Charity W Law

List of Publications by Year
in descending order

23 papers	32,459 citations	516215 16 h-index	676716 22 g-index
30 all docs	30 docs citations	30 times ranked	58365 citing authors

#	Article	IF	Citations
1	limma powers differential expression analyses for RNA-sequencing and microarray studies. Nucleic Acids Research, 2015, 43, e47-e47.	6.5	26,032
2	voom: precision weights unlock linear model analysis tools for RNA-seq read counts. Genome Biology, 2014, 15, R29.	13.9	4,603
3	RNA-seq analysis is easy as 1-2-3 with limma, Glimma and edgeR. F1000Research, 2016, 5, 1408.	0.8	394
4	RNA-seq analysis is easy as 1-2-3 with limma, Glimma and edgeR. F1000Research, 2016, 5, 1408.	0.8	368
5	RNA-seq analysis is easy as 1-2-3 with limma, Glimma and edgeR. F1000Research, 0, 5, 1408.	0.8	149
6	Glimma: interactive graphics for gene expression analysis. Bioinformatics, 2017, 33, 2050-2052.	1.8	128
7	Isoform prefiltering improves performance of count-based methods for analysis of differential transcript usage. Genome Biology, 2016, 17, 12.	3.8	116
8	Statistical methods for detecting differentially methylated loci and regions. Frontiers in Genetics, 2014, 5, 324.	1.1	99
9	Identification of quiescent and spatially restricted mammary stem cells that are hormone responsive. Nature Cell Biology, 2017, 19, 164-176.	4.6	99
10	Comprehensive characterization of single-cell full-length isoforms in human and mouse with long-read sequencing. Genome Biology, 2021, 22, 310.	3.8	83
11	Effective Adjunctive Therapy by an Innate Defense Regulatory Peptide in a Preclinical Model of Severe Malaria. Science Translational Medicine, 2012, 4, 135ra64.	5.8	81
12	The hematopoietic oncoprotein FOXP1 promotes tumor cell survival in diffuse large B-cell lymphoma by repressing S1PR2 signaling. Blood, 2016, 127, 1438-1448.	0.6	59
13	Easy and efficient ensemble gene set testing with EGSEA. F1000Research, 2017, 6, 2010.	0.8	53
14	Covering all your bases: incorporating intron signal from RNA-seq data. NAR Genomics and Bioinformatics, 2020, 2, lqaa073.	1.5	37
15	RNA-seq mixology: designing realistic control experiments to compare protocols and analysis methods. Nucleic Acids Research, 2017, 45, e30-e30.	6.5	34
16	The long and the short of it: unlocking nanopore long-read RNA sequencing data with short-read differential expression analysis tools. NAR Genomics and Bioinformatics, 2021, 3, lqab028.	1.5	26
17	A guide to creating design matrices for gene expression experiments. F1000Research, 2020, 9, 1444.	0.8	25
18	DNMT3L Is a Regulator of X Chromosome Compaction and Post-Meiotic Gene Transcription. PLoS ONE, 2011, 6, e18276.	1.1	20

#	Article	IF	Citations
19	The impact of influenza pulmonary infection and inflammation on vagal bronchopulmonary sensory neurons. FASEB Journal, 2021, 35, e21320.	0.2	14
20	Germline heterozygous mutations in Nxf1 perturb RNA metabolism and trigger thrombocytopenia and lymphopenia in mice. Blood Advances, 2020, 4, 1270-1283.	2.5	5
21	Homeostatic apoptosis prevents competition-induced atrophy in follicular B cells. Cell Reports, 2021, 36, 109430.	2.9	3
22	A functional genetic screen identifies aurora kinase b as an essential regulator of Sox9-positive mouse embryonic lung progenitor cells. Development (Cambridge), 2021, 148, .	1.2	2
23	Dashboard-style interactive plots for RNA-seq analysis are R Markdown ready with *Glimma* 2.0. NAR Genomics and Bioinformatics, 2021, 3, lqab116.	1.5	2