Jinze Liu

List of Publications by Year
in descending order

32	7,891	471509	526287
papers	**citations**	17	27
		h-index	**g-index**

33	33	33	13636
all docs	**docs citations**	**times ranked**	**citing authors**

#	Article	IF	Citations
1	Tumor Suppressor Par-4 Regulates Complement Factor C3 and Obesity. Frontiers in Oncology, 2022, 12, 860446.	2.8	1
2	Cytoplasmic synthesis of endogenous *Alu* complementary DNA via reverse transcription and implications in age-related macular degeneration. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	36
3	Recent Shrinkage and Fragmentation of Bluegrass Landscape in Kentucky. Remote Sensing, 2020, 12, 1815.	4.0	5
4	Loss of CLN3, the gene mutated in juvenile neuronal ceroid lipofuscinosis, leads to metabolic impairment and autophagy induction in retinal pigment epithelium. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2020, 1866, 165883.	3.8	24
5	HRV-Spark: Computing Heart Rate Variability Measures Using Apache Spark. , 2020, 2020, .		1
6	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
7	Exosomal lipids for classifying early and late stage non-small cell lung cancer. Analytica Chimica Acta, 2018, 1037, 256-264.	5.4	72
8	A novel data structure to support ultra-fast taxonomic classification of metagenomic sequences with *k*-mer signatures. Bioinformatics, 2018, 34, 171-178.	4.1	35
9	Discerning novel splice junctions derived from RNA-seq alignment: a deep learning approach. BMC Genomics, 2018, 19, 971.	2.8	26
10	SeqOthello: querying RNA-seq experiments at scale. Genome Biology, 2018, 19, 167.	8.8	31
11	iMapSplice: Alleviating reference bias through personalized RNA-seq alignment. PLoS ONE, 2018, 13, e0201554.	2.5	9
12	Classification of Whole Mammogram and Tomosynthesis Images Using Deep Convolutional Neural Networks. IEEE Transactions on Nanobioscience, 2018, 17, 237-242.	3.3	85
13	Latexin Inactivation Enhances Survival and Long-Term Engraftment of Hematopoietic Stem Cells and Expands the Entire Hematopoietic System in Mice. Stem Cell Reports, 2017, 8, 991-1004.	4.8	21
14	Whole mammogram image classification with convolutional neural networks. , 2017, , .		27
15	REC: fast sparse regression-based multicategory classification. Statistics and Its Interface, 2017, 10, 175-185.	0.3	1
16	DeepSplice: Deep classification of novel splice junctions revealed by RNA-seq. , 2016, , .		16
17	Annotation of the Protein Coding Regions of the Equine Genome. PLoS ONE, 2015, 10, e0124375.	2.5	29
18	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

#	Article	IF	Citations
19	Piecing the puzzle together: a revisit to transcript reconstruction problem in RNA-seq. BMC Bioinformatics, 2014, 15, S3.	2.6	1
20	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. Cell, 2014, 159, 676-690.	28.9	2,318
21	Circular RNAs are abundant, conserved, and associated with ALU repeats. Rna, 2013, 19, 141-157.	3.5	3,535
22	A Robust Method for Transcript Quantification with RNA-Seq Data. Journal of Computational Biology, 2013, 20, 167-187.	1.6	13
23	Plant-Symbiotic Fungi as Chemical Engineers: Multi-Genome Analysis of the Clavicipitaceae Reveals Dynamics of Alkaloid Loci. PLoS Genetics, 2013, 9, e1003323.	3.5	344
24	BlackOPs: increasing confidence in variant detection through mappability filtering. Nucleic Acids Research, 2013, 41, e178-e178.	14.5	19
25	DiffSplice: the genome-wide detection of differential splicing events with RNA-seq. Nucleic Acids Research, 2013, 41, e39-e39.	14.5	138
26	Analysis of Unannotated Equine Transcripts Identified by mRNA Sequencing. PLoS ONE, 2013, 8, e70125.	2.5	16
27	A Robust Method for Transcript Quantification with RNA-seq Data. Lecture Notes in Computer Science, 2012, , 127-147.	1.3	1
28	A Case Study of Recommendation Algorithms. , 2011, , .		2
29	FDM: a graph-based statistical method to detect differential transcription using RNA-seq data. Bioinformatics, 2011, 27, 2633-2640.	4.1	50
30	A probabilistic framework for aligning paired-end RNA-seq data. Bioinformatics, 2010, 26, 1950-1957.	4.1	23
31	MapSplice: Accurate mapping of RNA-seq reads for splice junction discovery. Nucleic Acids Research, 2010, 38, e178-e178.	14.5	946
32	Approximate Clustering on Distributed Data Streams. , 2008, , .		24