

# Saurav Mallik

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

45  
papers

617  
citations

15  
h-index

22  
g-index

51  
ext. papers

839  
ext. citations

5.3  
avg, IF

4.73  
L-index

#	Paper	IF	Citations
45	A Review of Computational Learning and IoT Applications to High-Throughput Array-Based Sequencing and Medical Imaging Data in Drug Discovery and Other Health Care Systems <b>2022</b> , 83-109		
44	A Deep Learning-Based Framework for Supporting Clinical Diagnosis of Glioblastoma Subtypes.. <i>Frontiers in Genetics</i> , <b>2022</b> , 13, 855420	4.5	1
43	An Ensemble-Based Deep Convolutional Neural Network for Computer-Aided Polyps Identification From Colonoscopy.. <i>Frontiers in Genetics</i> , <b>2022</b> , 13, 844391	4.5	5
42	Comparison of five supervised feature selection algorithms leading to top features and gene signatures from multi-omics data in cancer.. <i>BMC Bioinformatics</i> , <b>2022</b> , 23, 153	3.6	0
41	Molecular signatures identified by integrating gene expression and methylation in non-seminoma and seminoma of testicular germ cell tumours. <i>Epigenetics</i> , <b>2021</b> , 16, 162-176	5.7	9
40	Computational learning of features for automated colonic polyp classification. <i>Scientific Reports</i> , <b>2021</b> , 11, 4347	4.9	3
39	H19, a Long Non-coding RNA, Mediates Transcription Factors and Target Genes through Interference of MicroRNAs in Pan-Cancer. <i>Molecular Therapy - Nucleic Acids</i> , <b>2020</b> , 21, 180-191	10.7	11
38	Combinatorial Auction-Based Fog Service Allocation Mechanism for IoT Applications <b>2020</b> ,		6
37	MicroRNA and transcription factor co-regulatory networks and subtype classification of seminoma and non-seminoma in testicular germ cell tumors. <i>Scientific Reports</i> , <b>2020</b> , 10, 852	4.9	16
36	In silico ranking of phenolics for therapeutic effectiveness on cancer stem cells. <i>BMC Bioinformatics</i> , <b>2020</b> , 21, 499	3.6	4
35	Detecting methylation signatures in neurodegenerative disease by density-based clustering of applications with reducing noise. <i>Scientific Reports</i> , <b>2020</b> , 10, 22164	4.9	2
34	Identification of Serum miRNA Signature and Establishment of a Nomogram for Risk Stratification in Patients With Pancreatic Ductal Adenocarcinoma. <i>Annals of Surgery</i> , <b>2020</b> , 275,	7.8	9
33	Critical microRNAs and regulatory motifs in cleft palate identified by a conserved miRNA-TF-gene network approach in humans and mice. <i>Briefings in Bioinformatics</i> , <b>2020</b> , 21, 1465-1478	13.4	16
32	A Novel Graph Topology based GO-Similarity Measure for Signature Detection from Multi-Omics Data and its Application to Other Problems. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2020</b> , PP,	3	4
31	A Linear Regression and Deep Learning Approach for Detecting Reliable Genetic Alterations in Cancer Using DNA Methylation and Gene Expression Data. <i>Genes</i> , <b>2020</b> , 11,	4.2	11
30	Graph- and rule-based learning algorithms: a comprehensive review of their applications for cancer type classification and prognosis using genomic data. <i>Briefings in Bioinformatics</i> , <b>2020</b> , 21, 368-394	13.4	19
29	WeCoMXP: Weighted Connectivity Measure Integrating Co-Methylation, Co-Expression and Protein-Protein Interactions for Gene-Module Detection. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2020</b> , 17, 690-703	3	7

28	Machine Learning and Rule Mining Techniques in the Study of Gene Inactivation and RNA Interference <b>2019</b> ,		2
27	Multi-Objective Optimized Fuzzy Clustering for Detecting Cell Clusters from Single-Cell Expression Profiles. <i>Genes</i> , <b>2019</b> , 10,	4.2	7
26	Distance based knowledge retrieval through rule mining for complex biomarker recognition from tri-omics profiles. <i>International Journal of Computational Biology and Drug Design</i> , <b>2019</b> , 12, 105	0.4	1
25	An evaluation of supervised methods for identifying differentially methylated regions in Illumina methylation arrays. <i>Briefings in Bioinformatics</i> , <b>2019</b> , 20, 2224-2235	13.4	30
24	Identification of Multiview Gene Modules Using Mutual Information-Based Hypograph Mining. <i>IEEE Transactions on Systems, Man, and Cybernetics: Systems</i> , <b>2019</b> , 49, 1119-1130	7.3	17
23	Module-Based Knowledge Discovery for Multiple-Cytosine-Variant Methylation Profile <b>2018</b> , 169-186		1
22	DTFP-Growth: Dynamic Threshold-Based FP-Growth Rule Mining Algorithm Through Integrating Gene Expression, Methylation, and Protein-Protein Interaction Profiles. <i>IEEE Transactions on Nanobioscience</i> , <b>2018</b> , 17, 117-125	3.4	6
21	Hybrid Group Recommendation Using Modified Termite Colony Algorithm: A Context Towards Big Data. <i>Journal of Information and Knowledge Management</i> , <b>2018</b> , 17, 1850019	0.9	7
20	Detecting TF-miRNA-gene network based modules for 5hmC and 5mC brain samples: a intra- and inter-species case-study between human and rhesus. <i>BMC Genetics</i> , <b>2018</b> , 19, 9	2.6	17
19	Integrating Multiple Data Sources for Combinatorial Marker Discovery: A Study in Tumorigenesis. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2018</b> , 15, 673-687	3	17
18	Multi-Objective Optimization Approaches in Biological Learning System on Microarray Data <b>2018</b> , 159-180		1
17	Identification of gene signatures from RNA-seq data using Pareto-optimal cluster algorithm. <i>BMC Systems Biology</i> , <b>2018</b> , 12, 126	3.5	8
16	Identifying Epigenetic Biomarkers using Maximal Relevance and Minimal Redundancy Based Feature Selection for Multi-Omics Data. <i>IEEE Transactions on Nanobioscience</i> , <b>2017</b> , 16, 3-10	3.4	35
15	Towards integrated oncogenic marker recognition through mutual information-based statistically significant feature extraction: an association rule mining based study on cancer expression and methylation profiles. <i>Quantitative Biology</i> , <b>2017</b> , 5, 302-327	3.9	12
14	ConGEMs: Condensed Gene Co-Expression Module Discovery Through Rule-Based Clustering and Its Application to Carcinogenesis. <i>Genes</i> , <b>2017</b> , 9,	4.2	11
13	TrapRM: Transcriptomic and proteomic rule mining using weighted shortest distance based multiple minimum supports for multi-omics dataset <b>2017</b> ,		2
12	IDPT: Insights into potential intrinsically disordered proteins through transcriptomic analysis of genes for prostate carcinoma epigenetic data. <i>Gene</i> , <b>2016</b> , 586, 87-96	3.8	17
11	Co-evolutionary constraints of globular proteins correlate with their folding rates. <i>FEBS Letters</i> , <b>2015</b> , 589, 2179-85	3.8	10

10	MiRNA-TF-gene network analysis through ranking of biomolecules for multi-informative uterine leiomyoma dataset. <i>Journal of Biomedical Informatics</i> , <b>2015</b> , 57, 308-19	10.2	25
9	RANWAR: rank-based weighted association rule mining from gene expression and methylation data. <i>IEEE Transactions on Nanobioscience</i> , <b>2015</b> , 14, 59-66	3.4	37
8	Transcriptomic Analysis of mRNAs in Human Monocytic Cells Expressing the HIV-1 Nef Protein and Their Exosomes. <i>BioMed Research International</i> , <b>2015</b> , 2015, 492395	3	27
7	Analyzing large gene expression and methylation data profiles using StatBicRM: statistical biclustering-based rule mining. <i>PLoS ONE</i> , <b>2015</b> , 10, e0119448	3.7	26
6	Assembly constraints drive co-evolution among ribosomal constituents. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, 5352-63	20.1	12
5	A Survey and Comparative Study of Statistical Tests for Identifying Differential Expression from Microarray Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2014</b> , 11, 95-115	3	78
4	The HIV Nef protein modulates cellular and exosomal miRNA profiles in human monocytic cells. <i>Journal of Extracellular Vesicles</i> , <b>2014</b> , 3,	16.4	59
3	Integrated analysis of gene expression and genome-wide DNA methylation for tumor prediction: An association rule mining-based approach <b>2013</b> ,		14
2	Integrated Statistical and Rule-Mining Techniques for Dna Methylation and Gene Expression Data Analysis. <i>Journal of Artificial Intelligence and Soft Computing Research</i> , <b>2013</b> , 3, 101-115	5.1	11
1	Proposed Conceptual Model for Semantically Enabled Web Services Based On QoS. <i>Procedia Technology</i> , <b>2012</b> , 4, 579-583		1