Yasser El-Manzalawy

List of Publications by Year
in descending order

15 papers	**362** citations

1039406

9 h-index	

1199166

12 g-index	

23 all docs	**23** docs citations

23 times ranked	**592** citing authors

#	Article	IF	Citations
1	RNABindRPlus: A Predictor that Combines Machine Learning and Sequence Homology-Based Methods to Improve the Reliability of Predicted RNA-Binding Residues in Proteins. PLoS ONE, 2014, 9, e97725.	1.1	95
2	On Evaluating MHC-II Binding Peptide Prediction Methods. PLoS ONE, 2008, 3, e3268.	1.1	46
3	Min-redundancy and max-relevance multi-view feature selection for predicting ovarian cancer survival using multi-omics data. BMC Medical Genomics, 2018, 11, 71.	0.7	41
4	<p>Personalized Sleep Parameters Estimation from Actigraphy: A Machine Learning Approach</p>. Nature and Science of Sleep, 2019, Volume 11, 387-399.	1.4	32
5	Machine learning based refined differential gene expression analysis of pediatric sepsis. BMC Medical Genomics, 2020, 13, 122.	0.7	32
6	DockRank: Ranking docked conformations using partner-specific sequence homology-based protein interface prediction. Proteins: Structure, Function and Bioinformatics, 2014, 82, 250-267.	1.5	28
7	Biomarker discovery in inflammatory bowel diseases using network-based feature selection. PLoS ONE, 2019, 14, e0225382.	1.1	17
8	FastRNABindR: Fast and Accurate Prediction of Protein-RNA Interface Residues. PLoS ONE, 2016, 11, e0158445.	1.1	14
9	PlasmoSEP: Predicting surface-exposed proteins on the malaria parasite using semisupervised self-training and expert-annotated data. Proteomics, 2016, 16, 2967-2976.	1.3	13
10	Assessing the Effects of Data Selection and Representation on the Development of Reliable E. coli Sigma 70 Promoter Region Predictors. PLoS ONE, 2015, 10, e0119721.	1.1	9
11	CCA based multi-view feature selection for multi-omics data integration. , 2018, , .		8
12	Microbiomarkers Discovery in Inflammatory Bowel Diseases using Network-Based Feature Selection. , 2018, , .		6
13	Partner-specific prediction of RNA-binding residues in proteins: A critical assessment. Proteins: Structure, Function and Bioinformatics, 2019, 87, 198-211.	1.5	6
14	OASIS+: leveraging machine learning to improve the prognostic accuracy of OASIS severity score for predicting in-hospital mortality. BMC Medical Informatics and Decision Making, 2021, 21, 156.	1.5	3
15	Predictive and Comparative Network Analysis of the Gut Microbiota in Type 2 Diabetes. , 2017, , .		2