Yaohang Li

List of Publications by Year
in descending order

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134	6,123	87888	82547
papers	citations	38 h-index	72 g-index

135	135	135	4232
all docs	docs citations	times ranked	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	Feature and Nuclear Norm Minimization for Matrix Completion. IEEE Transactions on Knowledge and Data Engineering, 2022, 34, 2190-2199.	5.7	10
3	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
4	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
5	Biomedical data, computational methods and tools for evaluating diseaseâ€“disease associations. Briefings in Bioinformatics, 2022, 23, .	6.5	12
6	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
7	BACPI: a bi-directional attention neural network for compoundâ€“protein interaction and binding affinity prediction. Bioinformatics, 2022, 38, 1995-2002.	4.1	29
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	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
10	A deep matrix factorization based approach for single-cell RNA-seq data clustering. Methods, 2022, 205, 114-122.	3.8	4
11	Computational drug repositioning based on multi-similarities bilinear matrix factorization. Briefings in Bioinformatics, 2021, 22, .	6.5	49
12	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
13	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
14	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
15	PrGeFNE: Predicting disease-related genes by fast network embedding. Methods, 2021, 192, 3-12.	3.8	25
16	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
17	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
18	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

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19	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
20	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
21	DeepPPF: A deep learning framework for predicting protein family. Neurocomputing, 2021, 428, 19-29.	5.9	16
22	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
23	NIDM: network impulsive dynamics on multiplex biological network for disease-gene prediction. Briefings in Bioinformatics, 2021, 22, .	6.5	19
24	Essential Protein Prediction Based on node2vec and XGBoost. Journal of Computational Biology, 2021, 28, 687-700.	1.6	17
25	A novel graph attention model for predicting frequencies of drugâ€“side effects from multi-view data. Briefings in Bioinformatics, 2021, 22, .	6.5	21
26	De Novo Prediction of Drugâ€“Target Interactions Using Laplacian Regularized Schatten p-Norm Minimization. Journal of Computational Biology, 2021, 28, 660-673.	1.6	2
27	Multi-Label Classification of ICD-10 Coding & Clinical Notes Using MIMIC & CodiEsp. , 2021, , .		1
28	Protein interaction networks: centrality, modularity, dynamics, and applications. Frontiers of Computer Science, 2021, 15, 1.	2.4	24
29	Biomedical data and computational models for drug repositioning: a comprehensive review. Briefings in Bioinformatics, 2021, 22, 1604-1619.	6.5	110
30	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
31	Overlapping Protein Complexes Detection Based on Multi-level Topological Similarities. Lecture Notes in Computer Science, 2021, , 215-226.	1.3	1
32	Improving human essential protein prediction using only protein sequences via ensemble learning. , 2021, , .		2
33	A Hybrid Pooling Based Deep Learning Framework For Automated ICD Coding. , 2021, , .		3
34	Proteinâ€“protein interaction site prediction through combining local and global features with deep neural networks. Bioinformatics, 2020, 36, 1114-1120.	4.1	157
35	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
36	Constructing Disease Similarity Networks Based on Disease Module Theory. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 906-915.	3.0	29

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37	miRTRS: A Recommendation Algorithm for Predicting miRNA Targets. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 1032-1041.	3.0	10
38	Network-based methods for predicting essential genes or proteins: a survey. Briefings in Bioinformatics, 2020, 21, 566-583.	6.5	90
39	A disease inference method based on symptom extraction and bidirectional Long Short Term Memory networks. Methods, 2020, 173, 75-82.	3.8	14
40	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
41	DeepFrag-k: a fragment-based deep learning approach for protein fold recognition. BMC Bioinformatics, 2020, 21, 203.	2.6	5
42	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
43	An Adaptive Sparse Subspace Clustering for Cell Type Identification. Frontiers in Genetics, 2020, 11, 407.	2.3	18
44	SDLDA: lncRNA-disease association prediction based on singular value decomposition and deep learning. Methods, 2020, 179, 73-80.	3.8	61
45	Predicting Human lncRNA-Disease Associations Based on Geometric Matrix Completion. IEEE Journal of Biomedical and Health Informatics, 2020, 24, 2420-2429.	6.3	32
46	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
47	CLPred: a sequence-based protein crystallization predictor using BLSTM neural network. Bioinformatics, 2020, 36, i709-i717.	4.1	8
48	A novel approach based on deep residual learning to predict drugâ€™s anatomical therapeutic chemical code. , 2020, , .		4
49	Gaussian variant of Freivaldsâ€™ algorithm for efficient and reliable matrix product verification. Monte Carlo Methods and Applications, 2020, 26, 273-284.	0.8	2
50	Automatic ICD-9 coding via deep transfer learning. Neurocomputing, 2019, 324, 43-50.	5.9	79
51	A novel extended Pareto Optimality Consensus model for predicting essential proteins. Journal of Theoretical Biology, 2019, 480, 141-149.	1.7	9
52	Clinical big data and deep learning: Applications, challenges, and future outlooks. Big Data Mining and Analytics, 2019, 2, 288-305.	8.9	82
53	Drug repositioning based on bounded nuclear norm regularization. Bioinformatics, 2019, 35, i455-i463.	4.1	116
54	Network Connectivity, Centrality and Fragmentation in the Greek-Key Protein Topology. Protein Journal, 2019, 38, 497-505.	1.6	2

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55	Decoding the Structural Keywords in Protein Structure Universe. Journal of Computer Science and Technology, 2019, 34, 3-15.	1.5	4
56	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
57	DeepFunc: A Deep Learning Framework for Accurate Prediction of Protein Functions from Protein Sequences and Interactions. Proteomics, 2019, 19, e1900019.	2.2	72
58	Automatic ICD code assignment of Chinese clinical notes based on multilayer attention BiRNN. Journal of Biomedical Informatics, 2019, 91, 103114.	4.3	47
59	Tentative diagnosis prediction via deep understanding of patient narratives. , 2019, , .		3
60	HNEDTI: Prediction of drug-target interaction based on heterogeneous network embedding. , 2019, , .		7
61	LncRNAâ€“disease association prediction through combining linear and non-linear features with matrix factorization and deep learning techniques. , 2019, , .		7
62	Detecting protein complex based on hierarchical compressing network embedding. , 2019, , .		7
63	Overlap matrix completion for predicting drug-associated indications. PLoS Computational Biology, 2019, 15, e1007541.	3.2	35
64	DeepEP: a deep learning framework for identifying essential proteins. BMC Bioinformatics, 2019, 20, 506.	2.6	40
65	Automated ICD-9 Coding via A Deep Learning Approach. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1193-1202.	3.0	78
66	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
67	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
68	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
69	Overlap matrix completion for predicting drug-associated indications. , 2019, 15, e1007541.		0
70	Overlap matrix completion for predicting drug-associated indications. , 2019, 15, e1007541.		0
71	Overlap matrix completion for predicting drug-associated indications. , 2019, 15, e1007541.		0
72	Overlap matrix completion for predicting drug-associated indications. , 2019, 15, e1007541.		0

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73	Applications of deep learning to MRI images: A survey. Big Data Mining and Analytics, 2018, 1, 1-18.	8.9	195
74	Computational drug repositioning using low-rank matrix approximation and randomized algorithms. Bioinformatics, 2018, 34, 1904-1912.	4.1	183
75	Prediction of lncRNAâ€“disease associations based on inductive matrix completion. Bioinformatics, 2018, 34, 3357-3364.	4.1	227
76	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
77	Faster Matrix Completion Using Randomized SVD. , 2018, , .		24
78	A Deep Learning Framework for Identifying Essential Proteins Based on Protein-Protein Interaction Network and Gene Expression Data. , 2018, , .		12
79	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
80	Disease Inference with Symptom Extraction and Bidirectional Recurrent Neural Network. , 2018, , .		7
81	An interpretable boosting model to predict side effects of analgesics for osteoarthritis. BMC Systems Biology, 2018, 12, 105.	3.0	35
82	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
83	A survey of matrix completion methods for recommendation systems. Big Data Mining and Analytics, 2018, 1, 308-323.	8.9	92
84	LDAP: a web server for lncRNA-disease association prediction. Bioinformatics, 2017, 33, 458-460.	4.1	182
85	Identifying At-Risk Students for Early Interventionsâ€”A Time-Series Clustering Approach. IEEE Transactions on Emerging Topics in Computing, 2017, 5, 45-55.	4.6	62
86	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
87	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
88	Conformational Clusters of Phosphorylated Tyrosine. Journal of the American Chemical Society, 2017, 139, 17632-17638.	13.7	2
89	A breakdown-free block conjugate gradient method. BIT Numerical Mathematics, 2017, 57, 379-403.	2.0	18
90	Validating the Correctness of Outsourced Computational Tasks Using Pseudorandom Number Generators. , 2017, , .		1

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91	CytoCluster: A Cytoscape Plugin for Cluster Analysis and Visualization of Biological Networks. International Journal of Molecular Sciences, 2017, 18, 1880.	4.1	90
92	Predicting essential proteins based on subcellular localization, orthology and PPI networks. BMC Bioinformatics, 2016, 17, 279.	2.6	66
93	Drug repositioning based on comprehensive similarity measures and Bi-Random walk algorithm. Bioinformatics, 2016, 32, 2664-2671.	4.1	311
94	C-DEVA: Detection, evaluation, visualization and annotation of clusters from biological networks. BioSystems, 2016, 150, 78-86.	2.0	11
95	Big data-enabled multiscale serviceability analysis for aging bridgesâˆ†. Digital Communications and Networks, 2016, 2, 97-107.	5.0	31
96	An Apache Spark Implementation of Block Power Method for Computing Dominant Eigenvalues and Eigenvectors of Large-Scale Matrices. , 2016, , .		3
97	Coarse-Grained Contact Potential Helps Improve Fold Recognition Sensitivity in Template-Based Protein Structure Modeling. , 2016, , .		1
98	FLEXc: protein flexibility prediction using context-based statistics, predicted structural features, and sequence information. BMC Bioinformatics, 2016, 17, 281.	2.6	14
99	Predicting drugâ€“target interaction using positive-unlabeled learning. Neurocomputing, 2016, 206, 50-57.	5.9	83
100	RCD+: Fast loop modeling server. Nucleic Acids Research, 2016, 44, W395-W400.	14.5	54
101	A New Method for Predicting Protein Functions From Dynamic Weighted Interactome Networks. IEEE Transactions on Nanobioscience, 2016, 15, 131-139.	3.3	28
102	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
103	Prioritizing Disease Genes by Using Search Engine Algorithm. Current Bioinformatics, 2016, 11, 195-202.	1.5	22
104	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
105	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
106	CytoNCA: A cytoscape plugin for centrality analysis and evaluation of protein interaction networks. BioSystems, 2015, 127, 67-72.	2.0	813
107	An Implementation of Block Conjugate Gradient Algorithm on CPU-GPU Processors. , 2014, , .		3
108	Prediction of Essential Proteins Based on Overlapping Essential Modules. IEEE Transactions on Nanobioscience, 2014, 13, 415-424.	3.3	60

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109	Effective identification of essential proteins based on priori knowledge, network topology and gene expressions. Methods, 2014, 67, 325-333.	3.8	89
110	Context-Based Features Enhance Protein Secondary Structure Prediction Accuracy. Journal of Chemical Information and Modeling, 2014, 54, 992-1002.	5.4	52
111	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
112	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
113	Construction and application of dynamic protein interaction network based on time course gene expression data. Proteomics, 2013, 13, 301-312.	2.2	141
114	High-dimensional MRI data analysis using a large-scale manifold learning approach. Machine Vision and Applications, 2013, 24, 995-1014.	2.7	13
115	CONFORMATIONAL SAMPLING IN TEMPLATE-FREE PROTEIN LOOP STRUCTURE MODELING: AN OVERVIEW. Computational and Structural Biotechnology Journal, 2013, 5, e201302003.	4.1	17
116	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
117	Template-based prediction of protein 8-state secondary structures. , 2013, , .		1
118	An improved statistics-based backbone torsion potential energy for protein loop structure modeling. , 2013, , .		0
119	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
120	Identification of Essential Proteins Based on Edge Clustering Coefficient. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1070-1080.	3.0	254
121	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
122	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
123	Sampling Multiple Scoring Functions Can Improve Protein Loop Structure Prediction Accuracy. Journal of Chemical Information and Modeling, 2011, 51, 1656-1666.	5.4	17
124	A comparison of the functional modules identified from time course and static PPI network data. BMC Bioinformatics, 2011, 12, 339.	2.6	103
125	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
126	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

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127	Improving predicted protein loop structure ranking using a Pareto-optimality consensus method. BMC Structural Biology, 2010, 10, 22.	2.3	16
128	GPU-accelerated differential evolutionary Markov Chain Monte Carlo method for multi-objective optimization over continuous space. , 2010, , .		20
129	Identifying the overlapping complexes in protein interaction networks. International Journal of Data Mining and Bioinformatics, 2010, 4, 91.	0.1	36
130	Backbone Statistical Potential from Local Sequence-Structure Interactions in Protein Loops. Journal of Physical Chemistry B, 2010, 114, 1859-1869.	2.6	33
131	Integrating multiple scoring functions to improve protein loop structure conformation space sampling. , 2010, , .		5
132	Hybrid parallel tempering and simulated annealing method. Applied Mathematics and Computation, 2009, 212, 216-228.	2.2	25
133	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
134	Accelerated simulated tempering. Physics Letters, Section A: General, Atomic and Solid State Physics, 2004, 328, 274-283.	2.1	17