

# Feng Huang

## List of Publications by Year in descending order

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

Version: 2024-02-01

10  
papers

699  
citations

1163117

8  
h-index

1588992

8  
g-index

10  
all docs

10  
docs citations

10  
times ranked

411  
citing authors

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