

# Cong Shen

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1679690/publications.pdf>

Version: 2024-02-01

11  
papers

149  
citations

1478280

6  
h-index

1474057

9  
g-index

11  
all docs

11  
docs citations

11  
times ranked

72  
citing authors

#	ARTICLE	IF	CITATIONS
1	Multi-view Multichannel Attention Graph Convolutional Network for miRNA-disease association prediction. Briefings in Bioinformatics, 2021, 22, .	3.2	74
2	Incorporating Multisource Knowledge To Predict Drug Synergy Based on Graph Co-regularization. Journal of Chemical Information and Modeling, 2020, 60, 37-46.	2.5	14
3	Multiview Joint Learning-Based Method for Identifying Small-Molecule-Associated MiRNAs by Integrating Pharmacological, Genomics, and Network Knowledge. Journal of Chemical Information and Modeling, 2020, 60, 4085-4097.	2.5	13
4	Incorporating Clinical, Chemical and Biological Information for Predicting Small Molecule-microRNA Associations Based on Non-Negative Matrix Factorization. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2535-2545.	1.9	13
5	IDDKin: network-based influence deep diffusion model for enhancing prediction of kinase inhibitors. Bioinformatics, 2021, 36, 5481-5491.	1.8	13
6	Identification of Small Molecule-miRNA Associations with Graph Regularization Techniques in Heterogeneous Networks. Journal of Chemical Information and Modeling, 2020, 60, 6709-6721.	2.5	11
7	An In Silico Method for Predicting Drug Synergy Based on Multitask Learning. Interdisciplinary Sciences, Computational Life Sciences, 2021, 13, 299-311.	2.2	4
8	Metapath-Based Deep Convolutional Neural Network for Predicting miRNA-Target Association on Heterogeneous Network. Interdisciplinary Sciences, Computational Life Sciences, 2021, 13, 547-558.	2.2	3
9	Improving the Prediction of Potential Kinase Inhibitors with Feature Learning on Multisource Knowledge. Interdisciplinary Sciences, Computational Life Sciences, 2022, 14, 775-785.	2.2	3
10	Graph Attention Mechanism-based Deep Tensor Factorization for Predicting disease-associated miRNA-miRNA pairs. , 2021, , .		1
11	A Graph Convolutional Matrix Completion Method for miRNA-Disease Association Prediction. Lecture Notes in Computer Science, 2020, , 201-215.	1.0	0