Lei Wang

List of Publications by Year
in descending order

75 papers	1,702 citations	430442 18 h-index	301761 39 g-index
78 all docs	78 docs citations	78 times ranked	1056 citing authors

#	Article	IF	Citations
1	Predicting miRNA–disease association based on inductive matrix completion. Bioinformatics, 2018, 34, 4256-4265.	1.8	448
2	BNPMDA: Bipartite Network Projection for MiRNA–Disease Association prediction. Bioinformatics, 2018, 34, 3178-3186.	1.8	307
3	A Novel Method for LncRNA-Disease Association Prediction Based on an lncRNA-Disease Association Network. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 688-693.	1.9	92
4	AOPs-SVM: A Sequence-Based Classifier of Antioxidant Proteins Using a Support Vector Machine. Frontiers in Bioengineering and Biotechnology, 2019, 7, 224.	2.0	63
5	A Novel Probability Model for LncRNA–Disease Association Prediction Based on the Naïve Bayesian Classifier. Genes, 2018, 9, 345.	1.0	61
6	LDGRNMF: LncRNA-disease associations prediction based on graph regularized non-negative matrix factorization. Neurocomputing, 2021, 424, 236-245.	3.5	53
7	A novel collaborative filtering model for LncRNA-disease association prediction based on the Naïve Bayesian classifier. BMC Bioinformatics, 2019, 20, 396.	1.2	49
8	A Probabilistic Matrix Factorization Method for Identifying lncRNA-disease Associations. Genes, 2019, 10, 126.	1.0	45
9	A Novel Approach for Potential Human LncRNA-Disease Association Prediction Based on Local Random Walk. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1049-1059.	1.9	40
10	IIRWR: Internal Inclined Random Walk With Restart for LncRNA-Disease Association Prediction. IEEE Access, 2019, 7, 54034-54041.	2.6	33
11	Prediction of microRNA-disease associations based on distance correlation set. BMC Bioinformatics, 2018, 19, 141.	1.2	31
12	An iteration method for identifying yeast essential proteins from heterogeneous network. BMC Bioinformatics, 2019, 20, 355.	1.2	28
13	A Bidirectional Label Propagation Based Computational Model for Potential Microbe-Disease Association Prediction. Frontiers in Microbiology, 2019, 10, 684.	1.5	28
14	Predicting microRNA–disease associations from lncRNA–microRNA interactions via Multiview Multitask Learning. Briefings in Bioinformatics, 2021, 22, .	3.2	25
15	Imbalance Data Processing Strategy for Protein Interaction Sites Prediction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 985-994.	1.9	25
16	A Novel Human Microbe-Disease Association Prediction Method Based on the Bidirectional Weighted Network. Frontiers in Microbiology, 2019, 10, 676.	1.5	23
17	Identifying Microbe-Disease Association Based on a Novel Back-Propagation Neural Network Model. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2502-2513.	1.9	21
18	A Novel Approach based on Bipartite Network to Predict Human Microbe-Disease Associations. Current Bioinformatics, 2018, 13, 141-148.	0.7	20

#	Article	IF	Citations
19	A Novel Approach Based on a Weighted Interactive Network to Predict Associations of MiRNAs and Diseases. International Journal of Molecular Sciences, 2019, 20, 110.	1.8	20
20	Prediction of tumor metastasis from sequencing data in the era of genome sequencing. Briefings in Functional Genomics, 2019, 18, 412-418.	1.3	19
21	A clique base node scheduling method for wireless sensor networks. Journal of Network and Computer Applications, 2010, 33, 383-396.	5.8	18
22	A 2D graphical representation of the sequences of DNA based on triplets and its application. Eurasip Journal on Bioinformatics and Systems Biology, 2014, 2014, 1.	1.4	16
23	SIMILARITIES/DISSIMILARITIES ANALYSIS OF PROTEIN SEQUENCES BASED ON PCA-FFT. Journal of Biological Systems, 2017, 25, 29-45.	0.5	12
24	A Novel Network-Based Computational Model for Prediction of Potential LncRNA–Disease Association. International Journal of Molecular Sciences, 2019, 20, 1549.	1.8	11
25	A novel target convergence set based random walk with restart for prediction of potential LncRNA-disease associations. BMC Bioinformatics, 2019, 20, 626.	1.2	11
26	NPF:network propagation for protein function prediction. BMC Bioinformatics, 2020, 21, 355.	1.2	11
27	A Novel Model for Predicting Essential Proteins Based on Heterogeneous Protein-Domain Network. IEEE Access, 2020, 8, 8946-8958.	2.6	11
28	A Novel Approach Based on Point Cut Set to Predict Associations of Diseases and LncRNAs. Current Bioinformatics, 2019, 14, 333-343.	0.7	11
29	Review on predicting pairwise relationships between human microbes, drugs and diseases: from biological data to computational models. Briefings in Bioinformatics, 2022, 23, .	3.2	11
30	Resource multi-objective mapping algorithm based on virtualized network functions: RMMA. Applied Soft Computing Journal, 2018, 66, 220-231.	4.1	10
31	An Algorithm of Data Aggregation Based on Data Compression for Sensor Networks. Ruan Jian Xue Bao/Journal of Software, 2006, 17, 860.	0.3	10
32	Prioritizing Human Microbe-Disease Associations Utilizing a Node-Information-Based Link Propagation Method. IEEE Access, 2020, 8, 31341-31349.	2.6	9
33	A Novel Method to Predict Essential Proteins Based on Diffusion Distance Networks. IEEE Access, 2020, 8, 29385-29394.	2.6	9
34	An Iteration Method for Identifying Yeast Essential Proteins From Weighted PPI Network Based on Topological and Functional Features of Proteins. IEEE Access, 2020, 8, 90792-90804.	2.6	8
35	ADLD: A Novel Graphical Representation of Protein Sequences and Its Application. Computational and Mathematical Methods in Medicine, 2014, 2014, 1-15.	0.7	7
36	A Novel Method for Predicting Disease-Associated LncRNA-MiRNA Pairs Based on the Higher-Order Orthogonal Iteration. Computational and Mathematical Methods in Medicine, 2019, 2019, 1-13.	0.7	7

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37	Cluster based node scheduling method for wireless sensor networks. Science China Information Sciences, 2012, 55, 755-764.	2.7	6
38	A Novel Approach for Predicting Disease-lncRNA Associations Based on the Distance Correlation Set and Information of the miRNAs. Computational and Mathematical Methods in Medicine, 2018, 2018, 1-12.	0.7	6
39	A Novel Neighborhood-Based Computational Model for Potential MiRNA-Disease Association Prediction. Computational and Mathematical Methods in Medicine, 2019, 2019, 1-10.	0.7	6
40	A novel computational model for predicting potential LncRNA-disease associations based on both direct and indirect features of LncRNA-disease pairs. BMC Bioinformatics, 2020, 21, 555.	1.2	6
41	An iteration model for identifying essential proteins by combining comprehensive PPI network with biological information. BMC Bioinformatics, 2021, 22, 430.	1.2	6
42	A Novel Model for Predicting Associations between Diseases and LncRNA-miRNA Pairs Based on a Newly Constructed Bipartite Network. Computational and Mathematical Methods in Medicine, 2018, 2018, 1-11.	0.7	5
43	ICLRBBN: a tool for accurate prediction of potential lncRNA disease associations. Molecular Therapy - Nucleic Acids, 2021, 23, 501-511.	2.3	5
44	Method for Identifying Essential Proteins by Key Features of Proteins in a Novel Protein-Domain Network. Frontiers in Genetics, 2021, 12, 708162.	1.1	5
45	A Cross-entropy-based Method for Essential Protein Identification in Yeast Protein-protein Interaction Network. Current Bioinformatics, 2021, 16, 565-575.	0.7	5
46	Multi-Similarities Bilinear Matrix Factorization-Based Method for Predicting Human Microbe–Disease Associations. Frontiers in Genetics, 2021, 12, 754425.	1.1	5
47	MDADP: A Webserver Integrating Database and Prediction Tools for Microbe-Disease Associations. IEEE Journal of Biomedical and Health Informatics, 2022, 26, 3427-3434.	3.9	5
48	Similarities/Dissimilarities Analysis of Protein Sequences Based on Recurrence Quantification Analysis. Current Bioinformatics, 2015, 10, 112-119.	0.7	4
49	Efficient Orchestration of Virtualization Resource in RAN Based on Chemical Reaction Optimization and *Q*-Learning. IEEE Internet of Things Journal, 2022, 9, 3383-3396.	5.5	4
50	An Iterative Method for Predicting Essential Proteins Based on Multifeature Fusion and Linear Neighborhood Similarity. Frontiers in Aging Neuroscience, 2021, 13, 799500.	1.7	4
51	Key Distribution for Group-based Sensor Deployment Using a Novel Interconnection Graph. , 2007, , .		3
52	A self-organizing map based hybrid chemical reaction optimization algorithm for multiobjective optimization. Applied Intelligence, 2019, 49, 2266-2286.	3.3	3
53	Voronoi Tessellation Based Haar Wavelet Data Compression for Sensor Networks. , 2006, , .		2
54	Energy-saving routing protocol for Wireless Sensor Networks. , 2014, , .		2

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55	A novel privacy- and integrity-preserving approach for multidimensional data range queries in two-tiered wireless sensor networks. International Journal of Distributed Sensor Networks, 2019, 15, 155014771985589.	1.3	2
56	An Effective Graph Clustering Method to Identify Cancer Driver Modules. Frontiers in Bioengineering and Biotechnology, 2020, 8, 271.	2.0	2
57	A Novel Model for Identifying Essential Proteins Based on Key Target Convergence Sets. Frontiers in Genetics, 2021, 12, 721486.	1.1	2
58	Identification of essential proteins based on Local Random Walk and Adaptive Multi-View Multi-Label Learning. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	1.9	2
59	Privacy-preserving Data Aggregation Based on the P-function Set in Wireless Sensor Networks. , 2010, , .		1
60	An algorithm for fatigue pattern detection based on parallel Gabor and 1-nearest neighbor. , 2012, , .		1
61	Analysis of Similarities/Dissimilarities of DNA Sequences Based on Segment of Triplets. Journal of Computational and Theoretical Nanoscience, 2015, 12, 2601-2604.	0.4	1
62	A WIFI radio signals based adaptive positioning scheme. , 2015, , .		1
63	Method for predicting hot spot residues at protein-protein interface based on the extreme learning machine. , 2017, , .		1
64	A Novel Network-Based Computational Model for Prediction of Essential Proteins. IEEE Access, 2020, 8, 138141-138148.	2.6	1
65	Anti-Monitoring Algorithm for Mobile Object in Anisotropic Sensory Networks. Ruan Jian Xue Bao/Journal of Software, 2011, 22, 1389-1397.	0.3	1
66	Group Key Management Based on Random Perturbation in Wireless Sensor Networks. Ruan Jian Xue Bao/Journal of Software, 2014, 24, 873-886.	0.3	1
67	Similarities/Dissimilarities Analysis of Protein Sequences Based on the Appearance Model. Journal of Computational and Theoretical Nanoscience, 2017, 14, 1449-1460.	0.4	1
68	Distributed node scheduling method for wireless sensor networks. International Journal of Mobile Network Design and Innovation, 2009, 3, 53.	0.1	0
69	Applying DNA Computation to Integer-Planning Problem. Journal of Computational and Theoretical Nanoscience, 2009, 6, 1001-1007.	0.4	0
70	A new 2D graphical representation of protein sequence and its application. International Journal of Biomathematics, 2015, 08, 1550063.	1.5	0
71	A 2D Graphical Representation of Protein Sequence and Its Application. Journal of Computational and Theoretical Nanoscience, 2015, 12, 2369-2374.	0.4	0
72	YQuery: A Novel Privacy- and Integrity-Preserving Range Queries in Two-Tiered Sensor Networks. Lecture Notes in Electrical Engineering, 2018, , 959-966.	0.3	0

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73	LHNHLDA: A Novel Approach Based on LHN-2 Algorithm for Predicting Associations Between LncRNAs and Diseases. IEEE Access, 2020, 8, 198415-198424.	2.6	0
74	Security Using Dynamic Secret Based on Packet Loss Rate for Wireless Sensor Networks. , 2019, , .		0
75	An Iterative Method for Identifying Essential Proteins Based on Non-Negative Matrix Factorization. IEEE Access, 2020, 8, 226685-226696.	2.6	0