CITATION REPORT

List of articles citing

Oqtans: the RNA-seq workbench in the cloud for complete and reproducible quantitative transcriptome analy

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Bioinformatics, 2014, 30, 1300-1.

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#	Paper	IF	Citations
12	TRUFA: A User-Friendly Web Server for de novo RNA-seq Analysis Using Cluster Computing. *Evolutionary Bioinformatics*, **2015**, 11, 97-104	1.9	30
11	RAP: RNA-Seq Analysis Pipeline, a new cloud-based NGS web application. *BMC Genomics*, **2015**, 16, S3	4.5	58
10	. **2015**,		
9	From Big Data Analytics and Network Inference to Systems Modeling. **2016**, 113-144		
8	RNA-seq analysis in forest tree species: bioinformatic problems and solutions. *Tree Genetics and Genomes*, **2016**, 12, 1	2.1	20
7	Data-aware optimization of bioinformatics workflows in hybrid clouds. *Journal of Big Data*, **2016**, 3,	11.7	2
6	TRAPLINE: a standardized and automated pipeline for RNA sequencing data analysis, evaluation and annotation. *BMC Bioinformatics*, **2016**, 17, 21	3.6	28
5	Scalability and Validation of Big Data Bioinformatics Software. *Computational and Structural Biotechnology Journal*, **2017**, 15, 379-386	6.8	23
4	Hermes: Seamless delivery of containerized bioinformatics workflows in hybrid cloud (HTC) environments. *SoftwareX*, **2017**, 6, 217-224	2.7	7
3	CAFU: a Galaxy framework for exploring unmapped RNA-Seq data. *Briefings in Bioinformatics*, **2020**, 21, 676-686	13.4	6
2	Comparative transcriptome and histological analyses provide insights into the skin pigmentation in Minxian black fur sheep (Ovis aries). *PeerJ*, **2021**, 9, e11122	3.1	0
1	Current challenges and best practices for cell-free long RNA biomarker discovery. **2022**, 10,		1