Davis James McCarthy

List of Publications by Year
in descending order

36	47,084	270111	371746
papers	citations	25 h-index	37 g-index

53	53	53	89021
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	<tt>edgeR</tt>: a Bioconductor package for differential expression analysis of digital gene expression data. Bioinformatics, 2010, 26, 139-140.	1.8	32,955
2	Differential expression analysis of multifactor RNA-Seq experiments with respect to biological variation. Nucleic Acids Research, 2012, 40, 4288-4297.	6.5	4,474
3	Scater: pre-processing, quality control, normalization and visualization of single-cell RNA-seq data in R. Bioinformatics, 2017, 33, 1179-1186.	1.8	1,283
4	Count-based differential expression analysis of RNA sequencing data using R and Bioconductor. Nature Protocols, 2013, 8, 1765-1786.	5.5	1,124
5	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	13.7	952
6	A step-by-step workflow for low-level analysis of single-cell RNA-seq data with Bioconductor. F1000Research, 2016, 5, 2122.	0.8	822
7	Eleven grand challenges in single-cell data science. Genome Biology, 2020, 21, 31.	3.8	742
8	A step-by-step workflow for low-level analysis of single-cell RNA-seq data. F1000Research, 2016, 5, 2122.	0.8	654
9	Classification of low quality cells from single-cell RNA-seq data. Genome Biology, 2016, 17, 29.	3.8	572
10	Testing significance relative to a fold-change threshold is a TREAT. Bioinformatics, 2009, 25, 765-771.	1.8	570
11	Common genetic variation drives molecular heterogeneity in human iPSCs. Nature, 2017, 546, 370-375.	13.7	491
12	Benchmarking single-cell RNA-sequencing protocols for cell atlas projects. Nature Biotechnology, 2020, 38, 747-755.	9.4	313
13	Factors influencing success of clinical genome sequencing across a broad spectrum of disorders. Nature Genetics, 2015, 47, 717-726.	9.4	310
14	Detecting Differential Expression in RNA-sequence Data Using Quasi-likelihood with Shrunken Dispersion Estimates. Statistical Applications in Genetics and Molecular Biology, 2012, 11, .	0.2	282
15	Single-cell RNA-sequencing of differentiating iPS cells reveals dynamic genetic effects on gene expression. Nature Communications, 2020, 11, 810.	5.8	235
16	Tutorial: guidelines for the computational analysis of single-cell RNA sequencing data. Nature Protocols, 2021, 16, 1-9.	5.5	169
17	Choice of transcripts and software has a large effect on variant annotation. Genome Medicine, 2014, 6, 26.	3.6	158
18	Vireo: Bayesian demultiplexing of pooled single-cell RNA-seq data without genotype reference. Genome Biology, 2019, 20, 273.	3.8	152

#	Article	IF	Citations
19	f-scLVM: scalable and versatile factor analysis for single-cell RNA-seq. Genome Biology, 2017, 18, 212.	3.8	119
20	NOX1 loss-of-function genetic variants in patients with inflammatory bowel disease. Mucosal Immunology, 2018, 11, 562-574.	2.7	71
21	Properties of structural variants and short tandem repeats associated with gene expression and complex traits. Nature Communications, 2020, 11, 2927.	5.8	67
22	Visualization of Biomedical Data. Annual Review of Biomedical Data Science, 2018, 1, 275-304.	2.8	63
23	Combined single-cell profiling of expression and DNA methylation reveals splicing regulation and heterogeneity. Genome Biology, 2019, 20, 30.	3.8	61
24	Cardelino: computational integration of somatic clonal substructure and single-cell transcriptomes. Nature Methods, 2020, 17, 414-421.	9.0	48
25	Optimizing expression quantitative trait locus mapping workflows for single-cell studies. Genome Biology, 2021, 22, 188.	3.8	36
26	Erythrocytosis associated with a novel missense mutation in the BPGM gene. Haematologica, 2014, 99, e201-e204.	1.7	35
27	Method to Synchronize Cell Cycle of Human Pluripotent Stem Cells without Affecting Their Fundamental Characteristics. Stem Cell Reports, 2019, 12, 165-179.	2.3	35
28	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	2.4	31
29	MOZ and BMI1 play opposing roles during Hox gene activation in ES cells and in body segment identity specification in vivo. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 5437-5442.	3.3	28
30	Aliskiren increases bradykinin and tissue kallikrein mRNA levels in the heart. Clinical and Experimental Pharmacology and Physiology, 2011, 38, 623-631.	0.9	23
31	Discovery and quality analysis of a comprehensive set of structural variants and short tandem repeats. Nature Communications, 2020, 11, 2928.	5.8	22
32	Key signaling networks are dysregulated in patients with the adipose tissue disorder, lipedema. International Journal of Obesity, 2022, 46, 502-514.	1.6	15
33	Personalized genome structure via single gamete sequencing. Genome Biology, 2021, 22, 112.	3.8	10
34	Case Report: Hypoglycemia Due to a Novel Activating Glucokinase Variant in an Adult â€“ a Molecular Approach. Frontiers in Endocrinology, 2022, 13, 842937.	1.5	8
35	Differential Expression for RNA Sequencing (RNA-Seq) Data: Mapping, Summarization, Statistical Analysis, and Experimental Design. , 2012, , 169-190.		4
36	splatPop: simulating population scale single-cell RNA sequencing data. Genome Biology, 2021, 22, 341.	3.8	4