Debarka Sengupta

List of Publications by Year
in descending order

26 papers	1,739 citations	567281 15 h-index	526287 27 g-index
34 all docs	34 docs citations	34 times ranked	3337 citing authors

#	Article	IF	Citations
1	SelfE: Gene Selection via Self-Expression for Single-Cell Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 624-632.	3.0	0
2	Challenges and possible solutions for decoding extranasal olfactory receptors. FEBS Journal, 2021, 288, 4230-4241.	4.7	4
3	UniPath: a uniform approach for pathway and gene-set based analysis of heterogeneity in single-cell epigenome and transcriptome profiles. Nucleic Acids Research, 2021, 49, e13-e13.	14.5	9
4	The Cellular basis of loss of smell in 2019-nCoV-infected individuals. Briefings in Bioinformatics, 2021, 22, 873-881.	6.5	41
5	*Machine-OlF-Action*: a unified framework for developing and interpreting machine-learning models for chemosensory research. Bioinformatics, 2021, 37, 1769-1771.	4.1	6
6	Modeling expression ranks for noise-tolerant differential expression analysis of scRNA-seq data. Genome Research, 2021, 31, 689-697.	5.5	6
7	Big data analytics in single‐cell transcriptomics: Five grand opportunities. Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery, 2021, 11, e1414.	6.8	1
8	EcTracker: Tracking and elucidating ectopic expression leveraging large-scale scRNA-seq studies. Briefings in Bioinformatics, 2021, 22, .	6.5	0
9	OdoriFy: A conglomerate of artificial intelligence–driven prediction engines for olfactory decoding. Journal of Biological Chemistry, 2021, 297, 100956.	3.4	12
10	Hide and Seek: Outwitting Community Detection Algorithms. IEEE Transactions on Computational Social Systems, 2021, 8, 799-808.	4.4	20
11	Quantification of Age-Related Decline in Transcriptional Homeostasis. Journal of Molecular Biology, 2021, 433, 167179.	4.2	7
12	Recent Smell Loss Is the Best Predictor of COVID-19 Among Individuals With Recent Respiratory Symptoms. Chemical Senses, 2021, 46, .	2.0	119
13	deepMc: Deep Matrix Completion for Imputation of Single-Cell RNA-seq Data. Journal of Computational Biology, 2020, 27, 1011-1019.	1.6	19
14	Analysis of single-cell transcriptomes links enrichment of olfactory receptors with cancer cell differentiation status and prognosis. Communications Biology, 2020, 3, 506.	4.4	18
15	Molecular signature comprising 11 platelet-genes enables accurate blood-based diagnosis of NSCLC. BMC Genomics, 2020, 21, 744.	2.8	13
16	Integrative Analysis and Machine Learning Based Characterization of Single Circulating Tumor Cells. Journal of Clinical Medicine, 2020, 9, 1206.	2.4	42
17	Staging System to Predict the Risk of Relapse in Multiple Myeloma Patients Undergoing Autologous Stem Cell Transplantation. Frontiers in Oncology, 2019, 9, 633.	2.8	18
18	Improved dropClust R package with integrative analysis support for scRNA-seq data. Bioinformatics, 2019, , .	4.1	9

#	ARTICLE	IF	CITATIONS
19	McImpute: Matrix Completion Based Imputation for Single Cell RNA-seq Data. Frontiers in Genetics, 2019, 10, 9.	2.3	67
20	dropClust: efficient clustering of ultra-large scRNA-seq data. Nucleic Acids Research, 2018, 46, e36-e36.	14.5	94
21	Discovery of rare cells from voluminous single cell expression data. Nature Communications, 2018, 9, 4719.	12.8	91
22	AutoImpute: Autoencoder based imputation of single-cell RNA-seq data. Scientific Reports, 2018, 8, 16329.	3.3	128
23	CellAtlasSearch: a scalable search engine for single cells. Nucleic Acids Research, 2018, 46, W141-W147.	14.5	39
24	Structure-Aware Principal Component Analysis for Single-Cell RNA-seq Data. Journal of Computational Biology, 2018, 25, 1365-1373.	1.6	37
25	Reference component analysis of single-cell transcriptomes elucidates cellular heterogeneity in human colorectal tumors. Nature Genetics, 2017, 49, 708-718.	21.4	849
26	Topological patterns in microRNAâ€"gene regulatory network: studies in colorectal and breast cancer. Molecular BioSystems, 2013, 9, 1360.	2.9	28