

# 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  | KAICD: A knowledge attention-based deep learning framework for automatic ICD coding. <i>Neurocomputing</i> , 2022, 469, 376-383.  | 5.9 | 19        |
| 2  | 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        |
| 3  | BridgeDPI: a novel Graph Neural Network for predicting drug-protein interactions. <i>Bioinformatics</i> , 2022, 38, 2571-2578.  | 4.1 | 31        |
| 4  | DRCNNTLE: A deep recurrent convolutional neural network with transfer learning through pre-trained embeddings for automated ICD coding. <i>Methods</i> , 2022, 205, 97-105.                           | 3.8 | 3         |
| 5  | 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        |
| 6  | DMFLDA: A Deep Learning Framework for Predicting lncRNA-Disease Associations. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 2353-2363.                         | 3.0 | 38        |
| 7  | 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        |
| 8  | DeepPPF: A deep learning framework for predicting protein family. <i>Neurocomputing</i> , 2021, 428, 19-29.   | 5.9 | 16        |
| 9  | Essential Protein Prediction Based on node2vec and XGBoost. <i>Journal of Computational Biology</i> , 2021, 28, 687-700.  | 1.6 | 17        |
| 10 | Improving circRNA-disease association prediction by sequence and ontology representations with convolutional and recurrent neural networks. <i>Bioinformatics</i> , 2021, 36, 5656-5664.              | 4.1 | 21        |
| 11 | Improving human essential protein prediction using only protein sequences via ensemble learning. , 2021, , .  |     | 2         |
| 12 | Protein-protein interaction site prediction through combining local and global features with deep neural networks. <i>Bioinformatics</i> , 2020, 36, 1114-1120.                                       | 4.1 | 157       |
| 13 | Network-based methods for predicting essential genes or proteins: a survey. <i>Briefings in Bioinformatics</i> , 2020, 21, 566-583.   | 6.5 | 90        |
| 14 | NEDD: a network embedding based method for predicting drug-disease associations. <i>BMC Bioinformatics</i> , 2020, 21, 387.   | 2.6 | 23        |
| 15 | SDLDA: lncRNA-disease association prediction based on singular value decomposition and deep learning. <i>Methods</i> , 2020, 179, 73-80.  | 3.8 | 61        |
| 16 | NetEPD: A network-based essential protein discovery platform. <i>Tsinghua Science and Technology</i> , 2020, 25, 542-552.   | 6.1 | 15        |
| 17 | Ess-NEXC: Predict Essential Proteins by Constructing a Weighted Protein Interaction Network Based on Node Embedding and XGBoost. <i>Lecture Notes in Computer Science</i> , 2020, , 95-104.           | 1.3 | 4         |
| 18 | PROBselect: accurate prediction of protein-binding residues from proteins sequences via dynamic predictor-selection. <i>Bioinformatics</i> , 2020, 36, i735-i744.                                     | 4.1 | 19        |

| #  | ARTICLE   | IF  | CITATIONS |
|----|---|-----|-----------|
| 19 | Automatic ICD-9 coding via deep transfer learning. <i>Neurocomputing</i> , 2019, 324, 43-50.  | 5.9 | 79        |
| 20 | 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        |
| 21 | 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        |
| 22 | HNEDTI: Prediction of drug-target interaction based on heterogeneous network embedding. , 2019, , .   |     | 7         |
| 23 | LncRNAâ€™disease association prediction through combining linear and non-linear features with matrix factorization and deep learning techniques. , 2019, , .  |     | 7         |
| 24 | DeepEP: a deep learning framework for identifying essential proteins. <i>BMC Bioinformatics</i> , 2019, 20, 506.  | 2.6 | 40        |
| 25 | 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        |
| 26 | A Deep Learning Framework for Identifying Essential Proteins Based on Protein-Protein Interaction Network and Gene Expression Data. , 2018, , .   |     | 12        |
| 27 | Prediction of Drugâ€™Drug Interactions Based on Multiâ€™layer Feature Selection and Data Balance. <i>Chinese Journal of Electronics</i> , 2017, 26, 585-590.  | 1.5 | 4         |
| 28 | Effective prediction of three common diseases by combining SMOTE with Tomek links technique for imbalanced medical data. , 2016, , .  |     | 84        |