

Po-Yen Wu

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4096619/publications.pdf>

Version: 2024-02-01

18
papers

800
citations

1478505

6
h-index

1872680

6
g-index

18
all docs

18
docs citations

18
times ranked

2000
citing authors

#	ARTICLE	IF	CITATIONS
1	Impact of RNA-seq data analysis algorithms on gene expression estimation and downstream prediction. Scientific Reports, 2020, 10, 17925.	3.3	18
2	Machine learning-based method for automated well-log processing and interpretation. , 2018, , .		22
3	“Omic and Electronic Health Record Big Data Analytics for Precision Medicine. IEEE Transactions on Biomedical Engineering, 2017, 64, 263-273.	4.2	198
4	Integration of multi-modal biomedical data to predict cancer grade and patient survival. , 2016, 2016, 577-580.		11
5	Evaluating the impact of sequencing error correction for RNA-seq data with ERCC RNA spike-in controls. , 2016, 2016, 74-77.		4
6	The impact of RNA-seq aligners on gene expression estimation. , 2015, 2015, 462-471.		10
7	Comparison of RNA-seq and microarray-based models for clinical endpoint prediction. Genome Biology, 2015, 16, 133.	8.8	325
8	The impact of RNA-seq alignment pipeline on detection of differentially expressed genes. , 2014, 2012, 1376-1379.		1
9	Cardiovascular Transcriptomics and Epigenomics Using Next-Generation Sequencing. Circulation: Cardiovascular Genetics, 2014, 7, 701-710.	5.1	14
10	Detecting and correcting systematic variation in large-scale RNA sequencing data. Nature Biotechnology, 2014, 32, 888-895.	17.5	174
11	PHARM - Association Rule Mining for Predictive Health. IFMBE Proceedings, 2014, 42, 114-117.	0.3	6
12	An approach for assessing RNA-seq quantification algorithms in replication studies. , 2013, 2013, 15-18.		2
13	Systematic Assessment of RNA-Seq Quantification Tools Using Simulated Sequence Data. , 2013, 2013, .		2
14	The effect of human genome annotation complexity on RNA-Seq gene expression quantification. , 2012, 2012, 712-717.		7
15	Improving the flexibility of RNA-Seq data analysis pipelines. , 2012, 2012, 70-73.		1
16	Evaluation of normalization methods for RNA-Seq gene expression estimation. , 2011, 2011, 50-57.		4
17	Exploring the feasibility of next-generation sequencing and microarray data meta-analysis. , 2011, 2011, 7618-21.		1
18	A distributed system for fast alignment of next-generation sequencing data. , 2010, 2010, 579-584.		0