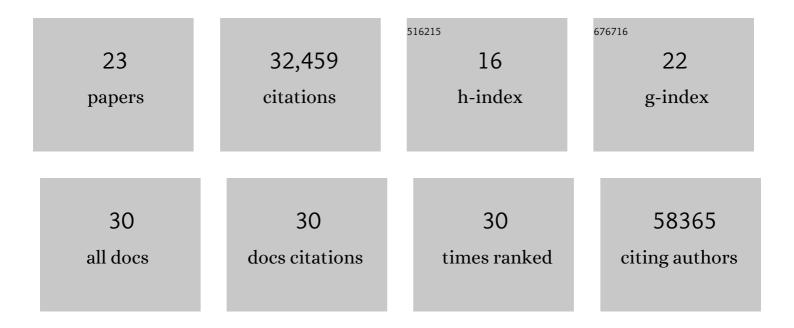
Charity W Law

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/518013/publications.pdf Version: 2024-02-01



| # | 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 with <i>Glimma</i> 2.0. NAR Genomics and Bioinformatics, 2021, 3, Iqab116. | 1.5 | 2 |
| 7 | Covering all your bases: incorporating intron signal from RNA-seq data. NAR Genomics and Bioinformatics, 2020, 2, Iqaa073. | 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 | lsoform 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 |

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| # | 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, Climma and edgeR. F1000Research, 0, 5, 1408. | 0.8 | 149 |