Cong Shen

List of Publications by Year in descending order

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

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		1478280	1474057
11	149	6	9
papers	citations	h-index	g-index
11	11	11	72
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	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
2	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
3	An In Silico Method for Predicting Drug Synergy Based on Multitask Learning. Interdisciplinary Sciences, Computational Life Sciences, 2021, 13, 299-311.	2.2	4
4	Multi-view Multichannel Attention Graph Convolutional Network for miRNA–disease association prediction. Briefings in Bioinformatics, 2021, 22, .	3.2	74
5	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
6	IDDkin: network-based influence deep diffusion model for enhancing prediction of kinase inhibitors. Bioinformatics, 2021, 36, 5481-5491.	1.8	13
7	Graph Attention Mechanism-based Deep Tensor Factorization for Predicting disease-associated miRNA-miRNA pairs. , 2021, , .		1
8	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
9	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
10	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
11	A Graph Convolutional Matrix Completion Method for miRNA-Disease Association Prediction. Lecture Notes in Computer Science, 2020, , 201-215.	1.0	0