

Stephanie C Hicks

List of Publications by Year in descending order

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Version: 2024-02-01

29
papers

3,995
citations

361296

20
h-index

477173

29
g-index

60
all docs

60
docs citations

60
times ranked

5267
citing authors

#	ARTICLE	IF	CITATIONS
1	Addressing the mean-correlation relationship in co-expression analysis. PLoS Computational Biology, 2022, 18, e1009954.	1.5	11
2	SpatialExperiment: infrastructure for spatially-resolved transcriptomics data in R using Bioconductor. Bioinformatics, 2022, 38, 3128-3131.	1.8	48
3	Differential expression of single-cell RNA-seq data using Tweedie models. Statistics in Medicine, 2022, 41, 3492-3510.	0.8	11
4	spatialLIBD: an R/Bioconductor package to visualize spatially-resolved transcriptomics data. BMC Genomics, 2022, 23, .	1.2	50
5	mbkmeans: Fast clustering for single cell data using mini-batch k-means. PLoS Computational Biology, 2021, 17, e1008625.	1.5	36
6	Transcriptome-scale spatial gene expression in the human dorsolateral prefrontal cortex. Nature Neuroscience, 2021, 24, 425-436.	7.1	418
7	Reproducible Research: A Retrospective. Annual Review of Public Health, 2021, 42, 79-93.	7.6	28
8	Reproducibility standards for machine learning in the life sciences. Nature Methods, 2021, 18, 1132-1135.	9.0	96
9	miQC: An adaptive probabilistic framework for quality control of single-cell RNA-sequencing data. PLoS Computational Biology, 2021, 17, e1009290.	1.5	38
10	Fast and memory-efficient scRNA-seq k-means clustering with various distances. , 2021, 2021, .		4
11	Genetic demultiplexing of pooled single-cell RNA-sequencing samples in cancer facilitates effective experimental design. GigaScience, 2021, 10, .	3.3	17
12	Single-nucleus transcriptome analysis reveals cell-type-specific molecular signatures across reward circuitry in the human brain. Neuron, 2021, 109, 3088-3103.e5.	3.8	95
13	Diagnosing Data Analytic Problems in the Classroom. Journal of Statistics and Data Science Education, 2021, 29, 267-276.	0.9	3
14	Orchestrating single-cell analysis with Bioconductor. Nature Methods, 2020, 17, 137-145.	9.0	488
15	A systematic evaluation of single-cell RNA-sequencing imputation methods. Genome Biology, 2020, 21, 218.	3.8	188
16	Eleven grand challenges in single-cell data science. Genome Biology, 2020, 21, 31.	3.8	742
17	TreeSummarizedExperiment: a S4 class for data with hierarchical structure. F1000Research, 2020, 9, 1246.	0.8	16
18	TreeSummarizedExperiment: a S4 class for data with hierarchical structure. F1000Research, 2020, 9, 1246.	0.8	11

#	ARTICLE	IF	CITATIONS
19	A practical guide to methods controlling false discoveries in computational biology. <i>Genome Biology</i> , 2019, 20, 118.	3.8	222
20	methylCC: technology-independent estimation of cell type composition using differentially methylated regions. <i>Genome Biology</i> , 2019, 20, 261.	3.8	13
21	Feature selection and dimension reduction for single-cell RNA-Seq based on a multinomial model. <i>Genome Biology</i> , 2019, 20, 295.	3.8	288
22	Missing data and technical variability in single-cell RNA-sequencing experiments. <i>Biostatistics</i> , 2018, 19, 562-578.	0.9	388
23	Smooth quantile normalization. <i>Biostatistics</i> , 2018, 19, 185-198.	0.9	78
24	A Guide to Teaching Data Science. <i>American Statistician</i> , 2018, 72, 382-391.	0.9	52
25	Analysis and correction of compositional bias in sparse sequencing count data. <i>BMC Genomics</i> , 2018, 19, 799.	1.2	85
26	Greater Data Science Ahead!. <i>Journal of Computational and Graphical Statistics</i> , 2017, 26, 770-771.	0.9	0
27	quantro: a data-driven approach to guide the choice of an appropriate normalization method. <i>Genome Biology</i> , 2015, 16, 117.	13.9	76
28	Evolutionary Action Score of <i>TP53</i> Coding Variants Is Predictive of Platinum Response in Head and Neck Cancer Patients. <i>Cancer Research</i> , 2015, 75, 1205-1215.	0.4	78
29	Evolutionary Action Score of <i>TP53</i> Identifies High-Risk Mutations Associated with Decreased Survival and Increased Distant Metastases in Head and Neck Cancer. <i>Cancer Research</i> , 2015, 75, 1527-1536.	0.4	139