

# Min Zeng

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3221855/publications.pdf>

Version: 2024-02-01

28  
papers

1,062  
citations

471509

17  
h-index

642732

23  
g-index

29  
all docs

29  
docs citations

29  
times ranked

663  
citing authors

#	ARTICLE	IF	CITATIONS
1	Proteinâ€“protein interaction site prediction through combining local and global features with deep neural networks. <i>Bioinformatics</i> , 2020, 36, 1114-1120.	4.1	157
2	Network-based methods for predicting essential genes or proteins: a survey. <i>Briefings in Bioinformatics</i> , 2020, 21, 566-583.	6.5	90
3	Effective prediction of three common diseases by combining SMOTE with Tomek links technique for imbalanced medical data. , 2016, , .		84
4	Automatic ICD-9 coding via deep transfer learning. <i>Neurocomputing</i> , 2019, 324, 43-50.	5.9	79
5	Automated ICD-9 Coding via A Deep Learning Approach. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1193-1202.	3.0	78
6	DeepFunc: A Deep Learning Framework for Accurate Prediction of Protein Functions from Protein Sequences and Interactions. <i>Proteomics</i> , 2019, 19, e1900019.	2.2	72
7	A deep learning framework for identifying essential proteins by integrating multiple types of biological information. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 18, 1-1.	3.0	65
8	SDLDA: lncRNA-disease association prediction based on singular value decomposition and deep learning. <i>Methods</i> , 2020, 179, 73-80.	3.8	61
9	Deep Matrix Factorization Improves Prediction of Human CircRNA-Disease Associations. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2021, 25, 891-899.	6.3	43
10	DeepEP: a deep learning framework for identifying essential proteins. <i>BMC Bioinformatics</i> , 2019, 20, 506.	2.6	40
11	DMFLDA: A Deep Learning Framework for Predicting lncRNAâ€“Disease Associations. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 2353-2363.	3.0	38
12	DeepLncLoc: a deep learning framework for long non-coding RNA subcellular localization prediction based on subsequence embedding. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	33
13	BridgeDPI: a novel Graph Neural Network for predicting drugâ€“protein interactions. <i>Bioinformatics</i> , 2022, 38, 2571-2578.	4.1	31
14	NEDD: a network embedding based method for predicting drug-disease associations. <i>BMC Bioinformatics</i> , 2020, 21, 387.	2.6	23
15	A Deep Learning Framework for Gene Ontology Annotations With Sequence- and Network-Based Information. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 2208-2217.	3.0	21
16	Improving circRNAâ€“disease association prediction by sequence and ontology representations with convolutional and recurrent neural networks. <i>Bioinformatics</i> , 2021, 36, 5656-5664.	4.1	21
17	KAICD: A knowledge attention-based deep learning framework for automatic ICD coding. <i>Neurocomputing</i> , 2022, 469, 376-383.	5.9	19
18	PROBselect: accurate prediction of protein-binding residues from proteins sequences via dynamic predictorÂ“selection. <i>Bioinformatics</i> , 2020, 36, i735-i744.	4.1	19

#	ARTICLE	IF	CITATIONS
19	Essential Protein Prediction Based on node2vec and XGBoost. Journal of Computational Biology, 2021, 28, 687-700.	1.6	17
20	DeepPPF: A deep learning framework for predicting protein family. Neurocomputing, 2021, 428, 19-29.	5.9	16
21	NetEPD: A network-based essential protein discovery platform. Tsinghua Science and Technology, 2020, 25, 542-552.	6.1	15
22	A Deep Learning Framework for Identifying Essential Proteins Based on Protein-Protein Interaction Network and Gene Expression Data. , 2018, , .		12
23	HNEDTI: Prediction of drug-target interaction based on heterogeneous network embedding. , 2019, , .		7
24	LncRNAâ€disease association prediction through combining linear and non-linear features with matrix factorization and deep learning techniques. , 2019, , .		7
25	Prediction of Drugâ€Drug Interactions Based on Multiâ€layer Feature Selection and Data Balance. Chinese Journal of Electronics, 2017, 26, 585-590.	1.5	4
26	Ess-NEXG: Predict Essential Proteins by Constructing a Weighted Protein Interaction Network Based on Node Embedding and XGBoost. Lecture Notes in Computer Science, 2020, , 95-104.	1.3	4
27	DRCNNTLE: A deep recurrent convolutional neural network with transfer learning through pre-trained embeddings for automated ICD coding. Methods, 2022, 205, 97-105.	3.8	3
28	Improving human essential protein prediction using only protein sequences via ensemble learning. , 2021, , .		2