

Wei Lan

List of Publications by Year in descending order

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47
papers

1,333
citations

489802

18
h-index

406436

35
g-index

49
all docs

49
docs citations

49
times ranked

1011
citing authors

#	ARTICLE	IF	CITATIONS
1	LDAP: a web server for lncRNA-disease association prediction. <i>Bioinformatics</i> , 2017, 33, 458-460.	1.8	182
2	Classification of Alzheimer's Disease Using Whole Brain Hierarchical Network. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 624-632.	1.9	142
3	Predicting MicroRNA-Disease Associations Based on Improved MicroRNA and Disease Similarities. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1774-1782.	1.9	116
4	Complex Brain Network Analysis and Its Applications to Brain Disorders: A Survey. <i>Complexity</i> , 2017, 2017, 1-27.	0.9	90
5	Predicting drug-target interaction using positive-unlabeled learning. <i>Neurocomputing</i> , 2016, 206, 50-57.	3.5	83
6	Computational approaches for prioritizing candidate disease genes based on PPI networks. <i>Tsinghua Science and Technology</i> , 2015, 20, 500-512.	4.1	64
7	DNRLMF-MDA: Predicting microRNA-Disease Associations Based on Similarities of microRNAs and Diseases. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 233-243.	1.9	59
8	ILDMSF: Inferring Associations Between Long Non-Coding RNA and Disease Based on Multi-Similarity Fusion. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 1106-1112.	1.9	57
9	LDICDL: lncRNA-Disease Association Identification Based on Collaborative Deep Learning. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 1715-1723.	1.9	47
10	GANLDA: Graph attention network for lncRNA-disease associations prediction. <i>Neurocomputing</i> , 2022, 469, 384-393.	3.5	43
11	Inferring lncRNA-disease associations based on graph autoencoder matrix completion. <i>Computational Biology and Chemistry</i> , 2020, 87, 107282.	1.1	40
12	A comprehensive survey on computational methods of non-coding RNA and disease association prediction. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	38
13	Improved ASD classification using dynamic functional connectivity and multi-task feature selection. <i>Pattern Recognition Letters</i> , 2020, 138, 82-87.	2.6	37
14	KGANLDA: predicting circRNA-disease associations based on knowledge graph attention network. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	33
15	A Framework for Integrating Multiple Biological Networks to Predict MicroRNA-Disease Associations. <i>IEEE Transactions on Nanobioscience</i> , 2017, 16, 100-107.	2.2	30
16	A novel method of predicting microRNA-disease associations based on microRNA, disease, gene and environment factor networks. <i>Methods</i> , 2017, 124, 69-77.	1.9	27
17	CircR2Cancer: a manually curated database of associations between circRNAs and cancers. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	27
18	Identifying Interactions Between Long Noncoding RNAs and Diseases Based on Computational Methods. <i>Methods in Molecular Biology</i> , 2018, 1754, 205-221.	0.4	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.	1.9	18
20	Identification of early mild cognitive impairment using multi-modal data and graph convolutional networks. BMC Bioinformatics, 2020, 21, 123.	1.2	17
21	SDTRLS: Predicting Drug-Target Interactions for Complex Diseases Based on Chemical Substructures. Complexity, 2017, 2017, 1-10.	0.9	15
22	GADTI: Graph Autoencoder Approach for DTI Prediction From Heterogeneous Network. Frontiers in Genetics, 2021, 12, 650821.	1.1	15
23	Inferring microRNA-Environmental Factor Interactions Based on Multiple Biological Information Fusion. Molecules, 2018, 23, 2439.	1.7	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.	1.9	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.	0.7	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.	1.9	12
28	miRTRS: A Recommendation Algorithm for Predicting miRNA Targets. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 1032-1041.	1.9	10
29	Predicting miRNA-Disease Association Based on Modularity Preserving Heterogeneous Network Embedding. Frontiers in Cell and Developmental Biology, 2021, 9, 603758.	1.8	10
30	Predicting drug-target interaction based on sequence and structure information. IFAC-PapersOnLine, 2015, 48, 12-16.	0.5	9
31	Identifying miRNA-disease association based on integrating miRNA topological similarity and functional similarity. Quantitative Biology, 2019, 7, 202-209.	0.3	7
32	Identifying Interactions Between Kinases and Substrates Based on Protein-Protein Interaction Network. Journal of Computational Biology, 2019, 26, 836-845.	0.8	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.	0.9	5
35	Survey of Network Embedding for Drug Analysis and Prediction. Current Protein and Peptide Science, 2021, 22, 237-250.	0.7	4
36	Predicting microRNA-environmental factor interactions based on bi-random walk and multi-label learning. , 2016, , .		3

#	ARTICLE	IF	CITATIONS
37	KSIMC: Predicting Kinase-Substrate Interactions Based on Matrix Completion. International Journal of Molecular Sciences, 2019, 20, 302.	1.8	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.	1.0	2
40	Polyphyletic Loss: Litchi Flower Detection with Occlusion. Journal of Physics: Conference Series, 2022, 2171, 012041.	0.3	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.	1.0	0
45	Predicting miRNA-disease interaction based on recommend method. Information Discovery and Delivery, 2019, 48, 35-40.	1.6	0
46	Editorial: Graph Embedding Methods for Multiple-Omics Data Analysis. Frontiers in Genetics, 2021, 12, 762274.	1.1	0
47	A Heterogeneous Graph Convolutional Network-Based Deep Learning Model to Identify miRNA-Disease Association. Lecture Notes in Computer Science, 2021, , 130-141.	1.0	0