Cheng Yan

List of Publications by Year
in descending order

15	312	1163117 8	1125743 13
papers	citations	h-index	g-index

15	15	15	211
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	DWNN-RLS: regularized least squares method for predicting circRNA-disease associations. BMC Bioinformatics, 2018, 19, 520.	2.6	68
2	DNRLMF-MDA:Predicting microRNA-Disease Associations Based on Similarities of microRNAs and Diseases. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 233-243.	3.0	59
3	BRWMDA:Predicting microbe-disease associations based on similarities and bi-random walk on disease and microbe networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 17, 1-1.	3.0	33
4	Predicting Drug-Drug Interactions Based on Integrated Similarity and Semi-Supervised Learning. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 168-179.	3.0	30
5	DDIGIP: predicting drug-drug interactions based on Gaussian interaction profile kernels. BMC Bioinformatics, 2019, 20, 538.	2.6	24
6	MCHMDA:Predicting Microbe-Disease Associations Based on Similarities and Low-Rank Matrix Completion. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 611-620.	3.0	21
7	SDTRLS: Predicting Drug-Target Interactions for Complex Diseases Based on Chemical Substructures. Complexity, 2017, 2017, 1-10.	1.6	15
8	A survey on predicting microbe-disease associations: biological data and computational methods. Briefings in Bioinformatics, 2021, 22, .	6.5	15
9	A Novel Drug Repositioning Approach Based on Collaborative Metric Learning. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 463-471.	3.0	11
10	PESM: predicting the essentiality of miRNAs based on gradient boosting machines and sequences. BMC Bioinformatics, 2020, 21, 111.	2.6	10
11	Prediction of Microbe-drug Associations Based on Chemical Structures and the KATZ Measure. Current Bioinformatics, 2021, 16, 807-819.	1.5	10
12	IILLS: predicting virus-receptor interactions based on similarity and semi-supervised learning. BMC Bioinformatics, 2019, 20, 651.	2.6	8
13	A novel approach based on deep residual learning to predict drugâ€™s anatomical therapeutic chemical code. , 2020, , .		4
14	Prediction of Virusâ€“Receptor Interactions Based on Improving Similarities. Journal of Computational Biology, 2021, 28, 650-659.	1.6	3
15	Identifying virus-receptor interactions through matrix completion with similarity fusion. , 2021, , .		1