Yaohang Li

List of Publications by Year
in descending order

134 papers	6,123 citations	87888 38 h-index	82547 72 g-index
135 all docs	135 docs citations	135 times ranked	4232 citing authors

#	Article	IF	Citations
1	CytoNCA: A cytoscape plugin for centrality analysis and evaluation of protein interaction networks. BioSystems, 2015, 127, 67-72.	2.0	813
2	Drug repositioning based on comprehensive similarity measures and Bi-Random walk algorithm. Bioinformatics, 2016, 32, 2664-2671.	4.1	311
3	Identification of Essential Proteins Based on Edge Clustering Coefficient. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1070-1080.	3.0	254
4	Prediction of lncRNA–disease associations based on inductive matrix completion. Bioinformatics, 2018, 34, 3357-3364.	4.1	227
5	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
6	Applications of deep learning to MRI images: A survey. Big Data Mining and Analytics, 2018, 1, 1-18.	8.9	195
7	Computational drug repositioning using low-rank matrix approximation and randomized algorithms. Bioinformatics, 2018, 34, 1904-1912.	4.1	183
8	LDAP: a web server for lncRNA-disease association prediction. Bioinformatics, 2017, 33, 458-460.	4.1	182
9	Protein–protein interaction site prediction through combining local and global features with deep neural networks. Bioinformatics, 2020, 36, 1114-1120.	4.1	157
10	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
11	Construction and application of dynamic protein interaction network based on time course gene expression data. Proteomics, 2013, 13, 301-312.	2.2	141
12	Drug repositioning based on bounded nuclear norm regularization. Bioinformatics, 2019, 35, i455-i463.	4.1	116
13	Biomedical data and computational models for drug repositioning: a comprehensive review. Briefings in Bioinformatics, 2021, 22, 1604-1619.	6.5	110
14	A comparison of the functional modules identified from time course and static PPI network data. BMC Bioinformatics, 2011, 12, 339.	2.6	103
15	A survey of matrix completion methods for recommendation systems. Big Data Mining and Analytics, 2018, 1, 308-323.	8.9	92
16	CytoCluster: A Cytoscape Plugin for Cluster Analysis and Visualization of Biological Networks. International Journal of Molecular Sciences, 2017, 18, 1880.	4.1	90
17	Network-based methods for predicting essential genes or proteins: a survey. Briefings in Bioinformatics, 2020, 21, 566-583.	6.5	90
18	Effective identification of essential proteins based on priori knowledge, network topology and gene expressions. Methods, 2014, 67, 325-333.	3.8	89

#	Article	IF	Citations
19	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
20	Predicting drug–target interaction using positive-unlabeled learning. Neurocomputing, 2016, 206, 50-57.	5.9	83
21	Clinical big data and deep learning: Applications, challenges, and future outlooks. Big Data Mining and Analytics, 2019, 2, 288-305.	8.9	82
22	Automatic ICD-9 coding via deep transfer learning. Neurocomputing, 2019, 324, 43-50.	5.9	79
23	Automated ICD-9 Coding via A Deep Learning Approach. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1193-1202.	3.0	78
24	DeepFunc: A Deep Learning Framework for Accurate Prediction of Protein Functions from Protein Sequences and Interactions. Proteomics, 2019, 19, e1900019.	2.2	72
25	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
26	Predicting essential proteins based on subcellular localization, orthology and PPI networks. BMC Bioinformatics, 2016, 17, 279.	2.6	66
27	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
28	Identifying At-Risk Students for Early Interventions—A Time-Series Clustering Approach. IEEE Transactions on Emerging Topics in Computing, 2017, 5, 45-55.	4.6	62
29	SDLDA: lncRNA-disease association prediction based on singular value decomposition and deep learning. Methods, 2020, 179, 73-80.	3.8	61
30	Prediction of Essential Proteins Based on Overlapping Essential Modules. IEEE Transactions on Nanobioscience, 2014, 13, 415-424.	3.3	60
31	RCD+: Fast loop modeling server. Nucleic Acids Research, 2016, 44, W395-W400.	14.5	54
32	Context-Based Features Enhance Protein Secondary Structure Prediction Accuracy. Journal of Chemical Information and Modeling, 2014, 54, 992-1002.	5.4	52
33	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
34	Computational drug repositioning based on multi-similarities bilinear matrix factorization. Briefings in Bioinformatics, 2021, 22, .	6.5	49
35	Automatic ICD code assignment of Chinese clinical notes based on multilayer attention BiRNN. Journal of Biomedical Informatics, 2019, 91, 103114.	4.3	47
36	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

#	Article	IF	Citations
37	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
38	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
39	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
40	Efficient Randomized Algorithms for the Fixed-Precision Low-Rank Matrix Approximation. SIAM Journal on Matrix Analysis and Applications, 2018, 39, 1339-1359.	1.4	41
41	DeepEP: a deep learning framework for identifying essential proteins. BMC Bioinformatics, 2019, 20, 506.	2.6	40
42	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
43	Identifying the overlapping complexes in protein interaction networks. International Journal of Data Mining and Bioinformatics, 2010, 4, 91.	0.1	36
44	Convergence Analysis of Markov Chain Monte Carlo Linear Solvers Using Ulam--von Neumann Algorithm. SIAM Journal on Numerical Analysis, 2013, 51, 2107-2122.	2.3	35
45	An interpretable boosting model to predict side effects of analgesics for osteoarthritis. BMC Systems Biology, 2018, 12, 105.	3.0	35
46	Overlap matrix completion for predicting drug-associated indications. PLoS Computational Biology, 2019, 15, e1007541.	3.2	35
47	Backbone Statistical Potential from Local Sequence-Structure Interactions in Protein Loops. Journal of Physical Chemistry B, 2010, 114, 1859-1869.	2.6	33
48	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
49	Predicting Human lncRNA-Disease Associations Based on Geometric Matrix Completion. IEEE Journal of Biomedical and Health Informatics, 2020, 24, 2420-2429.	6.3	32
50	Big data-enabled multiscale serviceability analysis for aging bridgesâ˜†. Digital Communications and Networks, 2016, 2, 97-107.	5.0	31
51	Constructing Disease Similarity Networks Based on Disease Module Theory. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 906-915.	3.0	29
52	BACPI: a bi-directional attention neural network for compoundâ€"protein interaction and binding affinity prediction. Bioinformatics, 2022, 38, 1995-2002.	4.1	29
53	A New Method for Predicting Protein Functions From Dynamic Weighted Interactome Networks. IEEE Transactions on Nanobioscience, 2016, 15, 131-139.	3.3	28
54	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

#	Article	IF	Citations
55	Hybrid parallel tempering and simulated annealing method. Applied Mathematics and Computation, 2009, 212, 216-228.	2.2	25
56	PrGeFNE: Predicting disease-related genes by fast network embedding. Methods, 2021, 192, 3-12.	3.8	25
57	Template-based C8-SCORPION: a protein 8-state secondary structure prediction method using structural information and context-based features. BMC Bioinformatics, 2014, 15, S3.	2.6	24
58	Faster Matrix Completion Using Randomized SVD. , 2018, , .		24
59	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
60	Protein interaction networks: centrality, modularity, dynamics, and applications. Frontiers of Computer Science, 2021, 15, 1.	2.4	24
61	Prioritizing Disease Genes by Using Search Engine Algorithm. Current Bioinformatics, 2016, 11, 195-202.	1.5	22
62	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
63	A novel graph attention model for predicting frequencies of drugâ€"side effects from multi-view data. Briefings in Bioinformatics, 2021, 22, .	6.5	21
64	GPU-accelerated differential evolutionary Markov Chain Monte Carlo method for multi-objective optimization over continuous space. , 2010, , .		20
65	KAICD: A knowledge attention-based deep learning framework for automatic ICD coding. Neurocomputing, 2022, 469, 376-383.	5.9	19
66	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
67	NIDM: network impulsive dynamics on multiplex biological network for disease-gene prediction. Briefings in Bioinformatics, 2021, 22, .	6.5	19
68	A breakdown-free block conjugate gradient method. BIT Numerical Mathematics, 2017, 57, 379-403.	2.0	18
69	An Adaptive Sparse Subspace Clustering for Cell Type Identification. Frontiers in Genetics, 2020, 11, 407.	2.3	18
70	A convolutional neural network and graph convolutional network-based method for predicting the classification of anatomical therapeutic chemicals. Bioinformatics, 2021, 37, 2841-2847.	4.1	18
71	Accelerated simulated tempering. Physics Letters, Section A: General, Atomic and Solid State Physics, 2004, 328, 274-283.	2.1	17
72	Sampling Multiple Scoring Functions Can Improve Protein Loop Structure Prediction Accuracy. Journal of Chemical Information and Modeling, 2011, 51, 1656-1666.	5.4	17

#	Article	IF	Citations
73	CONFORMATIONAL SAMPLING IN TEMPLATE-FREE PROTEIN LOOP STRUCTURE MODELING: AN OVERVIEW. Computational and Structural Biotechnology Journal, 2013, 5, e201302003.	4.1	17
74	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
75	Essential Protein Prediction Based on node2vec and XGBoost. Journal of Computational Biology, 2021, 28, 687-700.	1.6	17
76	Improving predicted protein loop structure ranking using a Pareto-optimality consensus method. BMC Structural Biology, 2010, 10, 22.	2.3	16
77	DEMCMC-GPU: An Efficient Multi-Objective Optimization Method with GPU Acceleration on the Fermi Architecture. New Generation Computing, 2011, 29, 163-184.	3.3	16
78	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
79	DeepPPF: A deep learning framework for predicting protein family. Neurocomputing, 2021, 428, 19-29.	5.9	16
80	MOMCMC: An efficient Monte Carlo method for multi-objective sampling over real parameter space. Computers and Mathematics With Applications, 2012, 64, 3542-3556.	2.7	14
81	FLEXc: protein flexibility prediction using context-based statistics, predicted structural features, and sequence information. BMC Bioinformatics, 2016, 17, 281.	2.6	14
82	A disease inference method based on symptom extraction and bidirectional Long Short Term Memory networks. Methods, 2020, 173, 75-82.	3.8	14
83	High-dimensional MRI data analysis using a large-scale manifold learning approach. Machine Vision and Applications, 2013, 24, 995-1014.	2.7	13
84	ICOSA: A Distance-Dependent, Orientation-Specific Coarse-Grained Contact Potential for Protein Structure Modeling. Journal of Molecular Biology, 2015, 427, 2562-2576.	4.2	12
85	A Deep Learning Framework for Identifying Essential Proteins Based on Protein-Protein Interaction Network and Gene Expression Data. , 2018, , .		12
86	Biomedical data, computational methods and tools for evaluating disease–disease associations. Briefings in Bioinformatics, 2022, 23, .	6.5	12
87	Building a Knowledge-Based Statistical Potential by Capturing High-Order Inter-residue Interactions and its Applications in Protein Secondary Structure Assessment. Journal of Chemical Information and Modeling, 2013, 53, 500-508.	5.4	11
88	C-DEVA: Detection, evaluation, visualization and annotation of clusters from biological networks. BioSystems, 2016, 150, 78-86.	2.0	11
89	A load-balancing workload distribution scheme for three-body interaction computation on Graphics Processing Units (GPU). Journal of Parallel and Distributed Computing, 2016, 87, 91-101.	4.1	11
90	A GPU-based large-scale Monte Carlo simulation method for systems with long-range interactions. Journal of Computational Physics, 2017, 338, 252-268.	3.8	11

#	ARTICLE	IF	CITATIONS
91	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
92	Biomedical Data and Deep Learning Computational Models for Predicting Compound-Protein Relations. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 2092-2110.	3.0	11
93	miRTRS: A Recommendation Algorithm for Predicting miRNA Targets. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 1032-1041.	3.0	10
94	Feature and Nuclear Norm Minimization for Matrix Completion. IEEE Transactions on Knowledge and Data Engineering, 2022, 34, 2190-2199.	5.7	10
95	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
96	A novel extended Pareto Optimality Consensus model for predicting essential proteins. Journal of Theoretical Biology, 2019, 480, 141-149.	1.7	9
97	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
98	CLPred: a sequence-based protein crystallization predictor using BLSTM neural network. Bioinformatics, 2020, 36, i709-i717.	4.1	8
99	Accelerating knowledge-based energy evaluation in protein structure modeling with Graphics Processing Units. Journal of Parallel and Distributed Computing, 2012, 72, 297-307.	4.1	7
100	Disease Inference with Symptom Extraction and Bidirectional Recurrent Neural Network. , 2018, , .		7
101	HNEDTI: Prediction of drug-target interaction based on heterogeneous network embedding. , 2019, , .		7
102	LncRNAâ€"disease association prediction through combining linear and non-linear features with matrix factorization and deep learning techniques. , 2019, , .		7
103	Detecting protein complex based on hierarchical compressing network embedding. , 2019, , .		7
104	Integrating multiple scoring functions to improve protein loop structure conformation space sampling. , 2010, , .		5
105	DeepFrag-k: a fragment-based deep learning approach for protein fold recognition. BMC Bioinformatics, 2020, 21, 203.	2.6	5
106	A comparison of topologically associating domain callers based on Hi-C data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, PP, 1-1.	3.0	5
107	Decoding the Structural Keywords in Protein Structure Universe. Journal of Computer Science and Technology, 2019, 34, 3-15.	1.5	4
108	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

#	Article	IF	Citations
109	A novel approach based on deep residual learning to predict drug's anatomical therapeutic chemical code. , 2020, , .		4
110	Accurate Prediction of Human Essential Proteins Using Ensemble Deep Learning. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	3.0	4
111	A deep matrix factorization based approach for single-cell RNA-seq data clustering. Methods, 2022, 205, 114-122.	3.8	4
112	An Implementation of Block Conjugate Gradient Algorithm on CPU-GPU Processors. , 2014, , .		3
113	An Apache Spark Implementation of Block Power Method for Computing Dominant Eigenvalues and Eigenvectors of Large-Scale Matrices. , 2016, , .		3
114	Tentative diagnosis prediction via deep understanding of patient narratives. , 2019, , .		3
115	A Hybrid Pooling Based Deep Learning Framework For Automated ICD Coding. , 2021, , .		3
116	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
117	Conformational Clusters of Phosphorylated Tyrosine. Journal of the American Chemical Society, 2017, 139, 17632-17638.	13.7	2
118	Network Connectivity, Centrality and Fragmentation in the Greek-Key Protein Topology. Protein Journal, 2019, 38, 497-505.	1.6	2
119	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
120	De Novo Prediction of Drug–Target Interactions Using Laplacian Regularized Schatten p-Norm Minimization. Journal of Computational Biology, 2021, 28, 660-673.	1.6	2
121	Gaussian variant of Freivalds' algorithm for efficient and reliable matrix product verification. Monte Carlo Methods and Applications, 2020, 26, 273-284.	0.8	2
122	Improving human essential protein prediction using only protein sequences via ensemble learning. , 2021, , .		2
123	Template-based prediction of protein 8-state secondary structures. , 2013, , .		1
124	Coarse-Grained Contact Potential Helps Improve Fold Recognition Sensitivity in Template-Based Protein Structure Modeling. , 2016, , .		1
125	Validating the Correctness of Outsourced Computational Tasks Using Pseudorandom Number Generators. , 2017, , .		1
126	RNPredATC: a deep residual learning-based model with applications to the prediction of drug-ATC code association. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	3.0	1

#	Article	IF	Citations
127	Multi-Label Classification of ICD-10 Coding & Clinical Notes Using MIMIC & CodiEsp. , 2021, , .		1
128	Overlapping Protein Complexes Detection Based on Multi-level Topological Similarities. Lecture Notes in Computer Science, 2021, , 215-226.	1.3	1
129	Extensive exploration of conformational space improves Rosetta results for short protein domains. Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference, 2008, 7, 203-9.	0.4	1
130	An improved statistics-based backbone torsion potential energy for protein loop structure modeling. , 2013, , .		0
131	Overlap matrix completion for predicting drug-associated indications. , 2019, 15, e1007541.		0
132	Overlap matrix completion for predicting drug-associated indications. , 2019, 15, e1007541.		0
133	Overlap matrix completion for predicting drug-associated indications. , 2019, 15, e1007541.		0
134	Overlap matrix completion for predicting drug-associated indications. , 2019, 15, e1007541.		0