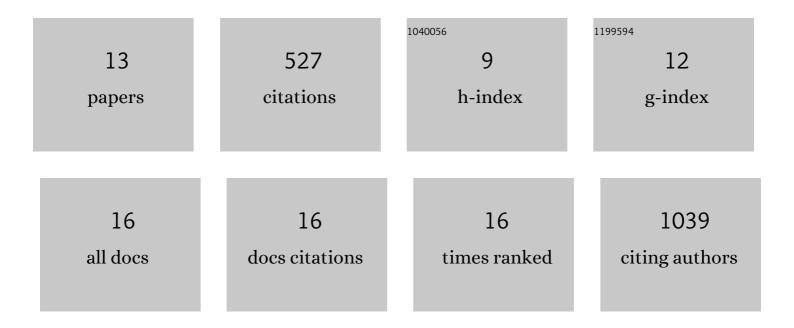


List of Publications by Year in descending order

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Vu Hu

#	ARTICLE	IF	CITATIONS
1	RNA-Seq identifies novel myocardial gene expression signatures of heart failure. Genomics, 2015, 105, 83-89.	2.9	220
2	Accounting for technical noise in differential expression analysis of single-cell RNA sequencing data. Nucleic Acids Research, 2017, 45, 10978-10988.	14.5	73
3	LIQA: long-read isoform quantification and analysis. Genome Biology, 2021, 22, 182.	8.8	49
4	Transcriptome-Wide Analysis Reveals Modulation of Human Macrophage Inflammatory Phenotype Through Alternative Splicing. Arteriosclerosis, Thrombosis, and Vascular Biology, 2016, 36, 1434-1447.	2.4	35
5	PennSeq: accurate isoform-specific gene expression quantification in RNA-Seq by modeling non-uniform read distribution. Nucleic Acids Research, 2014, 42, e20-e20.	14.5	33
6	Adipose tissue RNASeq reveals novel gene–nutrient interactions following n-3 PUFA supplementation and evoked inflammation in humans. Journal of Nutritional Biochemistry, 2016, 30, 126-132.	4.2	30
7	LongGF: computational algorithm and software tool for fast and accurate detection of gene fusions by long-read transcriptome sequencing. BMC Genomics, 2020, 21, 793.	2.8	22
8	Detecting differential alternative splicing events in scRNA-seq with or without Unique Molecular Identifiers. PLoS Computational Biology, 2020, 16, e1007925.	3.2	20
9	PennDiff: detecting differential alternative splicing and transcription by RNA sequencing. Bioinformatics, 2018, 34, 2384-2391.	4.1	14
10	Implications of Error-Prone Long-Read Whole-Genome Shotgun Sequencing on Characterizing Reference Microbiomes. IScience, 2020, 23, 101223.	4.1	10
11	Mapping Splicing Quantitative Trait Loci in RNA-Seq. Cancer Informatics, 2015, 14s1, CIN.S24832.	1.9	7
12	Mapping Splicing Quantitative Trait Loci in RNA-Seq. Cancer Informatics, 2014, 13s4, CIN.S13971.	1.9	6
13	Exploring strategy selection in populations via a continuous evolutionary game dynamics. , 2014, , .		3