Jiajie Peng

List of Publications by Year
in descending order

76	2,355	236925 25	233421 45
papers	citations	h-index	g-index

87	87	87	1878
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Identifying drugâ€“target interactions based on graph convolutional network and deep neural network. Briefings in Bioinformatics, 2021, 22, 2141-2150.	6.5	172
2	A learning-based framework for miRNA-disease association identification using neural networks. Bioinformatics, 2019, 35, 4364-4371.	4.1	142
3	LncRNA2Target: a database for differentially expressed genes after lncRNA knockdown or overexpression. Nucleic Acids Research, 2015, 43, D193-D196.	14.5	124
4	SemFunSim: A New Method for Measuring Disease Similarity by Integrating Semantic and Gene Functional Association. PLoS ONE, 2014, 9, e99415.	2.5	117
5	LncRNA2Function: a comprehensive resource for functional investigation of human lncRNAs based on RNA-seq data. BMC Genomics, 2015, 16, S2.	2.8	117
6	DeepLGP: a novel deep learning method for prioritizing lncRNA target genes. Bioinformatics, 2020, 36, 4466-4472.	4.1	106
7	InfAcrOnt: calculating cross-ontology term similarities using information flow by a random walk. BMC Genomics, 2018, 19, 919.	2.8	98
8	Predicting Parkinson's Disease Genes Based on Node2vec and Autoencoder. Frontiers in Genetics, 2019, 10, 226.	2.3	91
9	An end-to-end heterogeneous graph representation learning-based framework for drugâ€“target interaction prediction. Briefings in Bioinformatics, 2021, 22, .	6.5	87
10	Genome-wide survival study identifies a novel synaptic locus and polygenic score for cognitive progression in Parkinsonâ€™s disease. Nature Genetics, 2021, 53, 787-793.	21.4	82
11	Integrating multi-network topology for gene function prediction using deep neural networks. Briefings in Bioinformatics, 2021, 22, 2096-2105.	6.5	73
12	SC2disease: a manually curated database of single-cell transcriptome for human diseases. Nucleic Acids Research, 2021, 49, D1413-D1419.	14.5	65
13	A learning-based method for drug-target interaction prediction based on feature representation learning and deep neural network. BMC Bioinformatics, 2020, 21, 394.	2.6	54
14	Improving the measurement of semantic similarity by combining gene ontology and co-functional network: a random walk based approach. BMC Systems Biology, 2018, 12, 18.	3.0	52
15	Prediction and collection of proteinâ€“metabolite interactions. Briefings in Bioinformatics, 2021, 22, .	6.5	52
16	A novel method to measure the semantic similarity of HPO terms. International Journal of Data Mining and Bioinformatics, 2017, 17, 173.	0.1	51
17	Deep learningâ€based classification and mutation prediction from histopathological images of hepatocellular carcinoma. Clinical and Translational Medicine, 2020, 10, e102.	4.0	50
18	Combining gene ontology with deep neural networks to enhance the clustering of single cell RNA-Seq data. BMC Bioinformatics, 2019, 20, 284.	2.6	48

#	Article	IF	Citations
19	Predicting disease-related genes using integrated biomedical networks. BMC Genomics, 2017, 18, 1043.	2.8	46
20	Identifying term relations cross different gene ontology categories. BMC Bioinformatics, 2017, 18, 573.	2.6	46
21	Extending gene ontology with gene association networks. Bioinformatics, 2016, 32, 1185-1194.	4.1	42
22	Measuring semantic similarities by combining gene ontology annotations and gene co-function networks. BMC Bioinformatics, 2015, 16, 44.	2.6	39
23	Benchmarked approaches for reconstruction of inÂvitro cell lineages and in silico models of C. elegans and M. musculus developmental trees. Cell Systems, 2021, 12, 810-826.e4.	6.2	36
24	Classification and Prognosis Prediction from Histopathological Images of Hepatocellular Carcinoma by a Fully Automated Pipeline Based on Machine Learning. Annals of Surgical Oncology, 2020, 27, 2359-2369.	1.5	33
25	Measuring phenotype-phenotype similarity through the interactome. BMC Bioinformatics, 2018, 19, 114.	2.6	32
26	A pipeline for RNA-seq based eQTL analysis with automated quality control procedures. BMC Bioinformatics, 2021, 22, 403.	2.6	27
27	Towards integrative gene functional similarity measurement. BMC Bioinformatics, 2014, 15, S5.	2.6	26
28	InteGO2: a web tool for measuring and visualizing gene semantic similarities using Gene Ontology. BMC Genomics, 2016, 17, 530.	2.8	26
29	FSM: Fast and scalable network motif discovery for exploring higher-order network organizations. Methods, 2020, 173, 83-93.	3.8	26
30	An integrative approach for measuring semantic similarities using gene ontology. BMC Systems Biology, 2014, 8, S8.	3.0	20
31	Combining sequence and network information to enhance proteinâ€“protein interaction prediction. BMC Bioinformatics, 2020, 21, 537.	2.6	20
32	Reduction in TOM1 expression exacerbates Alzheimerâ€™s disease. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 3915-3916.	7.1	20
33	Joint detection of copy number variations in parent-offspring trios. Bioinformatics, 2016, 32, 1130-1137.	4.1	18
34	A novel subnetwork representation learning method for uncovering disease-disease relationships. Methods, 2021, 192, 77-84.	3.8	17
35	eQTLMAPT: Fast and Accurate eQTL Mediation Analysis With Efficient Permutation Testing Approaches. Frontiers in Genetics, 2019, 10, 1309.	2.3	17
36	A Generalized Topological Entropy for Analyzing the Complexity of DNA Sequences. PLoS ONE, 2014, 9, e88519.	2.5	16

#	Article	IF	Citations
37	Identifying consistent disease subnetworks using DNet. Methods, 2017, 131, 104-110.	3.8	16
38	Constructing Networks of Organelle Functional Modules in Arabidopsis. Current Genomics, 2016, 17, 427-438.	1.6	16
39	Enhancing discoveries of molecular QTL studies with small sample size using summary statistic imputation. Briefings in Bioinformatics, 2022, 23, .	6.5	15
40	Identifying cross-category relations in gene ontology and constructing genome-specific term association networks. BMC Bioinformatics, 2013, 14, S15.	2.6	14
41	Mining Relationships among Multiple Entities in Biological Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 769-776.	3.0	14
42	Predicting disease-related phenotypes using an integrated phenotype similarity measurement based on HPO. BMC Systems Biology, 2019, 13, 34.	3.0	12
43	DeepLearnMOR: a deep-learning framework for fluorescence image-based classification of organelle morphology. Plant Physiology, 2021, 186, 1786-1799.	4.8	12
44	LncDisAP: a computation model for LncRNA-disease association prediction based on multiple biological datasets. BMC Bioinformatics, 2019, 20, 582.	2.6	11
45	Prioritizing candidate diseases-related metabolites based on literature and functional similarity. BMC Bioinformatics, 2019, 20, 574.	2.6	9
46	Efficient Deep Reinforcement Learning via Adaptive Policy Transfer. , 2020, , .		9
47	Identifying emerging phenomenon in long temporal phenotyping experiments. Bioinformatics, 2020, 36, 568-577.	4.1	8
48	R-CRISPR: A Deep Learning Network to Predict Off-Target Activities with Mismatch, Insertion and Deletion in CRISPR-Cas9 System. Genes, 2021, 12, 1878.	2.4	8
49	An online tool for measuring and visualizing phenotype similarities using HPO. BMC Genomics, 2018, 19, 571.	2.8	7
50	TS-GOEA: a web tool for tissue-specific gene set enrichment analysis based on gene ontology. BMC Bioinformatics, 2019, 20, 572.	2.6	7
51	A novel method for predicting cell abundance based on single-cell RNA-seq data. BMC Bioinformatics, 2021, 22, 281.	2.6	7
52	A network-based method for brain disease gene prediction by integrating brain connectome and molecular network. Briefings in Bioinformatics, 2022, 23, .	6.5	7
53	Measuring phenotype semantic similarity using Human Phenotype Ontology. , 2016, , .		6
54	SpliVert: A Protein Multiple Sequence Alignment Refinement Method Based on Splitting-Splicing Vertically. Protein and Peptide Letters, 2020, 27, 295-302.	0.9	6

#	Article	IF	Citations
55	A Survey of Network Representation Learning Methods for Link Prediction in Biological Network. Current Pharmaceutical Design, 2020, 26, 3076-3084.	1.9	6
56	Integrated proteogenomic analysis revealed the metabolic heterogeneity in noncancerous liver tissues of patients with hepatocellular carcinoma. Journal of Hematology and Oncology, 2021, 14, 205.	17.0	6
57	Predicting Chromosome Flexibility from the Genomic Sequence Based on Deep Learning Neural Networks. Current Bioinformatics, 2021, 16, 1311-1319.	1.5	5
58	Explore potential disease related metabolites based on latent factor model. BMC Genomics, 2022, 23, 269.	2.8	5
59	Integrating Sequence and Network Information to Enhance Protein-Protein Interaction Prediction Using Graph Convolutional Networks. , 2019, , .		4
60	Predicting Hepatoma-Related Genes Based on Representation Learning of PPI network and Gene Ontology Annotations. , 2021, , .		4
61	Editorial: Data Mining and Statistical Methods for Knowledge Discovery in Diseases Based on Multimodal Omics. Frontiers in Genetics, 2022, 13, 895796.	2.3	4
62	Investigations on factors influencing HPO-based semantic similarity calculation. Journal of Biomedical Semantics, 2017, 8, 34.	1.6	3
63	Towards Gene Function Prediction via Multi-Networks Representation Learning. Proceedings of the AAAI Conference on Artificial Intelligence, 2019, 33, 10069-10070.	4.9	3
64	Integrating Multi-Network Topology via Deep Semi-supervised Node Embedding. , 2019, , .		3
65	Automatic Term Name Generation for Gene Ontology: Task and Dataset. , 2020, , .		3
66	Identifying Non-Math Students from Brain MRIs with an Ensemble Classifier Based on Subspace-Enhanced Contrastive Learning. Brain Sciences, 2022, 12, 908.	2.3	3
67	Measuring phenotype-phenotype similarity through the interactome. , 2017, , .		1
68	Identifying Representative Network Motifs for Inferring Higher-order Structure of Biological Networks. , 2018, , .		1
69	A novel method to measure the semantic similarity of HPO terms. International Journal of Data Mining and Bioinformatics, 2017, 17, 173.	0.1	1
70	Flexibility and rigidity index for chromosome packing, flexibility and dynamics analysis. Frontiers of Computer Science, 2022, 16, 1.	2.4	1
71	DCAE: Selecting Discriminative Genes on Single-cell RNA-seq Data for Cell-type Quantification. , 2021, , .		1
72	A web tool for measuring gene semantic similarities by combining gene ontology and gene co-function networks. , 2015, , .		0

#	Article	IF	Citations
73	Analyzing factors involved in the HPO-based semantic similarity calculation. , 2016, , .		0
74	TSGOE: A web tool for tissue-specific gene ontology enrichment. , 2018, , .		0
75	Predicting candidate disease-related lncRNAs based on network random walk. , 2018, , .		0
76	A deconvolution method for predicting cell abundance based on single cell RNA-seq data. , 2019, , .		0