

# Gaoshi Li

## List of Publications by Year in descending order

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Version: 2024-02-01

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	CytoNCA: A cytoscape plugin for centrality analysis and evaluation of protein interaction networks. <i>BioSystems</i> , 2015, 127, 67-72.	2.0	813
2	Drug repositioning based on comprehensive similarity measures and Bi-Random walk algorithm. <i>Bioinformatics</i> , 2016, 32, 2664-2671.	4.1	311
3	Identification of Essential Proteins Based on Edge Clustering Coefficient. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 1070-1080.	3.0	254
4	A survey of MRI-based brain tumor segmentation methods. <i>Tsinghua Science and Technology</i> , 2014, 19, 578-595.	6.1	252
5	Prediction of lncRNA-disease associations based on inductive matrix completion. <i>Bioinformatics</i> , 2018, 34, 3357-3364.	4.1	227
6	A new essential protein discovery method based on the integration of protein-protein interaction and gene expression data. <i>BMC Systems Biology</i> , 2012, 6, 15.	3.0	211
7	Modifying the DPPlus algorithm for identifying protein complexes based on new topological structures. <i>BMC Bioinformatics</i> , 2008, 9, 398.	2.6	209
8	Applications of deep learning to MRI images: A survey. <i>Big Data Mining and Analytics</i> , 2018, 1, 1-18.	8.9	195
9	Computational drug repositioning using low-rank matrix approximation and randomized algorithms. <i>Bioinformatics</i> , 2018, 34, 1904-1912.	4.1	183
10	LDAP: a web server for lncRNA-disease association prediction. <i>Bioinformatics</i> , 2017, 33, 458-460.	4.1	182
11	A Fast Hierarchical Clustering Algorithm for Functional Modules Discovery in Protein Interaction Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 607-620.	3.0	171
12	Protein-protein interaction site prediction through combining local and global features with deep neural networks. <i>Bioinformatics</i> , 2020, 36, 1114-1120.	4.1	157
13	A local average connectivity-based method for identifying essential proteins from the network level. <i>Computational Biology and Chemistry</i> , 2011, 35, 143-150.	2.3	152
14	Classification of Alzheimer's Disease Using Whole Brain Hierarchical Network. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 624-632.	3.0	142
15	Construction and application of dynamic protein interaction network based on time course gene expression data. <i>Proteomics</i> , 2013, 13, 301-312.	2.2	141
16	Towards the identification of protein complexes and functional modules by integrating PPI network and gene expression data. <i>BMC Bioinformatics</i> , 2012, 13, 109.	2.6	122
17	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.	3.0	116
18	SinNLRR: a robust subspace clustering method for cell type detection by non-negative and low-rank representation. <i>Bioinformatics</i> , 2019, 35, 3642-3650.	4.1	112

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19	Biomedical data and computational models for drug repositioning: a comprehensive review. <i>Briefings in Bioinformatics</i> , 2021, 22, 1604-1619.	6.5	110
20	Recent advances in clustering methods for protein interaction networks. <i>BMC Genomics</i> , 2010, 11, S10.	2.8	104
21	A comparison of the functional modules identified from time course and static PPI network data. <i>BMC Bioinformatics</i> , 2011, 12, 339.	2.6	103
22	ClusterViz: A Cytoscape APP for Cluster Analysis of Biological Network. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 815-822.	3.0	103
23	A survey of matrix completion methods for recommendation systems. <i>Big Data Mining and Analytics</i> , 2018, 1, 308-323.	8.9	92
24	CytoCluster: A Cytoscape Plugin for Cluster Analysis and Visualization of Biological Networks. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1880.	4.1	90
25	Complex Brain Network Analysis and Its Applications to Brain Disorders: A Survey. <i>Complexity</i> , 2017, 1-27.	1.6	90
26	Network-based methods for predicting essential genes or proteins: a survey. <i>Briefings in Bioinformatics</i> , 2020, 21, 566-583.	6.5	90
27	Effective identification of essential proteins based on priori knowledge, network topology and gene expressions. <i>Methods</i> , 2014, 67, 325-333.	3.8	89
28	A Topology Potential-Based Method for Identifying Essential Proteins from PPI Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 372-383.	3.0	88
29	Predicting drug-target interaction using positive-unlabeled learning. <i>Neurocomputing</i> , 2016, 206, 50-57.	5.9	83
30	United Complex Centrality for Identification of Essential Proteins from PPI Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 370-380.	3.0	80
31	Automatic ICD-9 coding via deep transfer learning. <i>Neurocomputing</i> , 2019, 324, 43-50.	5.9	79
32	Automated ICD-9 Coding via A Deep Learning Approach. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1193-1202.	3.0	78
33	Detecting Protein Complexes Based on Uncertain Graph Model. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 486-497.	3.0	77
34	DeepFunc: A Deep Learning Framework for Accurate Prediction of Protein Functions from Protein Sequences and Interactions. <i>Proteomics</i> , 2019, 19, e1900019.	2.2	72
35	DeepDSC: A Deep Learning Method to Predict Drug Sensitivity of Cancer Cell Lines. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 575-582.	3.0	67
36	Predicting essential proteins based on subcellular localization, orthology and PPI networks. <i>BMC Bioinformatics</i> , 2016, 17, 279.	2.6	66

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37	A deep learning framework for identifying essential proteins by integrating multiple types of biological information. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 18, 1-1.	3.0	65
38	Computational approaches for prioritizing candidate disease genes based on PPI networks. <i>Tsinghua Science and Technology</i> , 2015, 20, 500-512.	6.1	64
39	Integration of breast cancer gene signatures based on graph centrality. <i>BMC Systems Biology</i> , 2011, 5, S10.	3.0	62
40	SDLDA: lncRNA-disease association prediction based on singular value decomposition and deep learning. <i>Methods</i> , 2020, 179, 73-80.	3.8	61
41	DeepDTAF: a deep learning method to predict protein-ligand binding affinity. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	61
42	Prediction of Essential Proteins Based on Overlapping Essential Modules. <i>IEEE Transactions on Nanobioscience</i> , 2014, 13, 415-424.	3.3	60
43	BiXGBoost: a scalable, flexible boosting-based method for reconstructing gene regulatory networks. <i>Bioinformatics</i> , 2019, 35, 1893-1900.	4.1	59
44	Heterogeneous Network Model to Infer Human Disease-Long Intergenic Non-Coding RNA Associations. <i>IEEE Transactions on Nanobioscience</i> , 2015, 14, 175-183.	3.3	51
45	United neighborhood closeness centrality and orthology for predicting essential proteins. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 17, 1-1.	3.0	50
46	Automatic ICD code assignment of Chinese clinical notes based on multilayer attention BiRNN. <i>Journal of Biomedical Informatics</i> , 2019, 91, 103114.	4.3	47
47	Computational Drug Repositioning with Random Walk on a Heterogeneous Network. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1890-1900.	3.0	47
48	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.	1.7	46
49	Current challenges and solutions of <i>de novo</i> assembly. <i>Quantitative Biology</i> , 2019, 7, 90-109.	0.5	46
50	Control principles for complex biological networks. <i>Briefings in Bioinformatics</i> , 2019, 20, 2253-2266.	6.5	46
51	Predicting Protein Functions by Using Unbalanced Random Walk Algorithm on Three Biological Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 360-369.	3.0	45
52	Construction of Refined Protein Interaction Network for Predicting Essential Proteins. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1386-1397.	3.0	44
53	Improving protein function prediction using domain and protein complexes in PPI networks. <i>BMC Systems Biology</i> , 2014, 8, 35.	3.0	43
54	A fast and high performance multiple data integration algorithm for identifying human disease genes. <i>BMC Medical Genomics</i> , 2015, 8, S2.	1.5	43

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55	Deep Matrix Factorization Improves Prediction of Human CircRNA-Disease Associations. IEEE Journal of Biomedical and Health Informatics, 2021, 25, 891-899.	6.3	43
56	A Fast Agglomerate Algorithm for Mining Functional Modules in Protein Interaction Networks. , 2008, , ,		40
57	DeepEP: a deep learning framework for identifying essential proteins. BMC Bioinformatics, 2019, 20, 506.	2.6	40
58	Biological network motif detection and evaluation. BMC Systems Biology, 2011, 5, S5.	3.0	38
59	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
60	DMFLDA: A Deep Learning Framework for Predicting lncRNAâ€™Disease Associations. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2353-2363.	3.0	38
61	IDENTIFICATION OF ESSENTIAL PROTEINS FROM WEIGHTED PROTEINâ€™PROTEIN INTERACTION NETWORKS. Journal of Bioinformatics and Computational Biology, 2013, 11, 1341002.	0.8	37
62	Identifying the overlapping complexes in protein interaction networks. International Journal of Data Mining and Bioinformatics, 2010, 4, 91.	0.1	36
63	Identifying disease genes by integrating multiple data sources. BMC Medical Genomics, 2014, 7, S2.	1.5	36
64	HybridDock: A Hybrid Proteinâ€™Ligand Docking Protocol Integrating Protein- and Ligand-Based Approaches. Journal of Chemical Information and Modeling, 2016, 56, 1078-1087.	5.4	35
65	An interpretable boosting model to predict side effects of analgesics for osteoarthritis. BMC Systems Biology, 2018, 12, 105.	3.0	35
66	Identification of Hierarchical and Overlapping Functional Modules in PPI Networks. IEEE Transactions on Nanobioscience, 2012, 11, 386-393.	3.3	33
67	Disease gene identification by using graph kernels and Markov random fields. Science China Life Sciences, 2014, 57, 1054-1063.	4.9	33
68	A feature selection method for prediction essential protein. Tsinghua Science and Technology, 2015, 20, 491-499.	6.1	33
69	Network Output Controllability-Based Method for Drug Target Identification. IEEE Transactions on Nanobioscience, 2015, 14, 184-191.	3.3	33
70	BOSS: a novel scaffolding algorithm based on an optimized scaffold graph. Bioinformatics, 2017, 33, 169-176.	4.1	33
71	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
72	Essential Proteins Discovery from Weighted Protein Interaction Networks. Lecture Notes in Computer Science, 2010, , 89-100.	1.3	33

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73	Predicting Human lncRNA-Disease Associations Based on Geometric Matrix Completion. IEEE Journal of Biomedical and Health Informatics, 2020, 24, 2420-2429.	6.3	32
74	Research on the Auxiliary Classification and Diagnosis of Lung Cancer Subtypes Based on Histopathological Images. IEEE Access, 2021, 9, 53687-53707.	4.2	32
75	BridgeDPI: a novel Graph Neural Network for predicting drug-protein interactions. Bioinformatics, 2022, 38, 2571-2578.	4.1	31
76	BACPI: a bi-directional attention neural network for compound-protein interaction and binding affinity prediction. Bioinformatics, 2022, 38, 1995-2002.	4.1	29
77	A New Method for Predicting Protein Functions From Dynamic Weighted Interactome Networks. IEEE Transactions on Nanobioscience, 2016, 15, 131-139.	3.3	28
78	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
79	DyNetViewer: a Cytoscape app for dynamic network construction, analysis and visualization. Bioinformatics, 2018, 34, 1597-1599.	4.1	27
80	CircR2Cancer: a manually curated database of associations between circRNAs and cancers. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	3.0	27
81	<i>h</i> -measure: A new measurement for evaluating clusters in protein-protein interaction networks. Proteomics, 2013, 13, 291-300.	2.2	25
82	EPGA: <i>de novo</i> assembly using the distributions of reads and insert size. Bioinformatics, 2015, 31, 825-833.	4.1	25
83	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
84	Controllability and Its Applications to Biological Networks. Journal of Computer Science and Technology, 2019, 34, 16-34.	1.5	25
85	PrGeFNE: Predicting disease-related genes by fast network embedding. Methods, 2021, 192, 3-12.	3.8	25
86	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
87	Protein interaction networks: centrality, modularity, dynamics, and applications. Frontiers of Computer Science, 2021, 15, 1.	2.4	24
88	Prediction of disease genes using tissue-specified gene-gene network. BMC Systems Biology, 2014, 8, S3.	3.0	23
89	Discovering essential proteins based on PPI network and protein complex. International Journal of Data Mining and Bioinformatics, 2015, 12, 24.	0.1	23
90	NEDD: a network embedding based method for predicting drug-disease associations. BMC Bioinformatics, 2020, 21, 387.	2.6	23

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91	Identifying protein complexes from interaction networks based on clique percolation and distance restriction. BMC Genomics, 2010, 11, S10.	2.8	22
92	Identifying Dynamic Protein Complexes Based on Gene Expression Profiles and PPI Networks. BioMed Research International, 2014, 2014, 1-10.	1.9	22
93	Prioritizing Disease Genes by Using Search Engine Algorithm. Current Bioinformatics, 2016, 11, 195-202.	1.5	22
94	Identifying protein complexes based on density and modularity in protein-protein interaction network. BMC Systems Biology, 2013, 7, S12.	3.0	21
95	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
96	SSRE: Cell Type Detection Based on Sparse Subspace Representation and Similarity Enhancement. Genomics, Proteomics and Bioinformatics, 2021, 19, 282-291.	6.9	21
97	Improving circRNA disease association prediction by sequence and ontology representations with convolutional and recurrent neural networks. Bioinformatics, 2021, 36, 5656-5664.	4.1	21
98	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
99	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
100	EPGA2: memory-efficient <i>de novo</i> assembler. Bioinformatics, 2015, 31, 3988-3990.	4.1	19
101	Improving de novo Assembly Based on Read Classification. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 177-188.	3.0	19
102	KAICD: A knowledge attention-based deep learning framework for automatic ICD coding. Neurocomputing, 2022, 469, 376-383.	5.9	19
103	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
104	NIDM: network impulsive dynamics on multiplex biological network for disease-gene prediction. Briefings in Bioinformatics, 2021, 22, .	6.5	19
105	PROBselect: accurate prediction of protein-binding residues from proteins sequences via dynamic predictor selection. Bioinformatics, 2020, 36, i735-i744.	4.1	19
106	Identifying Individual-Cancer-Related Genes by Rebalancing the Training Samples. IEEE Transactions on Nanobioscience, 2016, 15, 309-315.	3.3	18
107	An Adaptive Sparse Subspace Clustering for Cell Type Identification. Frontiers in Genetics, 2020, 11, 407.	2.3	18
108	PECC: Correcting contigs based on paired-end read distribution. Computational Biology and Chemistry, 2017, 69, 178-184.	2.3	17

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109	CytoCtrlAnalyser: a Cytoscape app for biomolecular network controllability analysis. <i>Bioinformatics</i> , 2018, 34, 1428-1430.	4.1	17
110	A novel method of gene regulatory network structure inference from gene knock-out expression data. <i>Tsinghua Science and Technology</i> , 2019, 24, 446-455.	6.1	17
111	MEC: Misassembly Error Correction in Contigs based on Distribution of Paired-End Reads and Statistics of GC-contents. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 17, 847-857.	3.0	17
112	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.	3.0	17
113	Essential Protein Prediction Based on node2vec and XGBoost. <i>Journal of Computational Biology</i> , 2021, 28, 687-700.	1.6	17
114	Identifying multi-scale communities in networks by asymptotic surprise. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2019, 2019, 033403.	2.3	16
115	MGT-SM: A Method for Constructing Cellular Signal Transduction Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 417-424.	3.0	16
116	DeepPPF: A deep learning framework for predicting protein family. <i>Neurocomputing</i> , 2021, 428, 19-29.	5.9	16
117	Identifying Protein Complexes From Interactome Based on Essential Proteins and Local Fitness Method. <i>IEEE Transactions on Nanobioscience</i> , 2012, 11, 324-335.	3.3	15
118	Minimum steering node set of complex networks and its applications to biomolecular networks. <i>IET Systems Biology</i> , 2016, 10, 116-123.	1.5	15
119	NetEPD: A network-based essential protein discovery platform. <i>Tsinghua Science and Technology</i> , 2020, 25, 542-552.	6.1	15
120	Hierarchical Organization of Functional Modules in Weighted Protein Interaction Networks Using Clustering Coefficient. <i>Lecture Notes in Computer Science</i> , 2009, , 75-86.	1.3	14
121	Prediction of disease-related genes based on weighted tissue-specific networks by using DNA methylation. <i>BMC Medical Genomics</i> , 2014, 7, S4.	1.5	14
122	Re-alignment of the unmapped reads with base quality score. <i>BMC Bioinformatics</i> , 2015, 16, S8.	2.6	14
123	FLEXc: protein flexibility prediction using context-based statistics, predicted structural features, and sequence information. <i>BMC Bioinformatics</i> , 2016, 17, 281.	2.6	14
124	An Efficient Trimming Algorithm based on Multi-Feature Fusion Scoring Model for NGS Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 17, 728-738.	3.0	14
125	A disease inference method based on symptom extraction and bidirectional Long Short Term Memory networks. <i>Methods</i> , 2020, 173, 75-82.	3.8	14
126	Key residues influencing binding affinities of 2019-nCoV with ACE2 in different species. <i>Briefings in Bioinformatics</i> , 2021, 22, 963-975.	6.5	14



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127	Biomolecular Network Controllability With Drug Binding Information. IEEE Transactions on Nanobioscience, 2017, 16, 326-332.	3.3	13
128	SCOP: a novel scaffolding algorithm based on contig classification and optimization. Bioinformatics, 2019, 35, 1142-1150.	4.1	13
129	Predicting microRNA-disease associations by integrating multiple biological information. , 2015, , .		12
130	A Deep Learning Framework for Identifying Essential Proteins Based on Protein-Protein Interaction Network and Gene Expression Data. , 2018, , .		12
131	Biomedical data, computational methods and tools for evaluating disease-disease associations. Briefings in Bioinformatics, 2022, 23, .	6.5	12
132	C-DEVA: Detection, evaluation, visualization and annotation of clusters from biological networks. BioSystems, 2016, 150, 78-86.	2.0	11
133	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
134	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
135	A Method to Evaluate Genome-Wide Methylation in Archival Formalin-Fixed, Paraffin-Embedded Ovarian Epithelial Cells. PLoS ONE, 2014, 9, e104481.	2.5	11
136	A Novel Algorithm for Detecting Protein Complexes with the Breadth First Search. BioMed Research International, 2014, 2014, 1-8.	1.9	10
137	miRTRS: A Recommendation Algorithm for Predicting miRNA Targets. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 1032-1041.	3.0	10
138	Computer-Aided Diagnosis and Staging of Pancreatic Cancer Based on CT Images. IEEE Access, 2020, 8, 141705-141718.	4.2	10
139	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
140	MAC: Merging Assemblies by Using Adjacency Algebraic Model and Classification. Frontiers in Genetics, 2019, 10, 1396.	2.3	10
141	A sensitive repeat identification framework based on short and long reads. Nucleic Acids Research, 2021, 49, e100-e100.	14.5	10
142	A novel extended Pareto Optimality Consensus model for predicting essential proteins. Journal of Theoretical Biology, 2019, 480, 141-149.	1.7	9
143	A Novel Core-Attachment-Based Method to Identify Dynamic Protein Complexes Based on Gene Expression Profiles and PPI Networks. Proteomics, 2019, 19, e1800129.	2.2	9
144	Evaluation of Pathway Activation for a Single Sample Toward Inflammatory Bowel Disease Classification. Frontiers in Genetics, 2019, 10, 1401.	2.3	9

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145	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
146	Multimeric Stability of Human C-reactive Protein in Archived Specimens. PLoS ONE, 2013, 8, e58094.	2.5	8
147	A two-step logistic regression algorithm for identifying individual-cancer-related genes. , 2015, , .		8
148	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
149	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
150	A polygenic methylation prediction model associated with response to chemotherapy in epithelial ovarian cancer. Molecular Therapy - Oncolytics, 2021, 20, 545-555.	4.4	8
151	A logistic regression based algorithm for identifying human disease genes. , 2014, , .		7
152	Disease Inference with Symptom Extraction and Bidirectional Recurrent Neural Network. , 2018, , .		7
153	HNEDTI: Prediction of drug-target interaction based on heterogeneous network embedding. , 2019, , .		7
154	LncRNAâ€‘disease association prediction through combining linear and non-linear features with matrix factorization and deep learning techniques. , 2019, , .		7
155	Detecting protein complex based on hierarchical compressing network embedding. , 2019, , .		7
156	Bacon: a comprehensive computational benchmarking framework for evaluating targeted chromatin conformation capture-specific methodologies. Genome Biology, 2022, 23, 30.	8.8	7
157	Identification of Essential Proteins by Using Complexes and Interaction Network. Lecture Notes in Computer Science, 2014, , 255-265.	1.3	6
158	D3GRN: a data driven dynamic network construction method to infer gene regulatory networks. BMC Genomics, 2019, 20, 929.	2.8	6
159	Construction of the spatial and temporal active protein interaction network for identifying protein complexes. , 2016, , .		5
160	NetAUC: A network-based multi-biomarker identification method by AUC optimization. Methods, 2022, 198, 56-64.	3.8	5
161	Prioritization of candidate genes based on disease similarity and protein's proximity in PPI networks. , 2013, , .		4
162	Detecting SNP Combinations Discriminating Human Populations From HapMap Data. IEEE Transactions on Nanobioscience, 2015, 14, 220-228.	3.3	4

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163	Biomolecular Networks for Complex Diseases. Complexity, 2018, 2018, 1-3.	1.6	4
164	Decoding the Structural Keywords in Protein Structure Universe. Journal of Computer Science and Technology, 2019, 34, 3-15.	1.5	4
165	DoRC: Discovery of rare cells from ultra-large scRNA-seq data. , 2019, , .		4
166	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
167	HyMM: hybrid method for disease-gene prediction by integrating multiscale module structure. Briefings in Bioinformatics, 2022, 23, .	6.5	4
168	EPIXplorer: A web server for prediction, analysis and visualization of enhancer-promoter interactions. Nucleic Acids Research, 2022, 50, W290-W297.	14.5	4
169	Identification of Key Endometrial MicroRNAs and Their Target Genes Associated With Pathogenesis of Recurrent Implantation Failure by Integrated Bioinformatics Analysis. Frontiers in Genetics, 0, 13, .	2.3	4
170	A deep matrix factorization based approach for single-cell RNA-seq data clustering. Methods, 2022, 205, 114-122.	3.8	4
171	A new method for predicting essential proteins based on topology potential. , 2013, , .		3
172	The MSS of complex networks with centrality based preference and its application to biomolecular networks. , 2016, , .		3
173	Predicting microRNA-environmental factor interactions based on bi-random walk and multi-label learning. , 2016, , .		3
174	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
175	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
176	Tentative diagnosis prediction via deep understanding of patient narratives. , 2019, , .		3
177	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
178	A Hybrid Pooling Based Deep Learning Framework For Automated ICD Coding. , 2021, , .		3
179	DeepCI: a deep learning based clustering method for single cell RNA-seq data. , 2021, , .		3
180	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

#	ARTICLE	IF	CITATIONS
181	DRCNNTLe: A deep recurrent convolutional neural network with transfer learning through pre-trained embeddings for automated ICD coding. <i>Methods</i> , 2022, 205, 97-105.	3.8	3
182	Identifying protein complexes based on local fitness method. , 2012, , .		2
183	Systems Biology Approaches to Mining High Throughput Biological Data. <i>BioMed Research International</i> , 2015, 2015, 1-2.	1.9	2
184	Identifying protein complexes based on the integration of PPI network and gene expression data. <i>International Journal of Bioinformatics Research and Applications</i> , 2015, 11, 30.	0.2	2
185	MEC: Misassembly error correction in contigs using a combination of paired-end reads and GC-contents. , 2017, , .		2
186	VALiBS: a visual aligner for bisulfite sequences. <i>BMC Bioinformatics</i> , 2017, 18, 410.	2.6	2
187	CSA: a web service for the complete process of ChIP-Seq analysis. <i>BMC Bioinformatics</i> , 2019, 20, 515.	2.6	2
188	NIMCE: a gene regulatory network inference approach based on multi time delays causal entropy. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, PP, 1-1.	3.0	2
189	MADA: a web service for analysing DNA methylation array data. <i>BMC Bioinformatics</i> , 2020, 21, 403.	2.6	2
190	Identification of Prognostic and Heterogeneous Breast Cancer Biomarkers Based on Fusion Network and Multiple Scoring Strategies. <i>Lecture Notes in Computer Science</i> , 2019, , 529-534.	1.3	2
191	Improving human essential protein prediction using only protein sequences via ensemble learning. , 2021, , .		2
192	A New Measurement for Evaluating Clusters in Protein Interaction Networks. , 2011, , .		1
193	Identifying dynamic protein complexes based on gene expression profiles and PPI networks. , 2013, , .		1
194	Identifying Essential Proteins by Purifying Protein Interaction Networks. <i>Lecture Notes in Computer Science</i> , 2016, , 106-116.	1.3	1
195	DualRank: multiplex network-based dual ranking for heterogeneous complex disease analysis. , 2019, , .		1
196	LSSL: A Novel Scaffolding Method Based on Path Extension. <i>Lecture Notes in Computer Science</i> , 2017, , 428-438.	1.3	1
197	Overlapping Protein Complexes Detection Based on Multi-level Topological Similarities. <i>Lecture Notes in Computer Science</i> , 2021, , 215-226.	1.3	1
198	A clustering algorithm for identifying hierarchical and overlapping protein complexes in large PPI networks. , 2013, , .		0

#	ARTICLE	IF	CITATIONS
199	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
200	SPOC: Identification of Drug Targets in Biological Networks via Set Preference Output Control. Lecture Notes in Computer Science, 2020, , 26-37.	1.3	0
201	Guest Editorsâ€™ 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