

Weitai Yang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3034751/publications.pdf>

Version: 2024-02-01

21
papers

1,082
citations

687363

13
h-index

940533

16
g-index

21
all docs

21
docs citations

21
times ranked

624
citing authors

#	ARTICLE	IF	CITATIONS
1	Predicting potential drug-drug interactions by integrating chemical, biological, phenotypic and network data. <i>BMC Bioinformatics</i> , 2017, 18, 18.	2.6	231
2	The linear neighborhood propagation method for predicting long non-coding RNA-protein interactions. <i>Neurocomputing</i> , 2018, 273, 526-534.	5.9	171
3	A Fast Linear Neighborhood Similarity-Based Network Link Inference Method to Predict MicroRNA-Disease Associations. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 405-415.	3.0	89
4	A unified frame of predicting side effects of drugs by using linear neighborhood similarity. <i>BMC Systems Biology</i> , 2017, 11, 101.	3.0	70
5	Drug-Target Interaction Prediction through Label Propagation with Linear Neighborhood Information. <i>Molecules</i> , 2017, 22, 2056.	3.8	68
6	A network embedding-based multiple information integration method for the MiRNA-disease association prediction. <i>BMC Bioinformatics</i> , 2019, 20, 468.	2.6	62
7	Accurate Prediction of Transposon-Derived piRNAs by Integrating Various Sequential and Physicochemical Features. <i>PLoS ONE</i> , 2016, 11, e0153268.	2.5	52
8	Tensor decomposition with relational constraints for predicting multiple types of microRNA-disease associations. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	50
9	LncRNA-miRNA interaction prediction through sequence-derived linear neighborhood propagation method with information combination. <i>BMC Genomics</i> , 2019, 20, 946.	2.8	49
10	Predicting CircRNA-Disease Associations Through Linear Neighborhood Label Propagation Method. <i>IEEE Access</i> , 2019, 7, 83474-83483.	4.2	48
11	MVGCN: data integration through multi-view graph convolutional network for predicting links in biomedical bipartite networks. <i>Bioinformatics</i> , 2022, 38, 426-434.	4.1	40
12	Drug side effect prediction through linear neighborhoods and multiple data source integration. , 2016, , .		39
13	Predicting drug-disease associations based on the known association bipartite network. , 2017, , .		24
14	ACP-DA: Improving the Prediction of Anticancer Peptides Using Data Augmentation. <i>Frontiers in Genetics</i> , 2021, 12, 698477.	2.3	22
15	Predicting gene-disease associations from the heterogeneous network using graph embedding. , 2019, , .		21
16	SGNNMD: signed graph neural network for predicting deregulation types of miRNA-disease associations. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	14
17	LncRNA-miRNA interaction prediction from the heterogeneous network through graph embedding ensemble learning. , 2019, , .		12
18	MiRNA-Drug Resistance Association Prediction Through the Attentive Multimodal Graph Convolutional Network. <i>Frontiers in Pharmacology</i> , 2021, 12, 799108.	3.5	9

#	ARTICLE	IF	CITATIONS
19	ItLnc-BXE: A Bagging-XGBoost-Ensemble Method With Comprehensive Sequence Features for Identification of Plant lncRNAs. IEEE Access, 2020, 8, 68811-68819.	4.2	5
20	Detection of Cell Types from Single-cell RNA-seq Data using Similarity via Kernel Preserving Learning Embedding. , 2019, , .		4
21	Predicting Long non-coding RNAs through feature ensemble learning. BMC Genomics, 2020, 21, 865.	2.8	2