

Wei Peng

List of Publications by Year in descending order

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43
papers

1,191
citations

361413

20
h-index

395702

33
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43
all docs

43
docs citations

43
times ranked

793
citing authors

#	ARTICLE	IF	CITATIONS
1	Iteration method for predicting essential proteins based on orthology and protein-protein interaction networks. BMC Systems Biology, 2012, 6, 87.	3.0	128
2	XGBFEMF: An XGBoost-Based Framework for Essential Protein Prediction. IEEE Transactions on Nanobioscience, 2018, 17, 243-250.	3.3	100
3	Dynamic protein interaction network construction and applications. Proteomics, 2014, 14, 338-352.	2.2	88
4	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
5	Computational approaches for prioritizing candidate disease genes based on PPI networks. Tsinghua Science and Technology, 2015, 20, 500-512.	6.1	64
6	Computational approaches to predicting essential proteins: A survey. Proteomics - Clinical Applications, 2013, 7, 181-192.	1.6	59
7	Prediction of essential proteins based on gene expression programming. BMC Genomics, 2013, 14, S7.	2.8	54
8	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
9	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
10	Improving cancer driver gene identification using multi-task learning on graph convolutional network. Briefings in Bioinformatics, 2022, 23, .	6.5	45
11	GANLDA: Graph attention network for lncRNA-disease associations prediction. Neurocomputing, 2022, 469, 384-393.	5.9	43
12	Inferring lncRNA-disease associations based on graph autoencoder matrix completion. Computational Biology and Chemistry, 2020, 87, 107282.	2.3	40
13	A novel essential protein identification method based on PPI networks and gene expression data. BMC Bioinformatics, 2021, 22, 248.	2.6	35
14	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
15	A feature selection method for prediction essential protein. Tsinghua Science and Technology, 2015, 20, 491-499.	6.1	33
16	A Framework for Integrating Multiple Biological Networks to Predict MicroRNA-Disease Associations. IEEE Transactions on Nanobioscience, 2017, 16, 100-107.	3.3	30
17	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
18	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

#	ARTICLE	IF	CITATIONS
19	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
20	Predicting diabetes mellitus genes via protein-protein interaction and protein subcellular localization information. BMC Genomics, 2016, 17, 433.	2.8	23
21	A Novel Method for Identifying Essential Genes by Fusing Dynamic Protein-Protein Interactive Networks. Genes, 2019, 10, 31.	2.4	21
22	Network Embedding the Protein-Protein Interaction Network for Human Essential Genes Identification. Genes, 2020, 11, 153.	2.4	21
23	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
24	Identifying driver genes involving gene dysregulated expression, tissue-specific expression and gene-gene network. BMC Medical Genomics, 2019, 12, 168.	1.5	11
25	Identifying and ranking potential cancer drivers using representation learning on attributed network. Methods, 2021, 192, 13-24.	3.8	11
26	Predicting miRNA-Disease Association Based on Modularity Preserving Heterogeneous Network Embedding. Frontiers in Cell and Developmental Biology, 2021, 9, 603758.	3.7	10
27	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
28	An Analysis Platform of Road Traffic Management System Log Data Based on Distributed Storage and Parallel Computing Techniques. , 2016, , .		9
29	A novel extended Pareto Optimality Consensus model for predicting essential proteins. Journal of Theoretical Biology, 2019, 480, 141-149.	1.7	9
30	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
31	Identifying Cancer Subtypes Using a Residual Graph Convolution Model on a Sample Similarity Network. Genes, 2022, 13, 65.	2.4	8
32	A Novel Multi-Ensemble Method for Identifying Essential Proteins. Journal of Computational Biology, 2021, 28, 637-649.	1.6	6
33	Predicting protein functions through non-negative matrix factorization regularized by protein-protein interaction network and gene functional information. , 2019, , .		5
34	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
35	Prediction of circRNA-miRNA Associations Based on Network Embedding. Complexity, 2021, 2021, 1-10.	1.6	5
36	Multi-View Feature Aggregation for predicting microbe-disease association. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	3.0	5

#	ARTICLE	IF	CITATIONS
37	Identifying Human Essential Genes by Network Embedding Protein-Protein Interaction Network. Lecture Notes in Computer Science, 2019, , 127-137.	1.3	3
38	A multi-view approach for predicting microbedisease associations by fusing the linear and nonlinear features. , 2020, , .		2
39	DNRLCNN: A CNN Framework for Identifying MiRNAâ€Disease Associations Using Latent Feature Matrix Extraction with Positive Samples. Interdisciplinary Sciences, Computational Life Sciences, 2022, 14, 607-622.	3.6	2
40	A dividing-and-matching algorithm to detect conserved protein complexes via local network alignment. , 2013, , .		1
41	Predicting microRNA-disease associations by walking on four biological networks. , 2016, , .		1
42	Improved Multi-Source Color Transfer Algorithm by Saliency Filters. , 2018, , .		1
43	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