

Travers Ching

List of Publications by Citations

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Version: 2024-04-26

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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	Opportunities and obstacles for deep learning in biology and medicine. <i>Journal of the Royal Society Interface</i> , 2018 , 15,	4.1	780
20	Power analysis and sample size estimation for RNA-Seq differential expression. <i>Rna</i> , 2014 , 20, 1684-96	5.8	151
19	Cox-nnet: An artificial neural network method for prognosis prediction of high-throughput omics data. <i>PLoS Computational Biology</i> , 2018 , 14, e1006076	5	116
18	Single-Cell Transcriptomics Bioinformatics and Computational Challenges. <i>Frontiers in Genetics</i> , 2016 , 7, 163	4.5	80
17	A novel model to combine clinical and pathway-based transcriptomic information for the prognosis prediction of breast cancer. <i>PLoS Computational Biology</i> , 2014 , 10, e1003851	5	58
16	Alternative splicing promotes tumour aggressiveness and drug resistance in African American prostate cancer. <i>Nature Communications</i> , 2017 , 8, 15921	17.4	53
15	Detecting heterogeneity in single-cell RNA-Seq data by non-negative matrix factorization. <i>PeerJ</i> , 2017 , 5, e2888	3.1	49
14	Opportunities and obstacles for deep learning in biology and medicine		45
13	Genome-wide hypermethylation coupled with promoter hypomethylation in the chorioamniotic membranes of early onset pre-eclampsia. <i>Molecular Human Reproduction</i> , 2014 , 20, 885-904	4.4	42
12	Using single nucleotide variations in single-cell RNA-seq to identify subpopulations and genotype-phenotype linkage. <i>Nature Communications</i> , 2018 , 9, 4892	17.4	37
11	Genome-scale hypomethylation in the cord blood DNAs associated with early onset preeclampsia. <i>Clinical Epigenetics</i> , 2015 , 7, 21	7.7	34
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> , 2016 , 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> , 2016 , 7, 62-72	8.8	26
8	Multimodal Meta-Analysis of 1,494 Hepatocellular Carcinoma Samples Reveals Significant Impact of Consensus Driver Genes on Phenotypes. <i>Clinical Cancer Research</i> , 2019 , 25, 463-472	12.9	23
7	Non-coding yet non-trivial: a review on the computational genomics of lincRNAs. <i>BioData Mining</i> , 2015 , 8, 44	4.3	15
6	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> , 2016 , 15, 2026-38	5.6	12
5	A Novel FGFR3 Splice Variant Preferentially Expressed in African American Prostate Cancer Drives Aggressive Phenotypes and Docetaxel Resistance. <i>Molecular Cancer Research</i> , 2019 , 17, 2115-2125	6.6	5

4	Maternal cardiovascular-related single nucleotide polymorphisms, genes, and pathways associated with early-onset preeclampsia. <i>PLoS ONE</i> , 2019 , 14, e0222672	3.7	2
3	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> , 2018 , 1789, 205-220	1.4	1
2	Pan-cancer analysis of expressed somatic nucleotide variants in long intergenic non-coding RNA. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2018 , 23, 512-523	1.3	1
1	Glycerol-assisted degradation of dibenzothiophene by <i>Paraburkholderia</i> sp. C3 is associated with polyhydroxyalkanoate granulation. <i>Chemosphere</i> , 2021 , 291, 133054	8.4	0