

Travers Ching

List of Publications by Year in descending order

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Version: 2024-02-01

20
papers

2,435
citations

566801

15
h-index

752256

20
g-index

22
all docs

22
docs citations

22
times ranked

5016
citing authors

#	ARTICLE	IF	CITATIONS
1	Opportunities and obstacles for deep learning in biology and medicine. <i>Journal of the Royal Society Interface</i> , 2018, 15, 20170387.	1.5	1,282
2	Cox-nnet: An artificial neural network method for prognosis prediction of high-throughput omics data. <i>PLoS Computational Biology</i> , 2018, 14, e1006076.	1.5	241
3	Power analysis and sample size estimation for RNA-Seq differential expression. <i>Rna</i> , 2014, 20, 1684-1696.	1.6	204
4	Single-Cell Transcriptomics Bioinformatics and Computational Challenges. <i>Frontiers in Genetics</i> , 2016, 7, 163.	1.1	105
5	Alternative splicing promotes tumour aggressiveness and drug resistance in African American prostate cancer. <i>Nature Communications</i> , 2017, 8, 15921.	5.8	87
6	Detecting heterogeneity in single-cell RNA-Seq data by non-negative matrix factorization. <i>PeerJ</i> , 2017, 5, e2888.	0.9	77
7	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.	1.5	64
8	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.	1.3	54
9	Using single nucleotide variations in single-cell RNA-seq to identify subpopulations and genotype-phenotype linkage. <i>Nature Communications</i> , 2018, 9, 4892.	5.8	51
10	Genome-scale hypomethylation in the cord blood DNAs associated with early onset preeclampsia. <i>Clinical Epigenetics</i> , 2015, 7, 21.	1.8	41
11	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.	3.2	41
12	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.	1.6	37
13	Pan-Cancer Analyses Reveal Long Intergenic Non-Coding RNAs Relevant to Tumor Diagnosis, Subtyping and Prognosis. <i>EBioMedicine</i> , 2016, 7, 62-72.	2.7	33
14	Non-coding yet non-trivial: a review on the computational genomics of lincRNAs. <i>BioData Mining</i> , 2015, 8, 44.	2.2	20
15	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, 2026-2038.	1.8	16
16	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.	1.5	9
17	Maternal cardiovascular-related single nucleotide polymorphisms, genes, and pathways associated with early-onset preeclampsia. <i>PLoS ONE</i> , 2019, 14, e0222672.	1.1	6
18	Glycerol-assisted degradation of dibenzothiophene by <i>Paraburkholderia</i> sp. C3 is associated with polyhydroxyalkanoate granulation. <i>Chemosphere</i> , 2022, 291, 133054.	4.2	3

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19	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.	0.4	1
20	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.	0.7	1