

Susmita Datta

List of Publications by Year in descending order

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Version: 2024-02-01

22
papers

931
citations

949033

11
h-index

843174

20
g-index

22
all docs

22
docs citations

22
times ranked

1555
citing authors

#	ARTICLE	IF	CITATIONS
1	<scp>SAREV</scp>: A review on statistical analytics of single-cell RNA sequencing data. Wiley Interdisciplinary Reviews: Computational Statistics, 2022, 14, e1558.	2.1	2
2	Factors affecting live birth rates in donor oocytes from commercial egg banks vs. program egg donors: an analysis of 40,485 cycles from the Society for Assisted Reproductive Technology registry in 2016–2018. Fertility and Sterility, 2022, 117, 339-348.	0.5	8
3	Unraveling city-specific signature and identifying sample origin locations for the data from CAMDA MetaSUB challenge. Biology Direct, 2021, 16, 1.	1.9	21
4	Unraveling City-Specific Microbial Signatures and Identifying Sample Origins for the Data From CAMDA 2020 Metagenomic Geolocation Challenge. Frontiers in Genetics, 2021, 12, 659650.	1.1	1
5	Single-Cell Differential Network Analysis with Sparse Bayesian Factor Models. Frontiers in Genetics, 2021, 12, 810816.	1.1	0
6	A sparse Bayesian factor model for the construction of gene co-expression networks from single-cell RNA sequencing count data. BMC Bioinformatics, 2020, 21, 361.	1.2	12
7	Topical doxycycline monohydrate hydrogel 1% targeting proteases/PAR2 pathway is a novel therapeutic for atopic dermatitis. Experimental Dermatology, 2020, 29, 1171-1175.	1.4	3
8	Identification of city specific important bacterial signature for the MetaSUB CAMDA challenge microbiome data. Biology Direct, 2019, 14, 11.	1.9	23
9	Membrane proteomic analysis reveals overlapping and independent functions of <i>Streptococcus mutans</i> Ffh, YidC1, and YidC2. Molecular Oral Microbiology, 2019, 34, 131-152.	1.3	13
10	Detection of Differentially Expressed Genes in Discrete Single-Cell RNA Sequencing Data Using a Hurdle Model With Correlated Random Effects. Biometrics, 2019, 75, 1051-1062.	0.8	14
11	Pilot Study of Metabolomics and Psychoneurological Symptoms in Women With Early Stage Breast Cancer. Biological Research for Nursing, 2018, 20, 227-236.	1.0	24
12	The subgingival microbiome in patients with established rheumatoid arthritis. Rheumatology, 2018, 57, 1162-1172.	0.9	41
13	Unraveling bacterial fingerprints of city subways from microbiome 16S gene profiles. Biology Direct, 2018, 13, 10.	1.9	23
14	A novel statistical approach for identification of the master regulator transcription factor. BMC Bioinformatics, 2017, 18, 79.	1.2	20
15	Exploring the importance of cancer pathways by meta-analysis of differential protein expression networks in three different cancers. Biology Direct, 2016, 11, 65.	1.9	3
16	An integrative exploratory analysis of “omics data from the ICGC cancer genomes lung adenocarcinoma study. Systems Biomedicine (Austin, Tex), 2014, 2, 54-62.	0.7	3
17	dna: An R package for differential network analysis. Bioinformatics, 2014, 10, 233-234.	0.2	9
18	An adaptive optimal ensemble classifier via bagging and rank aggregation with applications to high dimensional data. BMC Bioinformatics, 2010, 11, 427.	1.2	37

#	ARTICLE	IF	CITATIONS
19	A statistical framework for differential network analysis from microarray data. BMC Bioinformatics, 2010, 11, 95.	1.2	134
20	RankAggreg, an R package for weighted rank aggregation. BMC Bioinformatics, 2009, 10, 62.	1.2	264
21	Reconstruction of genetic association networks from microarray data: a partial least squares approach. Bioinformatics, 2008, 24, 561-568.	1.8	60
22	Weighted rank aggregation of cluster validation measures: a Monte Carlo cross-entropy approach. Bioinformatics, 2007, 23, 1607-1615.	1.8	216