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	Reference component analysis of single-cell transcriptomes elucidates cellular heterogeneity in human colorectal tumors. Nature Genetics, 2017, 49, 708-718.	21.4	849
2	AutoImpute: Autoencoder based imputation of single-cell RNA-seq data. Scientific Reports, 2018, 8, 16329.	3.3	128
3	Recent Smell Loss Is the Best Predictor of COVID-19 Among Individuals With Recent Respiratory Symptoms. Chemical Senses, 2021, 46, .	2.0	119
4	dropClust: efficient clustering of ultra-large scRNA-seq data. Nucleic Acids Research, 2018, 46, e36-e36.	14.5	94
5	Discovery of rare cells from voluminous single cell expression data. Nature Communications, 2018, 9, 4719.	12.8	91
6	McImpute: Matrix Completion Based Imputation for Single Cell RNA-seq Data. Frontiers in Genetics, 2019, 10, 9.	2.3	67
7	Integrative Analysis and Machine Learning Based Characterization of Single Circulating Tumor Cells. Journal of Clinical Medicine, 2020, 9, 1206.	2.4	42
8	The Cellular basis of loss of smell in 2019-nCoV-infected individuals. Briefings in Bioinformatics, 2021, 22, 873-881.	6.5	41
9	CellAtlasSearch: a scalable search engine for single cells. Nucleic Acids Research, 2018, 46, W141-W147.	14.5	39
10	Structure-Aware Principal Component Analysis for Single-Cell RNA-seq Data. Journal of Computational Biology, 2018, 25, 1365-1373.	1.6	37
11	Topological patterns in microRNA–gene regulatory network: studies in colorectal and breast cancer. Molecular BioSystems, 2013, 9, 1360.	2.9	28
12	Hide and Seek: Outwitting Community Detection Algorithms. IEEE Transactions on Computational Social Systems, 2021, 8, 799-808.	4.4	20
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	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
15	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
16	Molecular signature comprising 11 platelet-genes enables accurate blood-based diagnosis of NSCLC. BMC Genomics, 2020, 21, 744.	2.8	13
17	OdoriFy: A conglomerate of artificial intelligence–driven prediction engines for olfactory decoding. Journal of Biological Chemistry, 2021, 297, 100956.	3.4	12
18	Improved dropClust R package with integrative analysis support for scRNA-seq data. Bioinformatics, 2019, , .	4.1	9

#	Article	IF	Citations
19	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
20	Quantification of Age-Related Decline in Transcriptional Homeostasis. Journal of Molecular Biology, 2021, 433, 167179.	4.2	7
21	<i>Machine-OlF-Action</i>: a unified framework for developing and interpreting machine-learning models for chemosensory research. Bioinformatics, 2021, 37, 1769-1771.	4.1	6
22	Modeling expression ranks for noise-tolerant differential expression analysis of scRNA-seq data. Genome Research, 2021, 31, 689-697.	5.5	6
23	Challenges and possible solutions for decoding extranasal olfactory receptors. FEBS Journal, 2021, 288, 4230-4241.	4.7	4
24	Big data analytics in single‐cell transcriptomics: Five grand opportunities. Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery, 2021, 11, e1414.	6.8	1
25	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
26	EcTracker: Tracking and elucidating ectopic expression leveraging large-scale scRNA-seq studies. Briefings in Bioinformatics, 2021, 22, .	6.5	0