Indika Kahanda

List of Publications by Year in descending order

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1478505 1125743 30 773 13 6 citations h-index g-index papers 41 41 41 879 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	8.8	308
2	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. Genome Biology, 2019, 20, 244.	8.8	261
3	PHENOstruct: Prediction of human phenotype ontology terms using heterogeneous data sources. F1000Research, 2015, 4, 259.	1.6	31
4	Genetic dissection of natural variation in oilseed traits of camelina by wholeâ€genome resequencing and QTL mapping. Plant Genome, 2021, 14, e20110.	2.8	24
5	Evaluating a variety of text-mined features for automatic protein function prediction with GOstruct. Journal of Biomedical Semantics, 2015, 6, 9.	1.6	20
6	A close look at protein function prediction evaluation protocols. GigaScience, 2015, 4, 41.	6.4	18
7	Quality assurance of bioinformatics software., 2018,,.		12
8	Pangenome-Wide Association Studies with Frequented Regions. , 2019, , .		10
9	Exploring Frequented Regions in Pan-Genomic Graphs. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1424-1435.	3.0	9
10	GOstruct 2.0., 2017, , .		8
11	Automatically Generating Psychiatric Case Notes From Digital Transcripts of Doctor-Patient Conversations. , 2019, , .		7
12	DeepACPpred: A Novel Hybrid CNN-RNN Architecture for Predicting Anti-Cancer Peptides. Advances in Intelligent Systems and Computing, 2021, , 60-69.	0.6	6
13	Relational similarity model for suggesting friends in online social networks. , 2011, , .		5
14	PPPred., 2019,,.		4
15	Metamorphic Testing for Quality Assurance of Protein Function Prediction Tools. , 2019, , .		4
16	MRpredT. , 2020, , .		4
17	Exploring Frequented Regions in Pan-Genomic Graphs. , 2017, , .		3
18	Overview of the BioCreative VI text-mining services for Kinome Curation Track. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	3

#	Article	lF	CITATIONS
19	ProPheno 1.0: An Online Dataset for Accelerating the Complete Characterization of the Human Protein-Phenotype Landscape in Biomedical Literature. , 2020, , .		3
20	Computational methods for the ab initio identification of novel microRNA in plants: a systematic review. PeerJ Computer Science, 2019, 5, e233.	4.5	3
21	BioSGAN: Protein-Phenotype Co-mention Classification Using Semi-Supervised Generative Adversarial Networks. , 2021, , .		2
22	miRNAFinder: A pre-microRNA classifier for plants and analysis of feature impact. , 2020, , .		1
23	Psychiatry Transcript Annotation: Process Study and Improvements. Proceedings of the International Symposium of Human Factors and Ergonomics in Healthcare, 2021, 10, 71-75.	0.3	1
24	Poster: Pangenome-Wide Association Studies with Frequented Regions. , 2019, , .		1
25	Deep semi-supervised learning ensemble framework for classifying co-mentions of human proteins and phenotypes. BMC Bioinformatics, 2021, 22, 500.	2.6	1
26	RDoC Task at BioNLP-OST 2019. , 2019, , .		1
27	miRNAFinder: A comprehensive web resource for plant Pre-microRNA classification. BioSystems, 2022, 215-216, 104662.	2.0	1
28	RDoCer: Information Retrieval and Sentence Extraction for Mental Health using Research Domain Criteria. , $2020, , .$		0
29	Vegetation Coverage in Marsh Grass Photography Using Convolutional Neural Networks. Proceedings of the International Florida Artificial Intelligence Research Society Conference, 2021, 34, .	0.3	0
30	DeepPPPred: Deep Ensemble Learning with Transformers, Recurrent and Convolutional Neural Networks for Human Protein-Phenotype Co-mention Classification., 2021,,.		0