Wei Lan

List of Publications by Year
in descending order

47 papers	1,333 citations	430874 18 h-index	361022 35 g-index
49 all docs	49 docs citations	49 times ranked	899 citing authors

#	Article	IF	Citations
1	LDAP: a web server for lncRNA-disease association prediction. Bioinformatics, 2017, 33, 458-460.	4.1	182
2	Classification of Alzheimer's Disease Using Whole Brain Hierarchical Network. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 624-632.	3.0	142
3	Predicting MicroRNA-Disease Associations Based on Improved MicroRNA and Disease Similarities. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1774-1782.	3.0	116
4	Complex Brain Network Analysis and Its Applications to Brain Disorders: A Survey. Complexity, 2017, 2017, 1-27.	1.6	90
5	Predicting drug–target interaction using positive-unlabeled learning. Neurocomputing, 2016, 206, 50-57.	5.9	83
6	Computational approaches for prioritizing candidate disease genes based on PPI networks. Tsinghua Science and Technology, 2015, 20, 500-512.	6.1	64
7	DNRLMF-MDA:Predicting microRNA-Disease Associations Based on Similarities of microRNAs and Diseases. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 233-243.	3.0	59
8	ILDMSF: Inferring Associations Between Long Non-Coding RNA and Disease Based on Multi-Similarity Fusion. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1106-1112.	3.0	57
9	LDICDL: LncRNA-Disease Association Identification Based on Collaborative Deep Learning. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 1715-1723.	3.0	47
10	GANLDA: Graph attention network for lncRNA-disease associations prediction. Neurocomputing, 2022, 469, 384-393.	5.9	43
11	Inferring LncRNA-disease associations based on graph autoencoder matrix completion. Computational Biology and Chemistry, 2020, 87, 107282.	2.3	40
12	A comprehensive survey on computational methods of non-coding RNA and disease association prediction. Briefings in Bioinformatics, 2021, 22, .	6.5	38
13	Improved ASD classification using dynamic functional connectivity and multi-task feature selection. Pattern Recognition Letters, 2020, 138, 82-87.	4.2	37
14	KGANCDA: predicting circRNA-disease associations based on knowledge graph attention network. Briefings in Bioinformatics, 2022, 23, .	6.5	33
15	A Framework for Integrating Multiple Biological Networks to Predict MicroRNA-Disease Associations. IEEE Transactions on Nanobioscience, 2017, 16, 100-107.	3.3	30
16	A novel method of predicting microRNA-disease associations based on microRNA, disease, gene and environment factor networks. Methods, 2017, 124, 69-77.	3.8	27
17	CircR2Cancer: a manually curated database of associations between circRNAs and cancers. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	3.0	27
18	Identifying Interactions Between Long Noncoding RNAs and Diseases Based on Computational Methods. Methods in Molecular Biology, 2018, 1754, 205-221.	0.9	19

#	Article	IF	Citations
19	Mining Featured Patterns of MiRNA Interaction Based on Sequence and Structure Similarity. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 415-422.	3.0	18
20	Identification of early mild cognitive impairment using multi-modal data and graph convolutional networks. BMC Bioinformatics, 2020, 21, 123.	2.6	17
21	SDTRLS: Predicting Drug-Target Interactions for Complex Diseases Based on Chemical Substructures. Complexity, 2017, 2017, 1-10.	1.6	15
22	GADTI: Graph Autoencoder Approach for DTI Prediction From Heterogeneous Network. Frontiers in Genetics, 2021, 12, 650821.	2.3	15
23	Inferring microRNA-Environmental Factor Interactions Based on Multiple Biological Information Fusion. Molecules, 2018, 23, 2439.	3.8	14
24	IGNSCDA: Predicting CircRNA-Disease Associations Based on Improved Graph Convolutional Network and Negative Sampling. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	3.0	13
25	Predicting microRNA-disease associations by integrating multiple biological information. , 2015, , .		12
26	Identification of Important Positions within miRNAs by Integrating Sequential and Structural Features. Current Protein and Peptide Science, 2014, 15, 591-597.	1.4	12
27	Predicting miRNA-Disease Associations From miRNA-Gene-Disease Heterogeneous Network With Multi-Relational Graph Convolutional Network Model. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2023, 20, 3363-3375.	3.0	12
28	miRTRS: A Recommendation Algorithm for Predicting miRNA Targets. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 1032-1041.	3.0	10
29	Predicting miRNA-Disease Association Based on Modularity Preserving Heterogeneous Network Embedding. Frontiers in Cell and Developmental Biology, 2021, 9, 603758.	3.7	10
30	Predicting drug-target interaction based on sequence and structure information. IFAC-PapersOnLine, 2015, 48, 12-16.	0.9	9
31	Identifying miRNAâ€disease association based on integrating miRNA topological similarity and functional similarity. Quantitative Biology, 2019, 7, 202-209.	0.5	7
32	Identifying Interactions Between Kinases and Substrates Based on Proteinâ€"Protein Interaction Network. Journal of Computational Biology, 2019, 26, 836-845.	1.6	5
33	Predicting protein functions through non-negative matrix factorization regularized by protein-protein interaction network and gene functional information. , 2019, , .		5
34	Prediction of circRNA-miRNA Associations Based on Network Embedding. Complexity, 2021, 2021, 1-10.	1.6	5
35	Survey of Network Embedding for Drug Analysis and Prediction. Current Protein and Peptide Science, 2021, 22, 237-250.	1.4	4
36	Predicting microRNA-environmental factor interactions based on bi-random walk and multi-label learning. , 2016, , .		3

#	Article	IF	Citations
37	KSIMC: Predicting Kinaseâ€"Substrate Interactions Based on Matrix Completion. International Journal of Molecular Sciences, 2019, 20, 302.	4.1	3
38	Predicting protein functions by using non-negative matrix factorisation with multi-networks co-regularisation. International Journal of Data Mining and Bioinformatics, 2020, 23, 318.	0.1	3
39	Predicting MicroRNA-Disease Associations by Random Walking on Multiple Networks. Lecture Notes in Computer Science, 2016, , 127-135.	1.3	2
40	Polyphyletic Loss: Litchi Flower Detection with Occlusion. Journal of Physics: Conference Series, 2022, 2171, 012041.	0.4	2
41	Predicting microRNA-disease associations by walking on four biological networks. , 2016, , .		1
42	Predicting protein functions by using non-negative matrix factorisation with multi-networks co-regularisation. International Journal of Data Mining and Bioinformatics, 2020, 23, 318.	0.1	1
43	Discovery of MicroRNA conservative sites in drosophila melanogaster. , 2011, , .		0
44	KSIBW: Predicting Kinase-Substrate Interactions Based on Bi-random Walk. Lecture Notes in Computer Science, 2018, , 151-162.	1.3	0
45	Predicting miRNA-disease interaction based on recommend method. Information Discovery and Delivery, 2019, 48, 35-40.	2.1	0
46	Editorial: Graph Embedding Methods for Multiple-Omics Data Analysis. Frontiers in Genetics, 2021, 12, 762274.	2.3	0
47	A Heterogeneous Graph Convolutional Network-Based Deep Learning Model to Identify miRNA-Disease Association. Lecture Notes in Computer Science, 2021, , 130-141.	1.3	0