Wei Peng

List of Publications by Year
in descending order

43 papers	1,191 citations	361413 20 h-index	395702 33 g-index
43 all docs	43 docs citations	43 times ranked	793 citing authors

#	Article	IF	Citations
1	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
2	Predicting Drug Response Based on Multi-Omics Fusion and Graph Convolution. IEEE Journal of Biomedical and Health Informatics, 2022, 26, 1384-1393.	6.3	34
3	Identifying Cancer Patient Subgroups by Finding Co-Modules From the Driver Mutation Profiles and Downstream Gene Expression Profiles. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 2863-2872.	3.0	5
4	GANLDA: Graph attention network for lncRNA-disease associations prediction. Neurocomputing, 2022, 469, 384-393.	5.9	43
5	Improving cancer driver gene identification using multi-task learning on graph convolutional network. Briefings in Bioinformatics, 2022, 23, .	6.5	45
6	Identifying Cancer Subtypes Using a Residual Graph Convolution Model on a Sample Similarity Network. Genes, 2022, 13, 65.	2.4	8
7	DNRLCNN: A CNN Framework for Identifying MiRNA–Disease Associations Using Latent Feature Matrix Extraction with Positive Samples. Interdisciplinary Sciences, Computational Life Sciences, 2022, 14, 607-622.	3.6	2
8	Identifying and ranking potential cancer drivers using representation learning on attributed network. Methods, 2021, 192, 13-24.	3.8	11
9	A novel essential protein identification method based on PPI networks and gene expression data. BMC Bioinformatics, 2021, 22, 248.	2.6	35
10	Predicting miRNA-Disease Association Based on Modularity Preserving Heterogeneous Network Embedding. Frontiers in Cell and Developmental Biology, 2021, 9, 603758.	3.7	10
11	A Novel Multi-Ensemble Method for Identifying Essential Proteins. Journal of Computational Biology, 2021, 28, 637-649.	1.6	6
12	Prediction of circRNA-miRNA Associations Based on Network Embedding. Complexity, 2021, 2021, 1-10.	1.6	5
13	Multi-View Feature Aggregation for predicting microbe-disease association. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	3.0	5
14	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
15	An Entropy-Based Method for Identifying Mutual Exclusive Driver Genes in Cancer. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 758-768.	3.0	25
16	Network Embedding the Protein–Protein Interaction Network for Human Essential Genes Identification. Genes, 2020, 11, 153.	2.4	21
17	Inferring LncRNA-disease associations based on graph autoencoder matrix completion. Computational Biology and Chemistry, 2020, 87, 107282.	2.3	40
18	A multi-view approach for predicting microbedisease associations by fusing the linear and nonlinear features. , 2020, , .		2

#	ARTICLE	IF	CITATIONS
19	A novel extended Pareto Optimality Consensus model for predicting essential proteins. Journal of Theoretical Biology, 2019, 480, 141-149.	1.7	9
20	A random walk-based method to identify driver genes by integrating the subcellular localization and variation frequency into bipartite graph. BMC Bioinformatics, 2019, 20, 238.	2.6	28
21	Identifying Human Essential Genes by Network Embedding Protein-Protein Interaction Network. Lecture Notes in Computer Science, 2019, , 127-137.	1.3	3
22	Identifying driver genes involving gene dysregulated expression, tissue-specific expression and gene-gene network. BMC Medical Genomics, 2019, 12, 168.	1.5	11
23	Predicting protein functions through non-negative matrix factorization regularized by protein-protein interaction network and gene functional information. , 2019, , .		5
24	A Novel Method for Identifying Essential Genes by Fusing Dynamic Protein–Protein Interactive Networks. Genes, 2019, 10, 31.	2.4	21
25	Improved Multi-Source Color Transfer Algorithm by Saliency Filters. , 2018, , .		1
26	XGBFEMF: An XGBoost-Based Framework for Essential Protein Prediction. IEEE Transactions on Nanobioscience, 2018, 17, 243-250.	3.3	100
27	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
28	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
29	A Framework for Integrating Multiple Biological Networks to Predict MicroRNA-Disease Associations. IEEE Transactions on Nanobioscience, 2017, 16, 100-107.	3.3	30
30	Predicting diabetes mellitus genes via protein-protein interaction and protein subcellular localization information. BMC Genomics, 2016, 17, 433.	2.8	23
31	Predicting microRNA-disease associations by walking on four biological networks. , 2016, , .		1
32	An Analysis Platform of Road Traffic Management System Log Data Based on Distributed Storage and Parallel Computing Techniques. , 2016, , .		9
33	Computational approaches for prioritizing candidate disease genes based on PPI networks. Tsinghua Science and Technology, 2015, 20, 500-512.	6.1	64
34	A feature selection method for prediction essential protein. Tsinghua Science and Technology, 2015, 20, 491-499.	6.1	33
35	Detecting conserved protein complexes using a dividing-and-matching algorithm and unequally lenient criteria for network comparison. Algorithms for Molecular Biology, 2015, 10, 21.	1.2	8
36	UDoNC: An Algorithm for Identifying Essential Proteins Based on Protein Domains and Protein-Protein Interaction Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 276-288.	3.0	75

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37	Identification of Protein Complexes Using Weighted PageRank-Nibble Algorithm and Core-Attachment Structure. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 179-192.	3.0	49
38	Dynamic protein interaction network construction and applications. Proteomics, 2014, 14, 338-352.	2.2	88
39	Predicting Protein Functions by Using Unbalanced Bi-Random Walk Algorithm on Protein-Protein Interaction Network and Functional Interrelationship Network. Current Protein and Peptide Science, 2014, 15, 529-539.	1.4	10
40	Prediction of essential proteins based on gene expression programming. BMC Genomics, 2013, 14, S7.	2.8	54
41	Computational approaches to predicting essential proteins: A survey. Proteomics - Clinical Applications, 2013, 7, 181-192.	1.6	59
42	A dividing-and-matching algorithm to detect conserved protein complexes via local network alignment. , 2013, , .		1
43	Iteration method for predicting essential proteins based on orthology and protein-protein interaction networks. BMC Systems Biology, 2012, 6, 87.	3.0	128