# Swarup Roy

List of Publications by Year
in descending order

| | | | |
|---|---|---|---|
| 47 papers | 449 citations | 840776<br>11 h-index | 794594<br>19 g-index |
| 54 all docs | 54 docs citations | 54 times ranked | 461 citing authors |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 1 | Reconstruction of gene co-expression network from microarray data using local expression patterns. BMC Bioinformatics, 2014, 15, S10. | 2.6 | 75 |
| 2 | Data science in unveiling COVID-19 pathogenesis and diagnosis: evolutionary origin to drug repurposing. Briefings in Bioinformatics, 2021, 22, 855-872. | 6.5 | 38 |
| 3 | CoBi: Pattern Based Co-Regulated Biclustering of Gene Expression Data. Pattern Recognition Letters, 2013, 34, 1669-1678. | 4.2 | 30 |
| 4 | Big data analytics in bioinformatics: architectures, techniques, tools and issues. Network Modeling Analysis in Health Informatics and Bioinformatics, 2016, 5, 1. | 2.1 | 28 |
| 5 | A detection framework for semantic code clones and obfuscated code. Expert Systems With Applications, 2018, 97, 405-420. | 7.6 | 28 |
| 6 | Characterizing genomic variants and mutations in SARS-CoV-2 proteins from Indian isolates. Gene Reports, 2021, 25, 101044. | 0.8 | 22 |
| 7 | 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 |
| 8 | Intrinsic-overlapping co-expression module detection with application to Alzheimer's Disease. Computational Biology and Chemistry, 2018, 77, 373-389. | 2.3 | 16 |
| 9 | A study on non-synonymous mutational patterns in structural proteins of SARS-CoV-2. Genome, 2021, 64, 1-14. | 2.0 | 15 |
| 10 | Comparative analysis of human coronaviruses focusing on nucleotide variability and synonymous codon usage patterns. Genomics, 2021, 113, 2177-2188. | 2.9 | 15 |
| 11 | 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 |
| 12 | 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 |
| 13 | 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 |
| 14 | 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 |
| 15 | 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 |
| 16 | Trends in quantitative association rule mining techniques. , 2015, , . | | 9 |
| 17 | Detecting intrinsic communities in evolving networks. Social Network Analysis and Mining, 2019, 9, 1. | 2.8 | 9 |
| 18 | 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 |

| # | Article | IF | Citations |
|---|---------|----|-----------|
| 19 | Unsupervised methods for finding protein complexes from PPI networks. Network Modeling Analysis in Health Informatics and Bioinformatics, 2015, 4, 1. | 2.1 | 7 |
| 20 | 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 |
| 21 | Pre-Processing: A Data Preparation Step. , 2019, , 463-471. |  | 6 |
| 22 | MODULA: A network module based local protein interaction network alignment method. , 2015, , . |  | 5 |
| 23 | Biological Network Inference from Microarray Data, Current Solutions, and Assessments. Methods in Molecular Biology, 2015, 1375, 155-167. | 0.9 | 5 |
| 24 | 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 |
| 25 | Mining strongly correlated item pairs in large transaction databases. International Journal of Data Mining, Modelling and Management, 2013, 5, 76. | 0.1 | 4 |
| 26 | Computational Methods for Detecting Functional Modules from Gene Regulatory Network. , 2016, , . |  | 4 |
| 27 | Causality Inference Techniques for In-Silico Gene Regulatory Network. Lecture Notes in Computer Science, 2013, , 432-443. | 1.3 | 4 |
| 28 | Complex Network Visualisation Using JavaScript: A Review. Lecture Notes in Networks and Systems, 2022, , 45-53. | 0.7 | 4 |
| 29 | Tools for in-Silico Reconstruction and Visualization of Gene Regulatory Networks (GRN). , 2015, , . |  | 3 |
| 30 | Analysis of Gene Expression Patterns Using Biclustering. Methods in Molecular Biology, 2015, 1375, 91-103. | 0.9 | 3 |
| 31 | Issues in Quantitative Association Rule Mining: A Big Data Perspective. Advances in Intelligent Systems and Computing, 2016, , 377-385. | 0.6 | 3 |
| 32 | pARACNE: A Parallel Inference Platform for Gene Regulatory Network Using ARACNe. Advances in Intelligent Systems and Computing, 2021, , 85-92. | 0.6 | 3 |
| 33 | 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 |
| 34 | Chemical Characterization of Interacting Genes in Few Subnetworks of Alzheimer's Disease. , 2018, , . |  | 2 |
| 35 | 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 |
| 36 | A new equivalence class based approach for discretizing quantitative data using Point Shift Mechanism. , 2015, , . |  | 1 |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 37 | Towards the assessment of GRN algorithms based on (disease) ontology. , 2015, , . | | 1 |
| 38 | Incremental Approach for Detecting Arbitrary and Embedded Cluster Structures. Lecture Notes in Computer Science, 2016, , 220-233. | 1.3 | 1 |
| 39 | Inferring Causal Gene Regulatory Networks Using Time-Delay Association Rules. Communications in Computer and Information Science, 2019, , 310-321. | 0.5 | 1 |
| 40 | Segmentation of cortical gray and white matters from MRI using density based clustering approach. , 2015, , . | | 0 |
| 41 | Network based algorithms for module extraction from RNASeq data: A quantitative assessment. , 2017, , . | | 0 |
| 42 | Preliminaries of graph theory. , 2020, , 7-24. | | 0 |
| 43 | Gene expression networks: inference and analysis. , 2020, , 95-131. | | 0 |
| 44 | Graph analysis. , 2020, , 25-51. | | 0 |
| 45 | Overlapping Community Detection inÂStatic and Dynamic Networks: AÂQualitative Assessment. Lecture Notes in Networks and Systems, 2021, , 113-123. | 0.7 | 0 |
| 46 | Inference and analysis of gene regulatory networks using data mining techniques. ACM SIGBioinformatics Record, 2020, 10, 1-2. | 0.3 | 0 |
| 47 | Functional module extraction from gene expression data using data mining techniques. ACM SIGBioinformatics Record, 2020, 10, 1-2. | 0.3 | 0 |