

# Ashish Anand

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2406102/publications.pdf>

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 Computationally Efficient Evolutionary Algorithm for Real-Parameter Optimization. <i>Evolutionary Computation</i> , 2002, 10, 371-395.	2.3	517
2	An approach for classification of highly imbalanced data using weighting and undersampling. <i>Amino Acids</i> , 2010, 39, 1385-1391.	1.2	134
3	Drug-drug interaction extraction from biomedical texts using long short-term memory network. <i>Journal of Biomedical Informatics</i> , 2018, 86, 15-24.	2.5	124
4	Relation extraction from clinical texts using domain invariant convolutional neural network. , 2016, , .		56
5	Predicting protein structural class by SVM with class-wise optimized features and decision probabilities. <i>Journal of Theoretical Biology</i> , 2008, 253, 375-380.	0.8	55
6	Disruption of the murine PIASx gene results in reduced testis weight. <i>Journal of Molecular Endocrinology</i> , 2005, 34, 645-654.	1.1	48
7	Multiclass cancer classification by support vector machines with class-wise optimized genes and probability estimates. <i>Journal of Theoretical Biology</i> , 2009, 259, 533-540.	0.8	35
8	Fog Computing: A New Era of Cloud Computing. , 2019, , .		13
9	What matters in a transferable neural network model for relation classification in the biomedical domain?. <i>Artificial Intelligence in Medicine</i> , 2018, 87, 60-66.	3.8	6
10	Feature Selection Approach for Quantitative Prediction of Transcriptional Activities. , 2006, , .		3
11	A novel fuzzy and multiobjective evolutionary algorithm based gene assignment for clustering short time series expression data. , 2007, , .		3
12	Rapid Reconstruction of Time-Varying Gene Regulatory Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 17, 278-291.	1.9	3
13	A New Family of Similarity Measures for Scoring Confidence of Protein Interactions Using Gene Ontology. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 19-30.	1.9	3
14	Impact of the Continuous Evolution of Gene Ontology on Similarity Measures. <i>Lecture Notes in Computer Science</i> , 2019, , 122-129.	1.0	3
15	Identification and analysis of transcription factor family-specific features derived from DNA and protein information. <i>Pattern Recognition Letters</i> , 2010, 31, 2097-2102.	2.6	2
16	Detection of Highly Overlapping Communities in Complex Networks. <i>Journal of Medical Imaging and Health Informatics</i> , 2015, 5, 1099-1103.	0.2	2
17	Impact of low-confidence interactions on computational identification of protein complexes. <i>Journal of Bioinformatics and Computational Biology</i> , 2020, 18, 2050025.	0.3	2
18	IQ-VQA: Intelligent Visual Question Answering. <i>Lecture Notes in Computer Science</i> , 2021, , 357-370.	1.0	2

#	ARTICLE	IF	CITATIONS
19	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
20	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
21	Prediction of Transcription Factor Families Using DNA Sequence Features. Lecture Notes in Computer Science, 2008, , 154-164.	1.0	1
22	Integration of functional information of genes in fuzzy clustering of short time series gene expression data. , 2010, , .		0