Feng Huang

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/240395/publications.pdf

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10	699	8 h-index	8
papers	citations		g-index
10	10	10	411 citing authors
all docs	docs citations	times ranked	

#	Article	IF	CITATIONS
1	MVGCN: data integration through multi-view graph convolutional network for predicting links in biomedical bipartite networks. Bioinformatics, 2022, 38, 426-434.	4.1	40
2	A heterogeneous network-based method with attentive meta-path extraction for predicting drug $\hat{a} \in \text{``target interactions.}$ Briefings in Bioinformatics, 2022, 23, .	6.5	15
3	A Fast Linear Neighborhood Similarity-Based Network Link Inference Method to Predict MicroRNA-Disease Associations. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 405-415.	3.0	89
4	Predicting Drug-Disease Associations via Multi-Task Learning Based on Collective Matrix Factorization. Frontiers in Bioengineering and Biotechnology, 2020, 8, 218.	4.1	17
5	Prediction of Drug-Disease Associations and Their Effects by Signed Network-Based Nonnegative Matrix Factorization. , $2018, , .$		8
6	HNGRNMF: Heterogeneous Network-based Graph Regularized Nonnegative Matrix Factorization for predicting events of microbe-disease associations. , 2018, , .		6
7	SFPEL-LPI: Sequence-based feature projection ensemble learning for predicting LncRNA-protein interactions. PLoS Computational Biology, 2018, 14, e1006616.	3.2	164
8	The Bi-Direction Similarity Integration Method for Predicting Microbe-Disease Associations. IEEE Access, 2018, 6, 38052-38061.	4.2	50
9	Predicting drug-disease associations by using similarity constrained matrix factorization. BMC Bioinformatics, 2018, 19, 233.	2.6	206
10	Predicting drug-disease associations and their therapeutic function based on the drug-disease association bipartite network. Methods, 2018, 145, 51-59.	3.8	104