

# Lun Hu

## List of Publications by Year in descending order

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Version: 2024-02-01

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 survey on computational models for predicting protein-protein interactions. Briefings in Bioinformatics, 2021, 22, .	6.5	92
2	Non-Negativity Constrained Missing Data Estimation for High-Dimensional and Sparse Matrices from Industrial Applications. IEEE Transactions on Cybernetics, 2020, 50, 1844-1855.	9.5	90
3	HiSCF: leveraging higher-order structures for clustering analysis in biological networks. Bioinformatics, 2021, 37, 542-550.	4.1	76
4	Fuzzy Clustering in a Complex Network Based on Content Relevance and Link Structures. IEEE Transactions on Fuzzy Systems, 2016, 24, 456-470.	9.8	70
5	Efficiently Detecting Protein Complexes from Protein Interaction Networks via Alternating Direction Method of Multipliers. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1922-1935.	3.0	64
6	HINGRL: predicting drug-disease associations with graph representation learning on heterogeneous information networks. Briefings in Bioinformatics, 2022, 23, .	6.5	60
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	A Variational Bayesian Framework for Cluster Analysis in a Complex Network. IEEE Transactions on Knowledge and Data Engineering, 2020, 32, 2115-2128.	5.7	54
9	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
10	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
11	Attention-based Knowledge Graph Representation Learning for Predicting Drug-drug Interactions. Briefings in Bioinformatics, 2022, 23, .	6.5	46
12	An Algorithm of Inductively Identifying Clusters from Attributed Graphs. IEEE Transactions on Big Data, 2020, , 1-1.	6.1	36
13	A gene-phenotype relationship extraction pipeline from the biomedical literature using a representation learning approach. Bioinformatics, 2018, 34, i386-i394.	4.1	35
14	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
15	Extracting Coevolutionary Features from Protein Sequences for Predicting Protein-Protein Interactions. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 155-166.	3.0	33
16	A Novel Method to Predict Drug-Target Interactions Based on Large-Scale Graph Representation Learning. Cancers, 2021, 13, 2111.	3.7	31
17	Incorporating the Coevolving Information of Substrates in Predicting HIV-1 Protease Cleavage Sites. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 2017-2028.	3.0	29
18	Discovering Variable-Length Patterns in Protein Sequences for Protein-Protein Interaction Prediction. IEEE Transactions on Nanobioscience, 2015, 14, 409-416.	3.3	24

#	ARTICLE	IF	CITATIONS
19	A density-based clustering approach for identifying overlapping protein complexes with functional preferences. BMC Bioinformatics, 2015, 16, 174.	2.6	24
20	Exploiting higher-order patterns for community detection in attributed graphs. Integrated Computer-Aided Engineering, 2021, 28, 207-218.	4.6	24
21	SANE: A sequence combined attentive network embedding model for COVID-19 drug repositioning. Applied Soft Computing Journal, 2021, 111, 107831.	7.2	23
22	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
23	Learning Latent Factors for Community Identification and Summarization. IEEE Access, 2018, 6, 30137-30148.	4.2	17
24	iGRLCDA: identifying circRNA-disease association based on graph representation learning. Briefings in Bioinformatics, 2022, 23, .	6.5	17
25	Efficiently predicting large-scale protein-protein interactions using MapReduce. Computational Biology and Chemistry, 2017, 69, 202-206.	2.3	13
26	A Novel Network-Based Algorithm for Predicting Protein-Protein Interactions Using Gene Ontology. Frontiers in Microbiology, 2021, 12, 735329.	3.5	11
27	Automatic hierarchy classification in venation networks using directional morphological filtering for hierarchical structure traits extraction. Computational Biology and Chemistry, 2019, 80, 187-194.	2.3	10
28	Predicting HIV-1 Protease Cleavage Sites With Positive-Unlabeled Learning. Frontiers in Genetics, 2021, 12, 658078.	2.3	10
29	Learning from low-rank multimodal representations for predicting disease-drug associations. BMC Medical Informatics and Decision Making, 2021, 21, 308.	3.0	10
30	InDel marker detection by integration of multiple softwares using machine learning techniques. BMC Bioinformatics, 2016, 17, 548.	2.6	8
31	Predicting Hospital Readmission of Diabetics using Deep Forest. , 2019, , .		8
32	A Multi-graph Deep Learning Model for Predicting Drug-Disease Associations. Lecture Notes in Computer Science, 2021, , 580-590.	1.3	8
33	Multi-view heterogeneous molecular network representation learning for protein-protein interaction prediction. BMC Bioinformatics, 2022, 23, .	2.6	8
34	An Efficient Computational Model for Large-Scale Prediction of Protein-Protein Interactions Based on Accurate and Scalable Graph Embedding. Frontiers in Genetics, 2021, 12, 635451.	2.3	7
35	A Novel Stochastic Block Model for Network-Based Prediction of Protein-Protein Interactions. Lecture Notes in Computer Science, 2020, , 621-632.	1.3	7
36	Phenotype Extraction Based on Word Embedding to Sentence Embedding Cascaded Approach. IEEE Transactions on Nanobioscience, 2018, 17, 172-180.	3.3	6

#	ARTICLE	IF	CITATIONS
37	Discovering second-order sub-structure associations in drug molecules for side-effect prediction. , 2017, , .		4
38	An Experimental Investigation into Promoting Mental Health Service Use on Social Media: Effects of Source and Comments. International Journal of Environmental Research and Public Health, 2020, 17, 7898.	2.6	4
39	Automatic Detection of Melanins and Sebums from Skin Images Using a Generative Adversarial Network. Cognitive Computation, 2022, 14, 1599-1608.	5.2	4
40	A fast algorithm to identify coevolutionary patterns from protein sequences based on tree-based data structure. , 2019, , .		3
41	Bar charts detection and analysis in biomedical literature of PubMed Central. AMIA ... Annual Symposium proceedings, 2017, 2017, 859-865.	0.2	3
42	Predicting Large-scale Protein-protein Interactions by Extracting Coevolutionary Patterns with MapReduce Paradigm. , 2021, , .		3
43	Does a Generic Price Pattern Exist? <i>An Alternative Approach to Technical Analysis</i>. Journal of Investing, 2012, 21, 69-77.	0.2	2
44	The identification of variable-length coevolutionary patterns for predicting HIV-1 protease cleavage sites. , 2020, , .		2
45	Identifying overlapping protein complexes in yeast protein interaction network via fuzzy clustering. , 2017, , .		0
46	An Ensemble Learning Algorithm for Predicting HIV-1 Protease Cleavage Sites. Lecture Notes in Computer Science, 2021, , 509-521.	1.3	0
47	Incorporating Generalized Momentum Method to Accelerate Clustering Analysis of Complex Networks. , 2021, , .		0
48	A deep learning algorithm for predicting protein-protein interactions with nonnegative latent factorization. , 2021, , .		0
49	Detection of Link Communities in Attributed Graphs via an Approximate Bayesian Generative Model. , 2022, , .		0