Yasser El-Manzalawy

List of Publications by Year in Descending Order

Source: https://exaly.com/author-pdf/4636977/yasser-el-manzalawy-publications-by-year.pdf
Version: 2024-04-24

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	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	3.6	2
18	Machine learning based refined differential gene expression analysis of pediatric sepsis. *BMC Medical Genomics*, **2020**, 13, 122	3.7	5
17	Biomarker discovery in inflammatory bowel diseases using network-based feature selection. *PLoS ONE*, **2019**, 14, e0225382	3.7	14
16	Personalized Sleep Parameters Estimation from Actigraphy: A Machine Learning Approach. *Nature and Science of Sleep*, **2019**, 11, 387-399	3.6	15
15	Partner-specific prediction of RNA-binding residues in proteins: A critical assessment. *Proteins: Structure, Function and Bioinformatics*, **2019**, 87, 198-211	4.2	3
14	CCA based multi-view feature selection for multi-omics data integration **2018**,		8
13	Min-redundancy and max-relevance multi-view feature selection for predicting ovarian cancer survival using multi-omics data. *BMC Medical Genomics*, **2018**, 11, 71	3.7	24
12	Microbiomarkers Discovery in Inflammatory Bowel Diseases using Network-Based Feature Selection **2018**,		6
11	Predictive and Comparative Network Analysis of the Gut Microbiota in Type 2 Diabetes **2017**,		2
10	FastRNABindR: Fast and Accurate Prediction of Protein-RNA Interface Residues. *PLoS ONE*, **2016**, 11, e0158445	3.7	13
9	PlasmoSEP: Predicting surface-exposed proteins on the malaria parasite using semisupervised self-training and expert-annotated data. *Proteomics*, **2016**, 16, 2967-2976	4.8	10
8	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	3.7	8
7	DockRank: ranking docked conformations using partner-specific sequence homology-based protein interface prediction. *Proteins: Structure, Function and Bioinformatics*, **2014**, 82, 250-67	4.2	22
6	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	3.7	71
5	On evaluating MHC-II binding peptide prediction methods. *PLoS ONE*, **2008**, 3, e3268	3.7	32
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

List of Publications

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