Parallel Applications. Journal of Supercomputing, 2003, 25, 199-214.	2.4	26
390	More Efficient Topological Sort Using Reconfigurable Optical Buses. Journal of Supercomputing, 2003, 24, 251-258.	2.4	12
391	A scalable HPF implementation of a finite-volume computational electromagnetics application on a CRAY T3E parallel system. Concurrency Computation Practice and Experience, 2003, 15, 607-621.	1.4	3
392	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.	4.0	26
393	An improved movement-based location management scheme for PCS network. , 2003, , .		1
394	Optimal Parallel Algorithms For Multiselection On Mesh-Connected Computers. International Journal of Computer Mathematics, 2003, 80, 165-179.	1.0	3
395	High-level vs low-level parallel programming for scientific computing. , 2002, , .		0
396	Optimal algorithms for the channel-assignment problem on a reconfigurable array of processors with wider bus networks. IEEE Transactions on Parallel and Distributed Systems, 2002, 13, 1124-1138.	4.0	2

#	ARTICLE	IF	CITATIONS
397	Generalized block shift network for clusters. IEEE Transactions on Circuits and Systems Part 1: Regular Papers, 2002, 49, 543-546.	0.1	0
398	Message routing and scheduling in optical multistage networks using simulated annealing. , 2002, , .		13
399	Parallel algorithms for median filtering on arrays with reconfigurable optical buses. , 2002, , .		0
400	Sublogarithmic deterministic selection on arrays with a reconfigurable optical bus. IEEE Transactions on Computers, 2002, 51, 702-707.	2.4	10
401	Efficient parallel algorithms for distance maps of 2D binary images using an optical bus. IEEE Transactions on Systems, Man and Cybernetics, Part A: Systems and Humans, 2002, 32, 228-236.	3.4	8
402	Gain-bandwidth characteristics of thin avalanche photodiodes. IEEE Transactions on Electron Devices, 2002, 49, 770-781.	1.6	44
403	Analysis of dynamic location management for PCS networks. IEEE Transactions on Vehicular Technology, 2002, 51, 1109-1119.	3.9	85
404	Introduction: Recent Developments in Parallel and Distributed Data Mining. Genetic Resources and Crop Evolution, 2002, 49, 491-501.	0.8	32
405	Fault tolerance in the Block-Shift Network. IEEE Transactions on Reliability, 2001, 50, 85-91.	3.5	10
406	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.	2.6	41
407	Optimally Scaling Permutation Routing on Reconfigurable Linear Arrays with Optical Buses. Journal of Parallel and Distributed Computing, 2000, 60, 1125-1136.	2.7	27
408	Title is missing!. Journal of Supercomputing, 2000, 15, 163-181.	2.4	33
409	EFFICIENT AND SCALABLE PARALLELIZATION OF TIME-DEPENDENT MAXWELL EQUATIONS SOLVER USING HIGH PERFORMANCE FORTRAN. , 2000, , .		4
410	Equivalent permutation capabilities between time division optical omega network and non-optical extra stage omega network. , 1999, , .		1
411	Parallel Computing on an Ethernet Cluster of Workstations: Opportunities and Constraints. Journal of Supercomputing, 1999, 13, 111-132.	2.4	3
412	Efficient fault-tolerant routing in multihop optical WDM networks. IEEE Transactions on Parallel and Distributed Systems, 1999, 10, 1012-1025.	4.0	22
413	Fast parallel selection on the linear array with reconfigurable pipelined bus system. , 1999, , .		2
414	An improved constant-time algorithm for computing the Radon and Hough transforms on a reconfigurable mesh. IEEE Transactions on Systems, Man and Cybernetics, Part A: Systems and Humans, 1999, 29, 417-421.	3.4	17



#	ARTICLE	IF	CITATIONS
415	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
416	Properties and performance of the block shift network. IEEE Transactions on Circuits and Systems Part 1: Regular Papers, 1997, 44, 93-102.	0.1	9
417	A MORE EFFICIENT CONSTANT TIME ALGORITHM FOR COMPUTING THE HOUGH TRANSFORM. Parallel Processing Letters, 1994, 04, 45-52.	0.4	10
418	Task allocation in distributed computer systems through an AI planner solver. , 0, , .		3
419	Communication-efficient algorithms on reconfigurable array of processors with spanning optical buses. , 0, , .		2
420	Quicksort on a linear array with a reconfigurable pipelined bus system. , 0, , .		19
421	A pipelined TDM optical bus with conditional delays. , 0, , .		14
422	Potentials and limitations of parallel computing on a cluster of workstations. , 0, , .		1
423	A constant-time algorithm for computing the Euclidean Distance Transform on reconfigurable meshes. , 0, , .		0
424	Fast nearest neighbor algorithms on a linear array with a reconfigurable pipelined bus system. , 0, , .		2
425	Permutation capability of optical multistage interconnection networks. , 0, , .		3
426	Efficient algorithms for fault-tolerant communication in optical WDM networks. , 0, , .		0
427	Optimally scaling permutation routing on reconfigurable linear arrays with optical buses. , 0, , .		2
428	New addressing schemes for pipelined optical buses. , 0, , .		1
429	Semigroup and prefix computations on improved generalized mesh-connected computers with multiple buses. , 0, , .		1
430	Continuous wavelet transform on reconfigurable meshes. , 0, , .		1
431	Parallel granular neural networks for fast credit card fraud detection. , 0, , .		70
432	Optimization techniques for parallel codes of irregular scientific computations. , 0, , .		0

#	ARTICLE	IF	CITATIONS
433	Evolutionary approach for message scheduling in optical Omega networks. , 0, , .		3
434	A new overflow replacement policy for efficient location management in mobile networks. , 0, , .		1
435	Implementation of a calendar application based on SyD coordination links. , 0, , .		5
436	Movement-based location management for 3G cellular networks. , 0, , .		1
437	Enforcing interdependencies and executing transactions atomically over autonomous mobile data stores using SyD link technology. , 0, , .		7
438	Factoring tertiary classification into binary classification improves neural network for protein secondary structure prediction. , 0, , .		0
439	Achieving proportional degradation areas for wireless adaptive multimedia networks. , 0, , .		1
440	Protein Secondary Structure Prediction using decision fusion of Genetic Algorithm and Simulated Annealing Algorithm. , 0, , .		1
441	An Adaptive Genetic Fuzzy Multi-path Routing Protocol for Wireless Ad Hoc Networks. , 0, , .		19
442	Rule Clustering and Super-rule Generation for Transmembrane Segments Prediction. , 0, , .		2
443	Gene Sequence Alignment on a Public Computing Platform. , 0, , .		7
444	Novel Hybrid Hierarchical-K-means Clustering Method (H-K-means) for Microarray Analysis. , 0, , .		31
445	Novel Clustering Algorithm Combined With DSSP Post Processing For Protein Sequence Motif Discovering. , 0, , .		1
446	Cysteine separations profiles on protein secondary structure infer disulfide connectivity. , 0, , .		4
447	Proteinâ€™Ligand Docking with Evolutionary Algorithms. , 0, , 167-195.		3
448	Evolutionary Feature Selection for Bioinformatics. , 0, , 117-139.		1
449	Evolutionary Algorithms for Cancer Chemotherapy Optimization. , 0, , 263-296.		9
450	Phylogenetic Inference Using Evolutionary Algorithms. , 0, , 237-262.		1

#	ARTICLE	IF	CITATIONS
451	Hybrid of Neural Classifier and Swarm Intelligence in Multiclass Cancer Diagnosis with Gene Expression Signatures. , 0, , 1-20.		1
452	Classifying Gene Expression Profiles with Evolutionary Computation. , 0, , 21-40.		0
453	Fuzzy Ontology-Based Text Mining System for Knowledge Acquisition, Ontology Enhancement, and Query Answering from Biomedical Texts. , 0, , 297-339.		1
454	Gene Networks and Evolutionary Computation. , 0, , 67-96.		1
455	Fuzzy-Granular Methods for Identifying Marker Genes from Microarray Expression Data. , 0, , 97-115.		1
456	Fuzzy Approaches for the Analysis CpG Island Methylation Patterns. , 0, , 141-165.		0
457	RNA Secondary Structure Prediction Employing Evolutionary Algorithms. , 0, , 197-223.		1
458	Identification of Marker Genes from High-Dimensional Microarray Data for Cancer Classification. , 0, , 71-87.		0
459	Current Methods for Protein Secondary-Structure Prediction Based on Support Vector Machines. , 0, , 1-26.		0
460	Comparison of Seven Methods for Mining Hidden Links. , 0, , 27-44.		1
461	RNA Interference and microRNA. , 0, , 113-144.		0
462	Voting Scheme-Based Evolutionary Kernel Machines for Drug Activity Comparisons. , 0, , 45-56.		0
463	Bioinformatics Analyses of Arabidopsis thaliana Tiling Array Expression Data. , 0, , 57-70.		0
464	Automatic Query Expansion with Keyphrases and POS Phrase Categorization for Effective Biomedical Text Mining. , 0, , 197-207.		0
465	Protein Structure Prediction using String Kernels. , 0, , 145-168.		4
466	Public Genomic Databases: Data Representation, Storage, and Access. , 0, , 169-195.		0
467	Patient Survival Prediction from Gene Expression Data. , 0, , 89-111.		0
468	On Comparing and Visualizing RNA Secondary Structures. , 0, , 233-249.		0

#	ARTICLE	IF	CITATIONS
469	Evolutionary Dynamics of Protein-Protein Interactions. , 0, , 209-231.		0
470	Integrative Analysis of Yeast Protein Translation Networks. , 0, , 251-266.		0
471	Identification of Transmembrane Proteins Using Variants of the Self-Organizing Feature Map Algorithm. , 0, , 267-293.		1
472	TriCluster: Mining Coherent Clusters in Three-Dimensional Microarray Data. , 0, , 295-317.		0
473	Clustering Methods in a Protein-Protein Interaction Network. , 0, , 319-355.		19
474	miR-193a-5p Promotes Pancreatic Cancer Cell Migration and Invasion Through SRSF6-Mediated Alternative Splicing of OGDHL and ECM1. SSRN Electronic Journal, 0, , .	0.4	3
475	Wiley Series on Bioinformatics: Computational Techniques and Engineering. , 0, , 364-364.		0
476	Generating and screening <i>de novo</i> compounds against given targets using ultrafast deep learning models as core components. Briefings in Bioinformatics, 0, , .	3.2	5
477	An Efficient Modern Strategy to Screen Drug Candidates Targeting RdRp of SARS-CoV-2 With Potentially High Selectivity and Specificity. Frontiers in Chemistry, 0, 10, .	1.8	7