

# Travers Ching

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

21  
papers

1,561  
citations

15  
h-index

22  
g-index

22  
ext. papers

2,085  
ext. citations

6.4  
avg, IF

4.55  
L-index

| #  | Paper   | IF   | Citations |
|----|---|------|-----------|
| 21 | Glycerol-assisted degradation of dibenzothiophene by Paraburkholderia sp. C3 is associated with polyhydroxyalkanoate granulation. <i>Chemosphere</i> , <b>2021</b> , 291, 133054  | 8.4  | 0         |
| 20 | Maternal cardiovascular-related single nucleotide polymorphisms, genes, and pathways associated with early-onset preeclampsia. <i>PLoS ONE</i> , <b>2019</b> , 14, e0222672   | 3.7  | 2         |
| 19 | A Novel FGFR3 Splice Variant Preferentially Expressed in African American Prostate Cancer Drives Aggressive Phenotypes and Docetaxel Resistance. <i>Molecular Cancer Research</i> , <b>2019</b> , 17, 2115-2125                           | 6.6  | 5         |
| 18 | Multimodal Meta-Analysis of 1,494 Hepatocellular Carcinoma Samples Reveals Significant Impact of Consensus Driver Genes on Phenotypes. <i>Clinical Cancer Research</i> , <b>2019</b> , 25, 463-472  | 12.9 | 23        |
| 17 | Opportunities and obstacles for deep learning in biology and medicine. <i>Journal of the Royal Society Interface</i> , <b>2018</b> , 15,  | 4.1  | 780       |
| 16 | Characterization of Plant Glycoproteins: Analysis of Plant Glycopeptide Mass Spectrometry Data with plantGlycoMS, a Package in the R Statistical Computing Environment. <i>Methods in Molecular Biology</i> , <b>2018</b> , 1789, 205-220 | 1.4  | 1         |
| 15 | Cox-nnet: An artificial neural network method for prognosis prediction of high-throughput omics data. <i>PLoS Computational Biology</i> , <b>2018</b> , 14, e1006076  | 5    | 116       |
| 14 | Pan-cancer analysis of expressed somatic nucleotide variants in long intergenic non-coding RNA. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , <b>2018</b> , 23, 512-523                                    | 1.3  | 1         |
| 13 | Using single nucleotide variations in single-cell RNA-seq to identify subpopulations and genotype-phenotype linkage. <i>Nature Communications</i> , <b>2018</b> , 9, 4892   | 17.4 | 37        |
| 12 | Alternative splicing promotes tumour aggressiveness and drug resistance in African American prostate cancer. <i>Nature Communications</i> , <b>2017</b> , 8, 15921  | 17.4 | 53        |
| 11 | Detecting heterogeneity in single-cell RNA-Seq data by non-negative matrix factorization. <i>PeerJ</i> , <b>2017</b> , 5, e2888   | 3.1  | 49        |
| 10 | Analysis of Microarray Data on Gene Expression and Methylation to Identify Long Non-coding RNAs in Non-small Cell Lung Cancer. <i>Scientific Reports</i> , <b>2016</b> , 6, 37233   | 4.9  | 31        |
| 9  | Pan-Cancer Analyses Reveal Long Intergenic Non-Coding RNAs Relevant to Tumor Diagnosis, Subtyping and Prognosis. <i>EBioMedicine</i> , <b>2016</b> , 7, 62-72   | 8.8  | 26        |
| 8  | Single-Cell Transcriptomics Bioinformatics and Computational Challenges. <i>Frontiers in Genetics</i> , <b>2016</b> , 7, 163  | 4.5  | 80        |
| 7  | Site-Specific N-Glycosylation Characterization of Windmill Palm Tree Peroxidase Using Novel Tools for Analysis of Plant Glycopeptide Mass Spectrometry Data. <i>Journal of Proteome Research</i> , <b>2016</b> , 15, 2026-38              | 5.6  | 12        |
| 6  | Genome-scale hypomethylation in the cord blood DNAs associated with early onset preeclampsia. <i>Clinical Epigenetics</i> , <b>2015</b> , 7, 21   | 7.7  | 34        |
| 5  | Non-coding yet non-trivial: a review on the computational genomics of lincRNAs. <i>BioData Mining</i> , <b>2015</b> , 8, 44   | 4.3  | 15        |

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|---|--|-----|-----|
| 4 | Genome-wide hypermethylation coupled with promoter hypomethylation in the chorioamniotic membranes of early onset pre-eclampsia. <i>Molecular Human Reproduction</i> , <b>2014</b> , 20, 885-904 | 4.4 | 42  |
| 3 | Power analysis and sample size estimation for RNA-Seq differential expression. <i>Rna</i> , <b>2014</b> , 20, 1684-96  | 5.8 | 151 |
| 2 | A novel model to combine clinical and pathway-based transcriptomic information for the prognosis prediction of breast cancer. <i>PLoS Computational Biology</i> , <b>2014</b> , 10, e1003851     | 5   | 58  |
| 1 | Opportunities and obstacles for deep learning in biology and medicine  |     | 45  |