

Lei Wang

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

63

papers

944

citations

14

h-index

29

g-index

78

ext. papers

1,369

ext. citations

4.1

avg, IF

4.98

L-index

#	Paper	IF	Citations
63	Predicting miRNA-disease association based on inductive matrix completion. <i>Bioinformatics</i> , 2018 , 34, 4256-4265	7.2	219
62	BNPMDA: Bipartite Network Projection for MiRNA-Disease Association prediction. <i>Bioinformatics</i> , 2018 , 34, 3178-3186	7.2	204
61	A Novel Method for LncRNA-Disease Association Prediction Based on an lncRNA-Disease Association Network. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019 , 16, 688-693	3.93	52
60	AOPs-SVM: A Sequence-Based Classifier of Antioxidant Proteins Using a Support Vector Machine. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019 , 7, 224	5.8	44
59	A Novel Probability Model for LncRNA-Disease Association Prediction Based on the Naïve Bayesian Classifier. <i>Genes</i> , 2018 , 9,	4.2	39
58	A novel collaborative filtering model for LncRNA-disease association prediction based on the Naïve Bayesian classifier. <i>BMC Bioinformatics</i> , 2019 , 20, 396	3.6	28
57	A Probabilistic Matrix Factorization Method for Identifying lncRNA-disease Associations. <i>Genes</i> , 2019 , 10,	4.2	26
56	Prediction of microRNA-disease associations based on distance correlation set. <i>BMC Bioinformatics</i> , 2018 , 19, 141	3.6	23
55	LDGRNMF: LncRNA-disease associations prediction based on graph regularized non-negative matrix factorization. <i>Neurocomputing</i> , 2021 , 424, 236-245	5.4	23
54	IIRWR: Internal Inclined Random Walk With Restart for LncRNA-Disease Association Prediction. <i>IEEE Access</i> , 2019 , 7, 54034-54041	3.5	19
53	An iteration method for identifying yeast essential proteins from heterogeneous network. <i>BMC Bioinformatics</i> , 2019 , 20, 355	3.6	18
52	A Novel Approach based on Bipartite Network to Predict Human Microbe-Disease Associations. <i>Current Bioinformatics</i> , 2018 , 13, 141-148	4.7	18
51	A Novel Approach for Potential Human LncRNA-Disease Association Prediction Based on Local Random Walk. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021 , 18, 1049-1059	3	17
50	A Bidirectional Label Propagation Based Computational Model for Potential Microbe-Disease Association Prediction. <i>Frontiers in Microbiology</i> , 2019 , 10, 684	5.7	14
49	Imbalance Data Processing Strategy for Protein Interaction Sites Prediction. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021 , 18, 985-994	3	13
48	A Novel Approach Based on a Weighted Interactive Network to Predict Associations of MiRNAs and Diseases. <i>International Journal of Molecular Sciences</i> , 2018 , 20,	6.3	11
47	Prediction of tumor metastasis from sequencing data in the era of genome sequencing. <i>Briefings in Functional Genomics</i> , 2019 , 18, 412-418	4.9	11

46	Predicting microRNA-disease associations from lncRNA-microRNA interactions via Multiview Multitask Learning. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	11
45	A Novel Network-Based Computational Model for Prediction of Potential lncRNA-Disease Association. <i>International Journal of Molecular Sciences</i> , 2019 , 20,	6.3	10
44	A 2D graphical representation of the sequences of DNA based on triplets and its application. <i>Eurasip Journal on Bioinformatics and Systems Biology</i> , 2014 , 2014, 1		9
43	A clique base node scheduling method for wireless sensor networks. <i>Journal of Network and Computer Applications</i> , 2010 , 33, 383-396	7.9	9
42	A Novel Approach Based on Point Cut Set to Predict Associations of Diseases and lncRNAs. <i>Current Bioinformatics</i> , 2019 , 14, 333-343	4.7	9
41	A Novel Human Microbe-Disease Association Prediction Method Based on the Bidirectional Weighted Network. <i>Frontiers in Microbiology</i> , 2019 , 10, 676	5.7	8
40	A novel target convergence set based random walk with restart for prediction of potential lncRNA-disease associations. <i>BMC Bioinformatics</i> , 2019 , 20, 626	3.6	8
39	SIMILARITIES/DISSIMILARITIES ANALYSIS OF PROTEIN SEQUENCES BASED ON PCA-FFT. <i>Journal of Biological Systems</i> , 2017 , 25, 29-45	1.6	7
38	Prioritizing Human Microbe-Disease Associations Utilizing a Node-Information-Based Link Propagation Method. <i>IEEE Access</i> , 2020 , 8, 31341-31349	3.5	6
37	A Novel Model for Predicting Essential Proteins Based on Heterogeneous Protein-Domain Network. <i>IEEE Access</i> , 2020 , 8, 8946-8958	3.5	6
36	Resource multi-objective mapping algorithm based on virtualized network functions: RMMA. <i>Applied Soft Computing Journal</i> , 2018 , 66, 220-231	7.5	6
35	ADLD: a novel graphical representation of protein sequences and its application. <i>Computational and Mathematical Methods in Medicine</i> , 2014 , 2014, 959753	2.8	6
34	A Novel Method to Predict Essential Proteins Based on Diffusion Distance Networks. <i>IEEE Access</i> , 2020 , 8, 29385-29394	3.5	5
33	An Algorithm of Data Aggregation Based on Data Compression for Sensor Networks. <i>Ruan Jian Xue Bao/Journal of Software</i> , 2006 , 17, 860		5
32	An Iteration Method for Identifying Yeast Essential Proteins From Weighted PPI Network Based on Topological and Functional Features of Proteins. <i>IEEE Access</i> , 2020 , 8, 90792-90804	3.5	5
31	A Novel Approach for Predicting Disease-lncRNA Associations Based on the Distance Correlation Set and Information of the miRNAs. <i>Computational and Mathematical Methods in Medicine</i> , 2018 , 2018, 6747453	2.8	5
30	A Novel Neighborhood-Based Computational Model for Potential MiRNA-Disease Association Prediction. <i>Computational and Mathematical Methods in Medicine</i> , 2019 , 2019, 5145646	2.8	4
29	Cluster based node scheduling method for wireless sensor networks. <i>Science China Information Sciences</i> , 2012 , 55, 755-764	3.4	4

28	NPF:network propagation for protein function prediction. <i>BMC Bioinformatics</i> , 2020 , 21, 355	3.6	4
27	A Novel Method for Predicting Disease-Associated LncRNA-MiRNA Pairs Based on the Higher-Order Orthogonal Iteration. <i>Computational and Mathematical Methods in Medicine</i> , 2019 , 2019, 7614850	2.8	3
26	A Novel Model for Predicting Associations between Diseases and LncRNA-miRNA Pairs Based on a Newly Constructed Bipartite Network. <i>Computational and Mathematical Methods in Medicine</i> , 2018 , 2018, 6789089	2.8	3
25	Similarities/Dissimilarities Analysis of Protein Sequences Based on Recurrence Quantification Analysis. <i>Current Bioinformatics</i> , 2015 , 10, 112-119	4.7	3
24	Key Distribution for Group-based Sensor Deployment Using a Novel Interconnection Graph 2007 ,		3
23	ICLRBBN: a tool for accurate prediction of potential lncRNA disease associations. <i>Molecular Therapy - Nucleic Acids</i> , 2021 , 23, 501-511	10.7	3
22	A Cross-entropy-based Method for Essential Protein Identification in Yeast Protein-protein Interaction Network. <i>Current Bioinformatics</i> , 2021 , 16, 565-575	4.7	3
21	A self-organizing map based hybrid chemical reaction optimization algorithm for multiobjective optimization. <i>Applied Intelligence</i> , 2019 , 49, 2266-2286	4.9	2
20	An Effective Graph Clustering Method to Identify Cancer Driver Modules. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020 , 8, 271	5.8	2
19	An Iterative Method for Predicting Essential Proteins Based on Multifeature Fusion and Linear Neighborhood Similarity.. <i>Frontiers in Aging Neuroscience</i> , 2021 , 13, 799500	5.3	2
18	A novel computational model for predicting potential LncRNA-disease associations based on both direct and indirect features of LncRNA-disease pairs. <i>BMC Bioinformatics</i> , 2020 , 21, 555	3.6	2
17	Method for Identifying Essential Proteins by Key Features of Proteins in a Novel Protein-Domain Network. <i>Frontiers in Genetics</i> , 2021 , 12, 708162	4.5	2
16	Identifying Microbe-Disease Association Based on a Novel Back-Propagation Neural Network Model. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021 , 18, 2502-2513	3	2
15	A novel privacy- and integrity-preserving approach for multidimensional data range queries in two-tiered wireless sensor networks. <i>International Journal of Distributed Sensor Networks</i> , 2019 , 15, 1550174771985589	1.7	1
14	Energy-saving routing protocol for Wireless Sensor Networks 2014 ,		1
13	A WIFI radio signals based adaptive positioning scheme 2015 ,		1
12	Privacy-preserving Data Aggregation Based on the P-function Set in Wireless Sensor Networks 2010 ,		1
11	A Novel Network-Based Computational Model for Prediction of Essential Proteins. <i>IEEE Access</i> , 2020 , 8, 138141-138148	3.5	1

10	Efficient Orchestration of Virtualization Resource in RAN Based on Chemical Reaction Optimization and Q-learning. <i>IEEE Internet of Things Journal</i> , 2021 , 1-1	10.7	1
9	Multi-Similarities Bilinear Matrix Factorization-Based Method for Predicting Human Microbe-Disease Associations. <i>Frontiers in Genetics</i> , 2021 , 12, 754425	4.5	0
8	Anti-Monitoring Algorithm for Mobile Object in Anisotropic Sensory Networks. <i>Ruan Jian Xue Bao/Journal of Software</i> , 2011 , 22, 1389-1397		0
7	A Novel Model for Identifying Essential Proteins Based on Key Target Convergence Sets. <i>Frontiers in Genetics</i> , 2021 , 12, 721486	4.5	0
6	An iteration model for identifying essential proteins by combining comprehensive PPI network with biological information. <i>BMC Bioinformatics</i> , 2021 , 22, 430	3.6	0
5	YQuery: A Novel Privacy- and Integrity-Preserving Range Queries in Two-Tiered Sensor Networks. <i>Lecture Notes in Electrical Engineering</i> , 2018 , 959-966	0.2	
4	A new 2D graphical representation of protein sequence and its application. <i>International Journal of Biomathematics</i> , 2015 , 08, 1550063	1.8	
3	Distributed node scheduling method for wireless sensor networks. <i>International Journal of Mobile Network Design and Innovation</i> , 2009 , 3, 53	0.4	
2	An Iterative Method for Identifying Essential Proteins Based on Non-Negative Matrix Factorization. <i>IEEE Access</i> , 2020 , 8, 226685-226696	3.5	
1	LHNHLDA: A Novel Approach Based on LHN-2 Algorithm for Predicting Associations Between LncRNAs and Diseases. <i>IEEE Access</i> , 2020 , 8, 198415-198424	3.5	