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List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/518013/publications.pdf

Version: 2024-02-01

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	The impact of influenza pulmonary infection and inflammation on vagal bronchopulmonary sensory neurons. FASEB Journal, 2021, 35, e21320.	0.2	14
2	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
3	Homeostatic apoptosis prevents competition-induced atrophy in follicular B cells. Cell Reports, 2021, 36, 109430.	2.9	3
4	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
5	Comprehensive characterization of single-cell full-length isoforms in human and mouse with long-read sequencing. Genome Biology, 2021, 22, 310.	3.8	83
6	Dashboard-style interactive plots for RNA-seq analysis are R Markdown ready withGlimma2.0. NAR Genomics and Bioinformatics, 2021, 3, lqab116.	1.5	2
7	Covering all your bases: incorporating intron signal from RNA-seq data. NAR Genomics and Bioinformatics, 2020, 2, lqaa073.	1.5	37
8	Germline heterozygous mutations in Nxf1 perturb RNA metabolism and trigger thrombocytopenia and lymphopenia in mice. Blood Advances, 2020, 4, 1270-1283.	2.5	5
9	A guide to creating design matrices for gene expression experiments. F1000Research, 2020, 9, 1444.	0.8	25
10	RNA-seq mixology: designing realistic control experiments to compare protocols and analysis methods. Nucleic Acids Research, 2017, 45, e30-e30.	6.5	34
11	Identification of quiescent and spatially restricted mammary stem cells that are hormone responsive. Nature Cell Biology, 2017, 19, 164-176.	4.6	99
12	Glimma: interactive graphics for gene expression analysis. Bioinformatics, 2017, 33, 2050-2052.	1.8	128
13	Easy and efficient ensemble gene set testing with EGSEA. F1000Research, 2017, 6, 2010.	0.8	53
14	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
15	Isoform prefiltering improves performance of count-based methods for analysis of differential transcript usage. Genome Biology, 2016, 17, 12.	3.8	116
16	RNA-seq analysis is easy as 1-2-3 with limma, Glimma and edgeR. F1000Research, 2016, 5, 1408.	0.8	368
17	RNA-seq analysis is easy as 1-2-3 with limma, Glimma and edgeR. F1000Research, 2016, 5, 1408.	0.8	394
18	limma powers differential expression analyses for RNA-sequencing and microarray studies. Nucleic Acids Research, 2015, 43, e47-e47.	6.5	26,032

#	Article	IF	Citations
19	Statistical methods for detecting differentially methylated loci and regions. Frontiers in Genetics, 2014, 5, 324.	1.1	99
20	voom: precision weights unlock linear model analysis tools for RNA-seq read counts. Genome Biology, 2014, 15, R29.	13.9	4,603
21	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
22	DNMT3L Is a Regulator of X Chromosome Compaction and Post-Meiotic Gene Transcription. PLoS ONE, 2011, 6, e18276.	1.1	20
23	RNA-seq analysis is easy as 1-2-3 with limma, Glimma and edgeR. F1000Research, 0, 5, 1408.	0.8	149