

Yasser El-Manzalawy

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

19
papers

241
citations

8
h-index

15
g-index

23
ext. papers

305
ext. citations

3.7
avg, IF

3.37
L-index

#	Paper	IF	Citations
19	RNABindRPlus: a predictor that combines machine learning and sequence homology-based methods to improve the reliability of predicted RNA-binding residues in proteins. <i>PLoS ONE</i> , 2014 , 9, e97725	3.7	71
18	On evaluating MHC-II binding peptide prediction methods. <i>PLoS ONE</i> , 2008 , 3, e3268	3.7	32
17	Min-redundancy and max-relevance multi-view feature selection for predicting ovarian cancer survival using multi-omics data. <i>BMC Medical Genomics</i> , 2018 , 11, 71	3.7	24
16	DockRank: ranking docked conformations using partner-specific sequence homology-based protein interface prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014 , 82, 250-67	4.2	22
15	Personalized Sleep Parameters Estimation from Actigraphy: A Machine Learning Approach. <i>Nature and Science of Sleep</i> , 2019 , 11, 387-399	3.6	15
14	Biomarker discovery in inflammatory bowel diseases using network-based feature selection. <i>PLoS ONE</i> , 2019 , 14, e0225382	3.7	14
13	FastRNABindR: Fast and Accurate Prediction of Protein-RNA Interface Residues. <i>PLoS ONE</i> , 2016 , 11, e0158445	3.7	13
12	PlasmoSEP: Predicting surface-exposed proteins on the malaria parasite using semisupervised self-training and expert-annotated data. <i>Proteomics</i> , 2016 , 16, 2967-2976	4.8	10
11	CCA based multi-view feature selection for multi-omics data integration 2018 ,		8
10	Assessing the effects of data selection and representation on the development of reliable E. coli sigma 70 promoter region predictors. <i>PLoS ONE</i> , 2015 , 10, e0119721	3.7	8
9	Microbiomarkers Discovery in Inflammatory Bowel Diseases using Network-Based Feature Selection 2018 ,		6
8	Machine learning based refined differential gene expression analysis of pediatric sepsis. <i>BMC Medical Genomics</i> , 2020 , 13, 122	3.7	5
7	Partner-specific prediction of RNA-binding residues in proteins: A critical assessment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019 , 87, 198-211	4.2	3
6	Predictive and Comparative Network Analysis of the Gut Microbiota in Type 2 Diabetes 2017 ,		2
5	OASIS +: leveraging machine learning to improve the prognostic accuracy of OASIS severity score for predicting in-hospital mortality. <i>BMC Medical Informatics and Decision Making</i> , 2021 , 21, 156	3.6	2
4	CCA based multi-view feature selection for multi-omics data integration		1
3	Proxi: a Python package for proximity network inference from metagenomic data		1

2	Min-Redundancy and Max-Relevance Multi-view Feature Selection for Predicting Ovarian Cancer Survival using Multi-omics Data	1
1	Biomarker discovery in inflammatory bowel diseases using network-based feature selection	1