

Ashish Anand

List of Publications by Year in descending order

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Version: 2024-02-01

22
papers

1,017
citations

1477746

6
h-index

887659

17
g-index

25
all docs

25
docs citations

25
times ranked

1062
citing authors

#	ARTICLE	IF	CITATIONS
1	A New Family of Similarity Measures for Scoring Confidence of Protein Interactions Using Gene Ontology. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 19-30.	1.9	3
2	Rapid Reconstruction of Time-varying Gene Regulatory Networks with Limited Main Memory. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1608-1619.	1.9	1
3	IQ-VQA: Intelligent Visual Question Answering. Lecture Notes in Computer Science, 2021, , 357-370.	1.0	2
4	Rapid Reconstruction of Time-Varying Gene Regulatory Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 278-291.	1.9	3
5	Impact of the Continuous Evolution of Gene Ontology on the Performance of Similarity Measures for Scoring Confidence of Protein Interactions. SN Computer Science, 2020, 1, 1.	2.3	1
6	Impact of low-confidence interactions on computational identification of protein complexes. Journal of Bioinformatics and Computational Biology, 2020, 18, 2050025.	0.3	2
7	Fog Computing: A New Era of Cloud Computing. , 2019, , .		13
8	Impact of the Continuous Evolution of Gene Ontology on Similarity Measures. Lecture Notes in Computer Science, 2019, , 122-129.	1.0	3
9	What matters in a transferable neural network model for relation classification in the biomedical domain?. Artificial Intelligence in Medicine, 2018, 87, 60-66.	3.8	6
10	Drug-drug interaction extraction from biomedical texts using long short-term memory network. Journal of Biomedical Informatics, 2018, 86, 15-24.	2.5	124
11	Relation extraction from clinical texts using domain invariant convolutional neural network. , 2016, , .		56
12	Detection of Highly Overlapping Communities in Complex Networks. Journal of Medical Imaging and Health Informatics, 2015, 5, 1099-1103.	0.2	2
13	An approach for classification of highly imbalanced data using weighting and undersampling. Amino Acids, 2010, 39, 1385-1391.	1.2	134
14	Identification and analysis of transcription factor family-specific features derived from DNA and protein information. Pattern Recognition Letters, 2010, 31, 2097-2102.	2.6	2
15	Integration of functional information of genes in fuzzy clustering of short time series gene expression data. , 2010, , .		0
16	Multiclass cancer classification by support vector machines with class-wise optimized genes and probability estimates. Journal of Theoretical Biology, 2009, 259, 533-540.	0.8	35
17	Predicting protein structural class by SVM with class-wise optimized features and decision probabilities. Journal of Theoretical Biology, 2008, 253, 375-380.	0.8	55
18	Prediction of Transcription Factor Families Using DNA Sequence Features. Lecture Notes in Computer Science, 2008, , 154-164.	1.0	1

#	ARTICLE	IF	CITATIONS
19	A novel fuzzy and multiobjective evolutionary algorithm based gene assignment for clustering short time series expression data. , 2007, , .		3
20	Feature Selection Approach for Quantitative Prediction of Transcriptional Activities. , 2006, , .		3
21	Disruption of the murine PIASx gene results in reduced testis weight. Journal of Molecular Endocrinology, 2005, 34, 645-654.	1.1	48
22	A Computationally Efficient Evolutionary Algorithm for Real-Parameter Optimization. Evolutionary Computation, 2002, 10, 371-395.	2.3	517