Saurav Mallik

List of Publications by Year
in descending order

50 papers	994 citations	430442 18 h-index	476904 29 g-index
51 all docs	51 docs citations	51 times ranked	963 citing authors

#	Article	IF	Citations
1	A Survey and Comparative Study of Statistical Tests for Identifying Differential Expression from Microarray Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 95-115.	1.9	105
2	The HIV Nef protein modulates cellular and exosomal miRNA profiles in human monocytic cells. Journal of Extracellular Vesicles, 2014, 3, .	5.5	80
3	An evaluation of supervised methods for identifying differentially methylated regions in Illumina methylation arrays. Briefings in Bioinformatics, 2019, 20, 2224-2235.	3.2	72
4	RANWAR: Rank-Based Weighted Association Rule Mining From Gene Expression and Methylation Data. IEEE Transactions on Nanobioscience, 2015, 14, 59-66.	2.2	51
5	MicroRNA and transcription factor co-regulatory networks and subtype classification of seminoma and non-seminoma in testicular germ cell tumors. Scientific Reports, 2020, 10, 852.	1.6	43
6	Identifying Epigenetic Biomarkers using Maximal Relevance and Minimal Redundancy Based Feature Selection for Multi-Omics Data. IEEE Transactions on Nanobioscience, 2017, 16, 3-10.	2.2	39
7	Transcriptomic Analysis of mRNAs in Human Monocytic Cells Expressing the HIV-1 Nef Protein and Their Exosomes. BioMed Research International, 2015, 2015, 1-10.	0.9	36
8	Graph- and rule-based learning algorithms: a comprehensive review of their applications for cancer type classification and prognosis using genomic data. Briefings in Bioinformatics, 2020, 21, 368-394.	3.2	34
9	Analyzing Large Gene Expression and Methylation Data Profiles Using StatBicRM: Statistical Biclustering-Based Rule Mining. PLoS ONE, 2015, 10, e0119448.	1.1	32
10	Critical microRNAs and regulatory motifs in cleft palate identified by a conserved miRNA–TF–gene network approach in humans and mice. Briefings in Bioinformatics, 2020, 21, 1465-1478.	3.2	30
11	MiRNA-TF-gene network analysis through ranking of biomolecules for multi-informative uterine leiomyoma dataset. Journal of Biomedical Informatics, 2015, 57, 308-319.	2.5	27
12	Identification of gene signatures from RNA-seq data using Pareto-optimal cluster algorithm. BMC Systems Biology, 2018, 12, 126.	3.0	27
13	H19, a Long Non-coding RNA, Mediates Transcription Factors and Target Genes through Interference of MicroRNAs in Pan-Cancer. Molecular Therapy - Nucleic Acids, 2020, 21, 180-191.	2.3	25
14	A Linear Regression and Deep Learning Approach for Detecting Reliable Genetic Alterations in Cancer Using DNA Methylation and Gene Expression Data. Genes, 2020, 11, 931.	1.0	24
15	Integrating Multiple Data Sources for Combinatorial Marker Discovery: A Study in Tumorigenesis. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 673-687.	1.9	24
16	Integrated analysis of gene expression and genome-wide DNA methylation for tumor prediction: An association rule mining-based approach. , 2013, , .		23
17	Identification of Multiview Gene Modules Using Mutual Information-Based Hypograph Mining. IEEE Transactions on Systems, Man, and Cybernetics: Systems, 2019, 49, 1119-1130.	5.9	23
18	Exosomal microRNAs (exoMIRs): micromolecules with macro impact in oral cancer. 3 Biotech, 2022, 12, .	1.1	22

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19	IDPT: Insights into potential intrinsically disordered proteins through transcriptomic analysis of genes for prostate carcinoma epigenetic data. Gene, 2016, 586, 87-96.	1.0	19
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. BMC Genetics, 2018, 19, 9.	2.7	19
21	ConGEMs: Condensed Gene Co-Expression Module Discovery Through Rule-Based Clustering and Its Application to Carcinogenesis. Genes, 2018, 9, 7.	1.0	18
22	An Ensemble-Based Deep Convolutional Neural Network for Computer-Aided Polyps Identification From Colonoscopy. Frontiers in Genetics, 2022, 13, 844391.	1.1	18
23	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. Quantitative Biology, 2017, 5, 302-327.	0.3	16
24	Multi-Objective Optimized Fuzzy Clustering for Detecting Cell Clusters from Single-Cell Expression Profiles. Genes, 2019, 10, 611.	1.0	14
25	Computational learning of features for automated colonic polyp classification. Scientific Reports, 2021, 11, 4347.	1.6	14
26	Identification of Serum miRNA Signature and Establishment of a Nomogram for Risk Stratification in Patients With Pancreatic Ductal Adenocarcinoma. Annals of Surgery, 2022, 275, e229-e237.	2.1	14
27	Assembly constraints drive co-evolution among ribosomal constituents. Nucleic Acids Research, 2015, 43, 5352-5363.	6.5	13
28	Combinatorial Auction-Based Fog Service Allocation Mechanism for IoT Applications. , 2020, , .		13
29	Molecular signatures identified by integrating gene expression and methylation in non-seminoma and seminoma of testicular germ cell tumours. Epigenetics, 2021, 16, 162-176.	1.3	12
30	Integrated Statistical and Rule-Mining Techniques for Dna Methylation and Gene Expression Data Analysis. Journal of Artificial Intelligence and Soft Computing Research, 2013, 3, 101-115.	3.5	12
31	Co–evolutionary constraints of globular proteins correlate with their folding rates. FEBS Letters, 2015, 589, 2179-2185.	1.3	10
32	DTFP-Growth: Dynamic Threshold-Based FP-Growth Rule Mining Algorithm Through Integrating Gene Expression, Methylation, and Protein–Protein Interaction Profiles. IEEE Transactions on Nanobioscience, 2018, 17, 117-125.	2.2	9
33	Hybrid Group Recommendation Using Modified Termite Colony Algorithm: A Context Towards Big Data. Journal of Information and Knowledge Management, 2018, 17, 1850019.	0.8	9
34	WeCoMXP: Weighted Connectivity Measure Integrating Co-Methylation, Co-Expression and Protein-Protein Interactions for Gene-Module Detection. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 17, 1-1.	1.9	9
35	In silico ranking of phenolics for therapeutic effectiveness on cancer stem cells. BMC Bioinformatics, 2020, 21, 499.	1.2	8
36	Comparison of five supervised feature selection algorithms leading to top features and gene signatures from multi-omics data in cancer. BMC Bioinformatics, 2022, 23, 153.	1.2	8

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37	Detecting methylation signatures in neurodegenerative disease by density-based clustering of applications with reducing noise. Scientific Reports, 2020, 10, 22164.	1.6	7
38	A Deep Learning–Based Framework for Supporting Clinical Diagnosis of Glioblastoma Subtypes. Frontiers in Genetics, 2022, 13, 855420.	1.1	6
39	Unsupervised Learning for Feature Representation Using Spatial Distribution of Amino Acids in Aldehyde Dehydrogenase (ALDH2) Protein Sequences. Mathematics, 2022, 10, 2228.	1.1	6
40	A Novel Graph Topology based GO-Similarity Measure for Signature Detection from Multi-Omics Data and its Application to Other Problems. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, PP, 1-1.	1.9	5
41	TrapRM: Transcriptomic and proteomic rule mining using weighted shortest distance based multiple minimum supports for multi-omics dataset. , 2017, , .		4
42	Novel Epigenetic Clock Biomarkers of Age-Related Macular Degeneration. Frontiers in Medicine, 0, 9, .	1.2	4
43	Machine Learning and Rule Mining Techniques in the Study of Gene Inactivation and RNA Interference. , 0, , .		2
44	Distance based knowledge retrieval through rule mining for complex biomarker recognition from tri-omics profiles. International Journal of Computational Biology and Drug Design, 2019, 12, 105.	0.3	2
45	Proposed Conceptual Model for Semantically Enabled Web Services Based On QoS. Procedia Technology, 2012, 4, 579-583.	1.1	1
46	Module-Based Knowledge Discovery for Multiple-Cytosine-Variant Methylation Profile. , 2018, , 169-186.		1
47	A Multi-classifier Model to Identify Mitochondrial Respiratory Gene Signatures in Human Cancer. , 2019, , .		1
48	Unsupervised Feature Selection Using an Integrated Strategy of Hierarchical Clustering with Singular Value Decomposition: An Integrative Biomarker Discovery Method with Application to Acute Myeloid Leukemia. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	1.9	1
49	Multi-Objective Optimization Approaches in Biological Learning System on Microarray Data. , 2018, , 159-180.		1
50	Negatively-Associated Maximal Frequent Geneset Mining on DNA Methylation Profile. , 2021, , .		0