

Jinze Liu

List of Publications by Year in descending order

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Version: 2024-02-01

32
papers

7,891
citations

471509

17
h-index

526287

27
g-index

33
all docs

33
docs citations

33
times ranked

13636
citing authors

#	ARTICLE	IF	CITATIONS
1	Circular RNAs are abundant, conserved, and associated with ALU repeats. <i>Rna</i> , 2013, 19, 141-157.	3.5	3,535
2	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. <i>Cell</i> , 2014, 159, 676-690.	28.9	2,318
3	MapSplice: Accurate mapping of RNA-seq reads for splice junction discovery. <i>Nucleic Acids Research</i> , 2010, 38, e178-e178.	14.5	946
4	Plant-Symbiotic Fungi as Chemical Engineers: Multi-Genome Analysis of the Clavicipitaceae Reveals Dynamics of Alkaloid Loci. <i>PLoS Genetics</i> , 2013, 9, e1003323.	3.5	344
5	DiffSplice: the genome-wide detection of differential splicing events with RNA-seq. <i>Nucleic Acids Research</i> , 2013, 41, e39-e39.	14.5	138
6	Classification of Whole Mammogram and Tomosynthesis Images Using Deep Convolutional Neural Networks. <i>IEEE Transactions on Nanobioscience</i> , 2018, 17, 237-242.	3.3	85
7	Exosomal lipids for classifying early and late stage non-small cell lung cancer. <i>Analytica Chimica Acta</i> , 2018, 1037, 256-264.	5.4	72
8	FDM: a graph-based statistical method to detect differential transcription using RNA-seq data. <i>Bioinformatics</i> , 2011, 27, 2633-2640.	4.1	50
9	Cytoplasmic synthesis of endogenous <i>Alu</i> complementary DNA via reverse transcription and implications in age-related macular degeneration. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	36
10	A novel data structure to support ultra-fast taxonomic classification of metagenomic sequences with <i>k</i> -mer signatures. <i>Bioinformatics</i> , 2018, 34, 171-178.	4.1	35
11	SeqOthello: querying RNA-seq experiments at scale. <i>Genome Biology</i> , 2018, 19, 167.	8.8	31
12	Annotation of the Protein Coding Regions of the Equine Genome. <i>PLoS ONE</i> , 2015, 10, e0124375.	2.5	29
13	Whole mammogram image classification with convolutional neural networks. , 2017, , .		27
14	Discerning novel splice junctions derived from RNA-seq alignment: a deep learning approach. <i>BMC Genomics</i> , 2018, 19, 971.	2.8	26
15	Approximate Clustering on Distributed Data Streams. , 2008, , .		24
16	Loss of CLN3, the gene mutated in juvenile neuronal ceroid lipofuscinosis, leads to metabolic impairment and autophagy induction in retinal pigment epithelium. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2020, 1866, 165883.	3.8	24
17	A probabilistic framework for aligning paired-end RNA-seq data. <i>Bioinformatics</i> , 2010, 26, 1950-1957.	4.1	23
18	Latexin Inactivation Enhances Survival and Long-Term Engraftment of Hematopoietic Stem Cells and Expands the Entire Hematopoietic System in Mice. <i>Stem Cell Reports</i> , 2017, 8, 991-1004.	4.8	21

#	ARTICLE	IF	CITATIONS
19	Tissue Restricted Splice Junctions Originate Not Only from Tissue-Specific Gene Loci, but Gene Loci with a Broad Pattern of Expression. PLoS ONE, 2015, 10, e0144302.	2.5	20
20	BlackOPs: increasing confidence in variant detection through mappability filtering. Nucleic Acids Research, 2013, 41, e178-e178.	14.5	19
21	Quaking orchestrates a post-transcriptional regulatory network of endothelial cell cycle progression critical to angiogenesis and metastasis. Oncogene, 2019, 38, 5191-5210.	5.9	19
22	Analysis of Unannotated Equine Transcripts Identified by mRNA Sequencing. PLoS ONE, 2013, 8, e70125.	2.5	16
23	DeepSplice: Deep classification of novel splice junctions revealed by RNA-seq. , 2016, , .		16
24	A Robust Method for Transcript Quantification with RNA-Seq Data. Journal of Computational Biology, 2013, 20, 167-187.	1.6	13
25	iMapSplice: Alleviating reference bias through personalized RNA-seq alignment. PLoS ONE, 2018, 13, e0201554.	2.5	9
26	Recent Shrinkage and Fragmentation of Bluegrass Landscape in Kentucky. Remote Sensing, 2020, 12, 1815.	4.0	5
27	A Case Study of Recommendation Algorithms. , 2011, , .		2
28	Piecing the puzzle together: a revisit to transcript reconstruction problem in RNA-seq. BMC Bioinformatics, 2014, 15, S3.	2.6	1
29	A Robust Method for Transcript Quantification with RNA-seq Data. Lecture Notes in Computer Science, 2012, , 127-147.	1.3	1
30	REC: fast sparse regression-based multcategory classification. Statistics and Its Interface, 2017, 10, 175-185.	0.3	1
31	HRV-Spark: Computing Heart Rate Variability Measures Using Apache Spark. , 2020, 2020, .		1
32	Tumor Suppressor Par-4 Regulates Complement Factor C3 and Obesity. Frontiers in Oncology, 2022, 12, 860446.	2.8	1