Gaoshi Li

List of Publications by Year
in descending order

201 papers	8,617 citations	53794 45 h-index	56724 83 g-index
208 all docs	208 docs citations	208 times ranked	5570 citing authors

#	Article	IF	Citations
1	KAICD: A knowledge attention-based deep learning framework for automatic ICD coding. Neurocomputing, 2022, 469, 376-383.	5.9	19
2	NetAUC: A network-based multi-biomarker identification method by AUC optimization. Methods, 2022, 198, 56-64.	3.8	5
3	DeepLncLoc: a deep learning framework for long non-coding RNA subcellular localization prediction based on subsequence embedding. Briefings in Bioinformatics, 2022, 23, .	6.5	33
4	Biomedical data, computational methods and tools for evaluating disease–disease associations. Briefings in Bioinformatics, 2022, 23, .	6.5	12
5	Bacon: a comprehensive computational benchmarking framework for evaluating targeted chromatin conformation capture-specific methodologies. Genome Biology, 2022, 23, 30.	8.8	7
6	BACPI: a bi-directional attention neural network for compound–protein interaction and binding affinity prediction. Bioinformatics, 2022, 38, 1995-2002.	4.1	29
7	Guest Editors' Introduction to the Special Section on Bioinformatics Research and Applications. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 166-167.	3.0	0
8	DeepDISOBind: accurate prediction of RNA-, DNA- and protein-binding intrinsically disordered residues with deep multi-task learning. Briefings in Bioinformatics, 2022, 23, .	6.5	28
9	SEPA: signaling entropy-based algorithm to evaluate personalized pathway activation for survival analysis on pan-cancer data. Bioinformatics, 2022, 38, 2536-2543.	4.1	3
10	BridgeDPI: a novel Graph Neural Network for predicting drug–protein interactions. Bioinformatics, 2022, 38, 2571-2578.	4.1	31
11	HyMM: hybrid method for disease-gene prediction by integrating multiscale module structure. Briefings in Bioinformatics, 2022, 23, .	6.5	4
12	EPIXplorer: A web server for prediction, analysis and visualization of enhancer-promoter interactions. Nucleic Acids Research, 2022, 50, W290-W297.	14.5	4
13	Temporal-Spatial Analysis of the Essentiality of Hub Proteins in Protein-Protein Interaction Networks. IEEE Transactions on Network Science and Engineering, 2022, 9, 3504-3514.	6.4	3
14	DRCNNTLe: A deep recurrent convolutional neural network with transfer learning through pre-trained embeddings for automated ICD coding. Methods, 2022, 205, 97-105.	3.8	3
15	A deep matrix factorization based approach for single-cell RNA-seq data clustering. Methods, 2022, 205, 114-122.	3.8	4
16	FUNMarker: Fusion Network-Based Method to Identify Prognostic and Heterogeneous Breast Cancer Biomarkers. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2483-2491.	3.0	10
17	A Deep Learning Framework for Gene Ontology Annotations With Sequence- and Network-Based Information. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2208-2217.	3.0	21
18	DMFLDA: A Deep Learning Framework for Predicting lncRNA–Disease Associations. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2353-2363.	3.0	38

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19	PrGeFNE: Predicting disease-related genes by fast network embedding. Methods, 2021, 192, 3-12.	3.8	25
20	Deep Matrix Factorization Improves Prediction of Human CircRNA-Disease Associations. IEEE Journal of Biomedical and Health Informatics, 2021, 25, 891-899.	6.3	43
21	An Ensemble Method to Reconstruct Gene Regulatory Networks Based on Multivariate Adaptive Regression Splines. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 347-354.	3.0	17
22	DeepDSC: A Deep Learning Method to Predict Drug Sensitivity of Cancer Cell Lines. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 575-582.	3.0	67
23	Deletion Detection Method Using the Distribution of Insert Size and a Precise Alignment Strategy. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1070-1081.	3.0	0
24	A Novel Drug Repositioning Approach Based on Collaborative Metric Learning. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 463-471.	3.0	11
25	Research on the Auxiliary Classification and Diagnosis of Lung Cancer Subtypes Based on Histopathological Images. IEEE Access, 2021, 9, 53687-53707.	4.2	32
26	DPCMNE: detecting protein complexes from protein-protein interaction networks via multi-level network embedding. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	3.0	19
27	SSRE: Cell Type Detection Based on Sparse Subspace Representation and Similarity Enhancement. Genomics, Proteomics and Bioinformatics, 2021, 19, 282-291.	6.9	21
28	A polygenic methylation prediction model associated with response to chemotherapy in epithelial ovarian cancer. Molecular Therapy - Oncolytics, 2021, 20, 545-555.	4.4	8
29	DeepPPF: A deep learning framework for predicting protein family. Neurocomputing, 2021, 428, 19-29.	5.9	16
30	DeepDTAF: a deep learning method to predict protein–ligand binding affinity. Briefings in Bioinformatics, 2021, 22, .	6.5	61
31	NIDM: network impulsive dynamics on multiplex biological network for disease-gene prediction. Briefings in Bioinformatics, 2021, 22, .	6.5	19
32	Essential Protein Prediction Based on node2vec and XGBoost. Journal of Computational Biology, 2021, 28, 687-700.	1.6	17
33	A sensitive repeat identification framework based on short and long reads. Nucleic Acids Research, 2021, 49, e100-e100.	14.5	10
34	Protein interaction networks: centrality, modularity, dynamics, and applications. Frontiers of Computer Science, 2021, 15, 1.	2.4	24
35	Key residues influencing binding affinities of 2019-nCoV with ACE2 in different species. Briefings in Bioinformatics, 2021, 22, 963-975.	6.5	14
36	Biomedical data and computational models for drug repositioning: a comprehensive review. Briefings in Bioinformatics, 2021, 22, 1604-1619.	6.5	110

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37	Improving circRNA–disease association prediction by sequence and ontology representations with convolutional and recurrent neural networks. Bioinformatics, 2021, 36, 5656-5664.	4.1	21
38	Overlapping Protein Complexes Detection Based on Multi-level Topological Similarities. Lecture Notes in Computer Science, 2021, , 215-226.	1.3	1
39	Improving human essential protein prediction using only protein sequences via ensemble learning. , 2021, , .		2
40	A Hybrid Pooling Based Deep Learning Framework For Automated ICD Coding. , 2021, , .		3
41	DeepCI: a deep learning based clustering method for single cell RNA-seq data. , 2021, , .		3
42	Protein–protein interaction site prediction through combining local and global features with deep neural networks. Bioinformatics, 2020, 36, 1114-1120.	4.1	157
43	GapReduce: A Gap Filling Algorithm Based on Partitioned Read Sets. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 877-886.	3.0	11
44	Identification of Protein Complexes by Using a Spatial and Temporal Active Protein Interaction Network. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 817-827.	3.0	24
45	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.	3.0	17
46	miRTRS: A Recommendation Algorithm for Predicting miRNA Targets. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 1032-1041.	3.0	10
47	Network-based methods for predicting essential genes or proteins: a survey. Briefings in Bioinformatics, 2020, 21, 566-583.	6.5	90
48	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.	3.0	14
49	Improving de novo Assembly Based on Read Classification. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 177-188.	3.0	19
50	A disease inference method based on symptom extraction and bidirectional Long Short Term Memory networks. Methods, 2020, 173, 75-82.	3.8	14
51	NIMCE: a gene regulatory network inference approach based on multi time delays causal entropy. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, PP, 1-1.	3.0	2
52	MADA: a web service for analysing DNA methylation array data. BMC Bioinformatics, 2020, 21, 403.	2.6	2
53	CircR2Cancer: a manually curated database of associations between circRNAs and cancers. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	3.0	27
54	Computer-Aided Diagnosis and Staging of Pancreatic Cancer Based on CT Images. IEEE Access, 2020, 8, 141705-141718.	4.2	10

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55	NEDD: a network embedding based method for predicting drug-disease associations. BMC Bioinformatics, 2020, 21, 387.	2.6	23
56	miRTMC: A miRNA Target Prediction Method Based on Matrix Completion Algorithm. IEEE Journal of Biomedical and Health Informatics, 2020, 24, 3630-3641.	6.3	8
57	An Adaptive Sparse Subspace Clustering for Cell Type Identification. Frontiers in Genetics, 2020, 11, 407.	2.3	18
58	SDLDA: lncRNA-disease association prediction based on singular value decomposition and deep learning. Methods, 2020, 179, 73-80.	3.8	61
59	Predicting Human lncRNA-Disease Associations Based on Geometric Matrix Completion. IEEE Journal of Biomedical and Health Informatics, 2020, 24, 2420-2429.	6.3	32
60	NetEPD: A network-based essential protein discovery platform. Tsinghua Science and Technology, 2020, 25, 542-552.	6.1	15
61	Ess-NEXG: Predict Essential Proteins by Constructing a Weighted Protein Interaction Network Based on Node Embedding and XGBoost. Lecture Notes in Computer Science, 2020, , 95-104.	1.3	4
62	PROBselect: accurate prediction of protein-binding residues from proteins sequences via dynamic predictorÂselection. Bioinformatics, 2020, 36, i735-i744.	4.1	19
63	SPOC: Identification of Drug Targets in Biological Networks via Set Preference Output Control. Lecture Notes in Computer Science, 2020, , 26-37.	1.3	0
64	Automatic ICD-9 coding via deep transfer learning. Neurocomputing, 2019, 324, 43-50.	5.9	79
65	A Novel Scaffolding Algorithm Based on Contig Error Correction and Path Extension. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 764-773.	3.0	8
66	A novel extended Pareto Optimality Consensus model for predicting essential proteins. Journal of Theoretical Biology, 2019, 480, 141-149.	1.7	9
67	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.	3.0	3
68	A Novel Coreâ€Attachmentâ€"Based Method to Identify Dynamic Protein Complexes Based on Gene Expression Profiles and PPI Networks. Proteomics, 2019, 19, e1800129.	2.2	9
69	Decoding the Structural Keywords in Protein Structure Universe. Journal of Computer Science and Technology, 2019, 34, 3-15.	1.5	4
70	Controllability and Its Applications to Biological Networks. Journal of Computer Science and Technology, 2019, 34, 16-34.	1.5	25
71	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.	3.0	65
72	Current challenges and solutions of *de novo* assembly. Quantitative Biology, 2019, 7, 90-109.	0.5	46

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73	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
74	A novel method of gene regulatory network structure inference from gene knock-out expression data. Tsinghua Science and Technology, 2019, 24, 446-455.	6.1	17
75	Identifying multi-scale communities in networks by asymptotic surprise. Journal of Statistical Mechanics: Theory and Experiment, 2019, 2019, 033403.	2.3	16
76	DeepFunc: A Deep Learning Framework for Accurate Prediction of Protein Functions from Protein Sequences and Interactions. Proteomics, 2019, 19, e1900019.	2.2	72
77	Automatic ICD code assignment of Chinese clinical notes based on multilayer attention BiRNN. Journal of Biomedical Informatics, 2019, 91, 103114.	4.3	47
78	Tentative diagnosis prediction via deep understanding of patient narratives. , 2019, , .		3
79	DoRC: Discovery of rare cells from ultra-large scRNA-seq data. , 2019, , .		4
80	HNEDTI: Prediction of drug-target interaction based on heterogeneous network embedding. , 2019, , .		7
81	LncRNAâ€"disease association prediction through combining linear and non-linear features with matrix factorization and deep learning techniques. , 2019, , .		7
82	Detecting protein complex based on hierarchical compressing network embedding. , 2019, , .		7
83	DualRank: multiplex network-based dual ranking for heterogeneous complex disease analysis. , 2019, , .		1
84	D3GRN: a data driven dynamic network construction method to infer gene regulatory networks. BMC Genomics, 2019, 20, 929.	2.8	6
85	CSA: a web service for the complete process of ChIP-Seq analysis. BMC Bioinformatics, 2019, 20, 515.	2.6	2
86	DeepEP: a deep learning framework for identifying essential proteins. BMC Bioinformatics, 2019, 20, 506.	2.6	40
87	SCOP: a novel scaffolding algorithm based on contig classification and optimization. Bioinformatics, 2019, 35, 1142-1150.	4.1	13
88	BiXGBoost: a scalable, flexible boosting-based method for reconstructing gene regulatory networks. Bioinformatics, 2019, 35, 1893-1900.	4.1	59
89	Control principles for complex biological networks. Briefings in Bioinformatics, 2019, 20, 2253-2266.	6.5	46
90	Automated ICD-9 Coding via A Deep Learning Approach. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1193-1202.	3.0	78

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91	Computational Drug Repositioning with Random Walk on a Heterogeneous Network. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1890-1900.	3.0	47
92	MGT-SM: A Method for Constructing Cellular Signal Transduction Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 417-424.	3.0	16
93	Construction of Refined Protein Interaction Network for Predicting Essential Proteins. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1386-1397.	3.0	44
94	Evaluation of Pathway Activation for a Single Sample Toward Inflammatory Bowel Disease Classification. Frontiers in Genetics, 2019, 10, 1401.	2.3	9
95	MAC: Merging Assemblies by Using Adjacency Algebraic Model and Classification. Frontiers in Genetics, 2019, 10, 1396.	2.3	10
96	Identification of Prognostic and Heterogeneous Breast Cancer Biomarkers Based on Fusion Network and Multiple Scoring Strategies. Lecture Notes in Computer Science, 2019, , 529-534.	1.3	2
97	Applications of deep learning to MRI images: A survey. Big Data Mining and Analytics, 2018, 1, 1-18.	8.9	195
98	CytoCtrlAnalyser: a Cytoscape app for biomolecular network controllability analysis. Bioinformatics, 2018, 34, 1428-1430.	4.1	17
99	Computational drug repositioning using low-rank matrix approximation and randomized algorithms. Bioinformatics, 2018, 34, 1904-1912.	4.1	183
100	DyNetViewer: a Cytoscape app for dynamic network construction, analysis and visualization. Bioinformatics, 2018, 34, 1597-1599.	4.1	27
101	Prediction of lncRNAâ€"disease associations based on inductive matrix completion. Bioinformatics, 2018, 34, 3357-3364.	4.1	227
102	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
103	Predicting MicroRNA-Disease Associations Based on Improved MicroRNA and Disease Similarities. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1774-1782.	3.0	116
104	Classification of Alzheimer's Disease Using Whole Brain Hierarchical Network. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 624-632.	3.0	142
105	A Deep Learning Framework for Identifying Essential Proteins Based on Protein-Protein Interaction Network and Gene Expression Data. , 2018, , .		12
106	United neighborhood closeness centrality and orthology for predicting essential proteins. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 17, 1-1.	3.0	50
107	Disease Inference with Symptom Extraction and Bidirectional Recurrent Neural Network. , 2018, , .		7
108	An interpretable boosting model to predict side effects of analgesics for osteoarthritis. BMC Systems Biology, 2018, 12, 105.	3.0	35

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109	Biomolecular Networks for Complex Diseases. Complexity, 2018, 2018, 1-3.	1.6	4
110	A survey of matrix completion methods for recommendation systems. Big Data Mining and Analytics, 2018, 1, 308-323.	8.9	92
111	LDAP: a web server for lncRNA-disease association prediction. Bioinformatics, 2017, 33, 458-460.	4.1	182
112	United Complex Centrality for Identification of Essential Proteins from PPI Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 370-380.	3.0	80
113	Predicting Protein Functions by Using Unbalanced Random Walk Algorithm on Three Biological Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 360-369.	3.0	45
114	ISEA: Iterative Seed-Extension Algorithm for De Novo Assembly Using Paired-End Information and Insert Size Distribution. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 916-925.	3.0	20
115	PECC: Correcting contigs based on paired-end read distribution. Computational Biology and Chemistry, 2017, 69, 178-184.	2.3	17
116	Biomolecular Network Controllability With Drug Binding Information. IEEE Transactions on Nanobioscience, 2017, 16, 326-332.	3.3	13
117	Classification of Schizophrenia Based on Individual Hierarchical Brain Networks Constructed From Structural MRI Images. IEEE Transactions on Nanobioscience, 2017, 16, 600-608.	3.3	38
118	Protein Inference from the Integration of Tandem MS Data and Interactome Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 1399-1409.	3.0	3
119	BOSS: a novel scaffolding algorithm based on an optimized scaffold graph. Bioinformatics, 2017, 33, 169-176.	4.1	33
120	MEC: Misassembly error correction in contigs using a combination of paired-end reads and GC-contents. , 2017, , .		2
121	CytoCluster: A Cytoscape Plugin for Cluster Analysis and Visualization of Biological Networks. International Journal of Molecular Sciences, 2017, 18, 1880.	4.1	90
122	Complex Brain Network Analysis and Its Applications to Brain Disorders: A Survey. Complexity, 2017, 2017, 1-27.	1.6	90
123	VAliBS: a visual aligner for bisulfite sequences. BMC Bioinformatics, 2017, 18, 410.	2.6	2
124	LSLS: A Novel Scaffolding Method Based on Path Extension. Lecture Notes in Computer Science, 2017, , 428-438.	1.3	1
125	Construction of the spatial and temporal active protein interaction network for identifying protein complexes. , 2016, , .		5
126	Predicting essential proteins based on subcellular localization, orthology and PPI networks. BMC Bioinformatics, 2016, 17, 279.	2.6	66

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127	A reliable neighbor-based method for identifying essential proteins by integrating gene expressions, orthology, and subcellular localization information. Tsinghua Science and Technology, 2016, 21, 668-677.	6.1	25
128	The MSS of complex networks with centrality based preference and its application to biomolecular networks. , 2016, , .		3
129	Predicting microRNA-environmental factor interactions based on bi-random walk and multi-label learning. , 2016, , .		3
130	Identifying Essential Proteins by Purifying Protein Interaction Networks. Lecture Notes in Computer Science, 2016, , 106-116.	1.3	1
131	Drug repositioning based on comprehensive similarity measures and Bi-Random walk algorithm. Bioinformatics, 2016, 32, 2664-2671.	4.1	311
132	C-DEVA: Detection, evaluation, visualization and annotation of clusters from biological networks. BioSystems, 2016, 150, 78-86.	2.0	11
133	Minimum steering node set of complex networks and its applications to biomolecular networks. IET Systems Biology, 2016, 10, 116-123.	1.5	15
134	FLEXc: protein flexibility prediction using context-based statistics, predicted structural features, and sequence information. BMC Bioinformatics, 2016, 17, 281.	2.6	14
135	Identifying Individual-Cancer-Related Genes by Rebalancing the Training Samples. IEEE Transactions on Nanobioscience, 2016, 15, 309-315.	3.3	18
136	Predicting drug–target interaction using positive-unlabeled learning. Neurocomputing, 2016, 206, 50-57.	5.9	83
137	A New Method for Predicting Protein Functions From Dynamic Weighted Interactome Networks. IEEE Transactions on Nanobioscience, 2016, 15, 131-139.	3.3	28
138	HybridDock: A Hybrid Protein–Ligand Docking Protocol Integrating Protein- and Ligand-Based Approaches. Journal of Chemical Information and Modeling, 2016, 56, 1078-1087.	5.4	35
139	Prioritizing Disease Genes by Using Search Engine Algorithm. Current Bioinformatics, 2016, 11, 195-202.	1.5	22
140	Computational approaches for prioritizing candidate disease genes based on PPI networks. Tsinghua Science and Technology, 2015, 20, 500-512.	6.1	64
141	A feature selection method for prediction essential protein. Tsinghua Science and Technology, 2015, 20, 491-499.	6.1	33
142	A fast and high performance multiple data integration algorithm for identifying human disease genes. BMC Medical Genomics, 2015, 8, S2.	1.5	43
143	Re-alignment of the unmapped reads with base quality score. BMC Bioinformatics, 2015, 16, S8.	2.6	14
144	Systems Biology Approaches to Mining High Throughput Biological Data. BioMed Research International, 2015, 2015, 1-2.	1.9	2

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145	Predicting microRNA-disease associations by integrating multiple biological information. , 2015, , .		12
146	A two-step logistic regression algorithm for identifying individual-cancer-related genes. , 2015, , .		8
147	Identifying protein complexes based on the integration of PPI network and gene expression data. International Journal of Bioinformatics Research and Applications, 2015, 11, 30.	0.2	2
148	Discovering essential proteins based on PPI network and protein complex. International Journal of Data Mining and Bioinformatics, 2015, 12, 24.	0.1	23
149	Heterogeneous Network Model to Infer Human Disease-Long Intergenic Non-Coding RNA Associations. IEEE Transactions on Nanobioscience, 2015, 14, 175-183.	3.3	51
150	Network Output Controllability-Based Method for Drug Target Identification. IEEE Transactions on Nanobioscience, 2015, 14, 184-191.	3.3	33
151	Detecting SNP Combinations Discriminating Human Populations From HapMap Data. IEEE Transactions on Nanobioscience, 2015, 14, 220-228.	3.3	4
152	ClusterViz: A Cytoscape APP for Cluster Analysis of Biological Network. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 815-822.	3.0	103
153	A Topology Potential-Based Method for Identifying Essential Proteins from PPI Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 372-383.	3.0	88
154	EPGA2: memory-efficient <i>de novo</i> assembler. Bioinformatics, 2015, 31, 3988-3990.	4.1	19
155	CytoNCA: A cytoscape plugin for centrality analysis and evaluation of protein interaction networks. BioSystems, 2015, 127, 67-72.	2.0	813
156	EPGA: <i>de novo</i> assembly using the distributions of reads and insert size. Bioinformatics, 2015, 31, 825-833.	4.1	25
157	Identifying Dynamic Protein Complexes Based on Gene Expression Profiles and PPI Networks. BioMed Research International, 2014, 2014, 1-10.	1.9	22
158	A logistic regression based algorithm for identifying human disease genes. , 2014, , .		7
159	A Novel Algorithm for Detecting Protein Complexes with the Breadth First Search. BioMed Research International, 2014, 2014, 1-8.	1.9	10
160	Prediction of Essential Proteins Based on Overlapping Essential Modules. IEEE Transactions on Nanobioscience, 2014, 13, 415-424.	3.3	60
161	Identification of Essential Proteins by Using Complexes and Interaction Network. Lecture Notes in Computer Science, 2014, , 255-265.	1.3	6
162	A survey of MRI-based brain tumor segmentation methods. Tsinghua Science and Technology, 2014, 19, 578-595.	6.1	252

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163	Prioritization of orphan disease-causing genes using topological feature and GO similarity between proteins in interaction networks. Science China Life Sciences, 2014, 57, 1064-1071.	4.9	20
164	Disease gene identification by using graph kernels and Markov random fields. Science China Life Sciences, 2014, 57, 1054-1063.	4.9	33
165	Effective identification of essential proteins based on priori knowledge, network topology and gene expressions. Methods, 2014, 67, 325-333.	3.8	89
166	Detecting Protein Complexes Based on Uncertain Graph Model. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 486-497.	3.0	77
167	Improving protein function prediction using domain and protein complexes in PPI networks. BMC Systems Biology, 2014, 8, 35.	3.0	43
168	Prediction of disease genes using tissue-specified gene-gene network. BMC Systems Biology, 2014, 8, S3.	3.0	23
169	Prediction of disease-related genes based on weighted tissue-specific networks by using DNA methylation. BMC Medical Genomics, 2014, 7, S4.	1.5	14
170	Identifying disease genes by integrating multiple data sources. BMC Medical Genomics, 2014, 7, S2.	1.5	36
171	A Method to Evaluate Genome-Wide Methylation in Archival Formalin-Fixed, Paraffin-Embedded Ovarian Epithelial Cells. PLoS ONE, 2014, 9, e104481.	2.5	11
172	An effective method for refining predicted protein complexes based on protein activity and the mechanism of protein complex formation. BMC Systems Biology, 2013, 7, 28.	3.0	8
173	Identifying protein complexes based on density and modularity in protein-protein interaction network. BMC Systems Biology, 2013, 7, S12.	3.0	21
174	A new method for predicting essential proteins based on topology potential. , 2013, , .		3
175	A clustering algorithm for identifying hierarchical and overlapping protein complexes in large PPI networks. , 2013, , .		0
176	Identifying dynamic protein complexes based on gene expression profiles and PPI networks. , 2013, , .		1
177	Prioritization of candidate genes based on disease similarity and protein's proximity in PPI networks. , 2013, , .		4
178	Construction and application of dynamic protein interaction network based on time course gene expression data. Proteomics, 2013, 13, 301-312.	2.2	141
179	<i>hF‑measure</i>: A new measurement for evaluating clusters in protein–protein interaction networks. Proteomics, 2013, 13, 291-300.	2.2	25
180	IDENTIFICATION OF ESSENTIAL PROTEINS FROM WEIGHTED PROTEIN–PROTEIN INTERACTION NETWORKS. Journal of Bioinformatics and Computational Biology, 2013, 11, 1341002.	0.8	37

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181	Multimeric Stability of Human C-reactive Protein in Archived Specimens. PLoS ONE, 2013, 8, e58094.	2.5	8
182	Identification of Hierarchical and Overlapping Functional Modules in PPI Networks. IEEE Transactions on Nanobioscience, 2012, 11, 386-393.	3.3	33
183	Identifying Protein Complexes From Interactome Based on Essential Proteins and Local Fitness Method. IEEE Transactions on Nanobioscience, 2012, 11, 324-335.	3.3	15
184	Identifying protein complexes based on local fitness method. , 2012, , .		2
185	Towards the identification of protein complexes and functional modules by integrating PPI network and gene expression data. BMC Bioinformatics, 2012, 13, 109.	2.6	122
186	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
187	Identification of Essential Proteins Based on Edge Clustering Coefficient. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1070-1080.	3.0	254
188	A Fast Hierarchical Clustering Algorithm for Functional Modules Discovery in Protein Interaction Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 607-620.	3.0	171
189	A New Measurement for Evaluating Clusters in Protein Interaction Networks. , 2011, , .		1
190	A comparison of the functional modules identified from time course and static PPI network data. BMC Bioinformatics, 2011, 12, 339.	2.6	103
191	Integration of breast cancer gene signatures based on graph centrality. BMC Systems Biology, 2011, 5, S10.	3.0	62
192	Biological network motif detection and evaluation. BMC Systems Biology, 2011, 5, S5.	3.0	38
193	A local average connectivity-based method for identifying essential proteins from the network level. Computational Biology and Chemistry, 2011, 35, 143-150.	2.3	152
194	Identifying protein complexes from interaction networks based on clique percolation and distance restriction. BMC Genomics, 2010, 11, S10.	2.8	22
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