

Swarup Roy

List of Publications by Year in descending order

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Version: 2024-02-01

47
papers

449
citations

840776

11
h-index

794594

19
g-index

54
all docs

54
docs citations

54
times ranked

461
citing authors

#	ARTICLE	IF	CITATIONS
1	Complex Network Visualisation Using JavaScript: A Review. Lecture Notes in Networks and Systems, 2022, , 45-53.	0.7	4
2	Mapping sequence to feature vector using numerical representation of codons targeted to amino acids for alignment-free sequence analysis. Gene, 2021, 766, 145096.	2.2	11
3	Overlapping Community Detection in Static and Dynamic Networks: A Qualitative Assessment. Lecture Notes in Networks and Systems, 2021, , 113-123.	0.7	0
4	Data science in unveiling COVID-19 pathogenesis and diagnosis: evolutionary origin to drug repurposing. Briefings in Bioinformatics, 2021, 22, 855-872.	6.5	38
5	Characterizing genomic variants and mutations in SARS-CoV-2 proteins from Indian isolates. Gene Reports, 2021, 25, 101044.	0.8	22
6	A study on non-synonymous mutational patterns in structural proteins of SARS-CoV-2. Genome, 2021, 64, 1-14.	2.0	15
7	A scheme for inferring viral-host associations based on codon usage patterns identifies the most affected signaling pathways during COVID-19. Journal of Biomedical Informatics, 2021, 118, 103801.	4.3	11
8	Comparative analysis of human coronaviruses focusing on nucleotide variability and synonymous codon usage patterns. Genomics, 2021, 113, 2177-2188.	2.9	15
9	Analyzing host-viral interactome of SARS-CoV-2 for identifying vulnerable host proteins during COVID-19 pathogenesis. Infection, Genetics and Evolution, 2021, 93, 104921.	2.3	21
10	pARACNE: A Parallel Inference Platform for Gene Regulatory Network Using ARACNe. Advances in Intelligent Systems and Computing, 2021, , 85-92.	0.6	3
11	Mutation-Induced Long-Range Allosteric Interactions in the Spike Protein Determine the Infectivity of SARS-CoV-2 Emerging Variants. ACS Omega, 2021, 6, 31305-31320.	3.5	8
12	Assessing the Effectiveness of Causality Inference Methods for Gene Regulatory Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 56-70.	3.0	12
13	Prioritizing disease biomarkers using functional module based network analysis: A multilayer consensus driven scheme. Computers in Biology and Medicine, 2020, 126, 104023.	7.0	7
14	Preliminaries of graph theory. , 2020, , 7-24.		0
15	Gene expression networks: inference and analysis. , 2020, , 95-131.		0
16	Graph analysis. , 2020, , 25-51.		0
17	InOvIn: A fuzzy-rough approach for detecting overlapping communities with intrinsic structures in evolving networks. Applied Soft Computing Journal, 2020, 89, 106096.	7.2	15
18	Inference and analysis of gene regulatory networks using data mining techniques. ACM SIGBioinformatics Record, 2020, 10, 1-2.	0.3	0

#	ARTICLE	IF	CITATIONS
19	Functional module extraction from gene expression data using data mining techniques. ACM SIGBioinformatics Record, 2020, 10, 1-2.	0.3	0
20	Pre-Processing: A Data Preparation Step. , 2019, , 463-471.		6
21	Detecting intrinsic communities in evolving networks. Social Network Analysis and Mining, 2019, 9, 1.	2.8	9
22	Functional module extraction by ensembling the ensembles of selective module detectors. International Journal of Computational Biology and Drug Design, 2019, 12, 345.	0.3	2
23	A data reduction scheme for active authentication of legitimate smartphone owner using informative apps ranking. Digital Communications and Networks, 2019, 5, 205-213.	5.0	5
24	Qualitative assessment of functional module detectors on microarray and RNASeq data. Network Modeling Analysis in Health Informatics and Bioinformatics, 2019, 8, 1.	2.1	12
25	Inferring Causal Gene Regulatory Networks Using Time-Delay Association Rules. Communications in Computer and Information Science, 2019, , 310-321.	0.5	1
26	A detection framework for semantic code clones and obfuscated code. Expert Systems With Applications, 2018, 97, 405-420.	7.6	28
27	Chemical Characterization of Interacting Genes in Few Subnetworks of Alzheimer's Disease. , 2018, , .		2
28	Intrinsic-overlapping co-expression module detection with application to Alzheimer's Disease. Computational Biology and Chemistry, 2018, 77, 373-389.	2.3	16
29	Network based algorithms for module extraction from RNASeq data: A quantitative assessment. , 2017, , .		0
30	Incremental Approach for Detecting Arbitrary and Embedded Cluster Structures. Lecture Notes in Computer Science, 2016, , 220-233.	1.3	1
31	Big data analytics in bioinformatics: architectures, techniques, tools and issues. Network Modeling Analysis in Health Informatics and Bioinformatics, 2016, 5, 1.	2.1	28
32	Computational Methods for Detecting Functional Modules from Gene Regulatory Network. , 2016, , .		4
33	Issues in Quantitative Association Rule Mining: A Big Data Perspective. Advances in Intelligent Systems and Computing, 2016, , 377-385.	0.6	3
34	Segmentation of cortical gray and white matters from MRI using density based clustering approach. , 2015, , .		0
35	A new equivalence class based approach for discretizing quantitative data using Point Shift Mechanism. , 2015, , .		1
36	Towards the assessment of GRN algorithms based on (disease) ontology. , 2015, , .		1

#	ARTICLE	IF	CITATIONS
37	MODULA: A network module based local protein interaction network alignment method. , 2015, , .		5
38	Tools for in-Silico Reconstruction and Visualization of Gene Regulatory Networks (GRN). , 2015, , .		3
39	Unsupervised methods for finding protein complexes from PPI networks. Network Modeling Analysis in Health Informatics and Bioinformatics, 2015, 4, 1.	2.1	7
40	Analysis of Gene Expression Patterns Using Biclustering. Methods in Molecular Biology, 2015, 1375, 91-103.	0.9	3
41	Trends in quantitative association rule mining techniques. , 2015, , .		9
42	Biological Network Inference from Microarray Data, Current Solutions, and Assessments. Methods in Molecular Biology, 2015, 1375, 155-167.	0.9	5
43	Detecting protein complexes using connectivity among nodes in a PPI Network. Network Modeling Analysis in Health Informatics and Bioinformatics, 2015, 4, 1.	2.1	2
44	Reconstruction of gene co-expression network from microarray data using local expression patterns. BMC Bioinformatics, 2014, 15, S10.	2.6	75
45	CoBi: Pattern Based Co-Regulated Biclustering of Gene Expression Data. Pattern Recognition Letters, 2013, 34, 1669-1678.	4.2	30
46	Mining strongly correlated item pairs in large transaction databases. International Journal of Data Mining, Modelling and Management, 2013, 5, 76.	0.1	4
47	Causality Inference Techniques for In-Silico Gene Regulatory Network. Lecture Notes in Computer Science, 2013, , 432-443.	1.3	4