

Lun Hu

List of Publications by Year in descending order

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49
papers

1,187
citations

361413

20
h-index

395702

33
g-index

52
all docs

52
docs citations

52
times ranked

592
citing authors

#	ARTICLE	IF	CITATIONS
1	A Distributed Framework for Large-scale Protein-protein Interaction Data Analysis and Prediction Using MapReduce. IEEE/CAA Journal of Automatica Sinica, 2022, 9, 160-172.	13.1	52
2	Automatic Detection of Melanins and Sebums from Skin Images Using a Generative Adversarial Network. Cognitive Computation, 2022, 14, 1599-1608.	5.2	4
3	Identifying Protein Complexes From Protein-Protein Interaction Networks Based on Fuzzy Clustering and GO Semantic Information. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 2882-2893.	3.0	18
4	A Fast Fuzzy Clustering Algorithm for Complex Networks via a Generalized Momentum Method. IEEE Transactions on Fuzzy Systems, 2022, 30, 3473-3485.	9.8	50
5	Attention-based Knowledge Graph Representation Learning for Predicting Drug-drug Interactions. Briefings in Bioinformatics, 2022, 23, .	6.5	46
6	iGRLCDA: identifying circRNAâ€™disease association based on graph representation learning. Briefings in Bioinformatics, 2022, 23, .	6.5	17
7	A deep learning method for repurposing antiviral drugs against new viruses via multi-view nonnegative matrix factorization and its application to SARS-CoV-2. Briefings in Bioinformatics, 2022, 23, .	6.5	56
8	HINGRL: predicting drugâ€™disease associations with graph representation learning on heterogeneous information networks. Briefings in Bioinformatics, 2022, 23, .	6.5	60
9	Multi-view heterogeneous molecular network representation learning for proteinâ€™protein interaction prediction. BMC Bioinformatics, 2022, 23, .	2.6	8
10	Detection of Link Communities in Attributed Graphs via an Approximate Bayesian Generative Model. , 2022, , .		0
11	HiSCF: leveraging higher-order structures for clustering analysis in biological networks. Bioinformatics, 2021, 37, 542-550.	4.1	76
12	An Effective Link-Based Clustering Algorithm for Detecting Overlapping Protein Complexes in Protein-Protein Interaction Networks. IEEE Transactions on Network Science and Engineering, 2021, 8, 3275-3289.	6.4	34
13	An Ensemble Learning Algorithm for Predicting HIV-1 Protease Cleavage Sites. Lecture Notes in Computer Science, 2021, , 509-521.	1.3	0
14	A Multi-graph Deep Learning Model for Predicting Drug-Disease Associations. Lecture Notes in Computer Science, 2021, , 580-590.	1.3	8
15	An Efficient Computational Model for Large-Scale Prediction of Proteinâ€™Protein Interactions Based on Accurate and Scalable Graph Embedding. Frontiers in Genetics, 2021, 12, 635451.	2.3	7
16	A survey on computational models for predicting proteinâ€™protein interactions. Briefings in Bioinformatics, 2021, 22, .	6.5	92
17	Exploiting higher-order patterns for community detection in attributed graphs. Integrated Computer-Aided Engineering, 2021, 28, 207-218.	4.6	24
18	Predicting HIV-1 Protease Cleavage Sites With Positive-Unlabeled Learning. Frontiers in Genetics, 2021, 12, 658078.	2.3	10

#	ARTICLE	IF	CITATIONS
19	A Novel Method to Predict Drug-Target Interactions Based on Large-Scale Graph Representation Learning. <i>Cancers</i> , 2021, 13, 2111.	3.7	31
20	A Novel Network-Based Algorithm for Predicting Protein-Protein Interactions Using Gene Ontology. <i>Frontiers in Microbiology</i> , 2021, 12, 735329.	3.5	11
21	SANE: A sequence combined attentive network embedding model for COVID-19 drug repositioning. <i>Applied Soft Computing Journal</i> , 2021, 111, 107831.	7.2	23
22	Incorporating Generalized Momentum Method to Accelerate Clustering Analysis of Complex Networks. , 2021, , .		0
23	Learning from low-rank multimodal representations for predicting disease-drug associations. <i>BMC Medical Informatics and Decision Making</i> , 2021, 21, 308.	3.0	10
24	Predicting Large-scale Protein-protein Interactions by Extracting Coevolutionary Patterns with MapReduce Paradigm. , 2021, , .		3
25	A deep learning algorithm for predicting protein-protein interactions with nonnegative latent factorization. , 2021, , .		0
26	Incorporating the Coevolving Information of Substrates in Predicting HIV-1 Protease Cleavage Sites. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 17, 2017-2028.	3.0	29
27	A Variational Bayesian Framework for Cluster Analysis in a Complex Network. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2020, 32, 2115-2128.	5.7	54
28	Non-Negativity Constrained Missing Data Estimation for High-Dimensional and Sparse Matrices from Industrial Applications. <i>IEEE Transactions on Cybernetics</i> , 2020, 50, 1844-1855.	9.5	90
29	An Experimental Investigation into Promoting Mental Health Service Use on Social Media: Effects of Source and Comments. <i>International Journal of Environmental Research and Public Health</i> , 2020, 17, 7898.	2.6	4
30	An Algorithm of Inductively Identifying Clusters from Attributed Graphs. <i>IEEE Transactions on Big Data</i> , 2020, , 1-1.	6.1	36
31	A Novel Stochastic Block Model for Network-Based Prediction of Protein-Protein Interactions. <i>Lecture Notes in Computer Science</i> , 2020, , 621-632.	1.3	7
32	The identification of variable-length coevolutionary patterns for predicting HIV-1 protease cleavage sites. , 2020, , .		2
33	Automatic hierarchy classification in venation networks using directional morphological filtering for hierarchical structure traits extraction. <i>Computational Biology and Chemistry</i> , 2019, 80, 187-194.	2.3	10
34	A fast algorithm to identify coevolutionary patterns from protein sequences based on tree-based data structure. , 2019, , .		3
35	Predicting Hospital Readmission of Diabetics using Deep Forest. , 2019, , .		8
36	Efficiently Detecting Protein Complexes from Protein Interaction Networks via Alternating Direction Method of Multipliers. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1922-1935.	3.0	64

#	ARTICLE	IF	CITATIONS
37	A geneâ€“phenotype relationship extraction pipeline from the biomedical literature using a representation learning approach. <i>Bioinformatics</i> , 2018, 34, i386-i394.	4.1	35
38	Learning Latent Factors for Community Identification and Summarization. <i>IEEE Access</i> , 2018, 6, 30137-30148.	4.2	17
39	Phenotype Extraction Based on Word Embedding to Sentence Embedding Cascaded Approach. <i>IEEE Transactions on Nanobioscience</i> , 2018, 17, 172-180.	3.3	6
40	Extracting Coevolutionary Features from Protein Sequences for Predicting Protein-Protein Interactions. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 155-166.	3.0	33
41	Efficiently predicting large-scale protein-protein interactions using MapReduce. <i>Computational Biology and Chemistry</i> , 2017, 69, 202-206.	2.3	13
42	Identifying overlapping protein complexes in yeast protein interaction network via fuzzy clustering. , 2017, , .		0
43	Discovering second-order sub-structure associations in drug molecules for side-effect prediction. , 2017, , .		4
44	Bar charts detection and analysis in biomedical literature of PubMed Central. <i>AMIA ... Annual Symposium proceedings</i> , 2017, 2017, 859-865.	0.2	3
45	InDel marker detection by integration of multiple softwares using machine learning techniques. <i>BMC Bioinformatics</i> , 2016, 17, 548.	2.6	8
46	Fuzzy Clustering in a Complex Network Based on Content Relevance and Link Structures. <i>IEEE Transactions on Fuzzy Systems</i> , 2016, 24, 456-470.	9.8	70
47	Discovering Variable-Length Patterns in Protein Sequences for Protein-Protein Interaction Prediction. <i>IEEE Transactions on Nanobioscience</i> , 2015, 14, 409-416.	3.3	24
48	A density-based clustering approach for identifying overlapping protein complexes with functional preferences. <i>BMC Bioinformatics</i> , 2015, 16, 174.	2.6	24
49	Does a Generic Price Pattern Exist? <i>An Alternative Approach to Technical Analysis</i>. <i>Journal of Investing</i> , 2012, 21, 69-77.	0.2	2