Ling-Hong Hung

List of Publications by Year
in descending order

20	914	933447 10	940533 16
papers	citations	h-index	g-index

30	30	30	1852
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A graphical, interactive and GPU-enabled workflow to process long-read sequencing data. BMC Genomics, 2021, 22, 626.	2.8	7
2	An Investigation on Public Cloud Performance Variation for an RNA Sequencing Workflow. , 2020, , .		2
3	Characterizing Performance Variation of Genomic Data Analysis Workflows on the Public Cloud. , 2020, , .		1
4	Building Containerized Workflows Using the BioDepot-Workflow-Builder. Cell Systems, 2019, 9, 508-514.e3.	6.2	18
5	Integration of Multiple Data Sources for Gene Network Inference Using Genetic Perturbation Data. Journal of Computational Biology, 2019, 26, 1113-1129.	1.6	7
6	Holistic optimization of an RNA-seq workflow for multi-threaded environments. Bioinformatics, 2019, 35, 4173-4175.	4.1	4
7	Using BioDepot-workflow-builder to Access Public Databases in a Containerized Environment. , 2019, , .		0
8	Reproducible Bioconductor workflows using browser-based interactive notebooks and containers. Journal of the American Medical Informatics Association: JAMIA, 2018, 25, 4-12.	4.4	23
9	Hot-starting software containers for STAR aligner. GigaScience, 2018, 7, .	6.4	9
10	Using BioDepot-workflow-Builder to Create and Execute Reproducible Bioinformatics Workflows. , 2018, , .		0
11	GUIdock: Using Docker Containers with a Common Graphics User Interface to Address the Reproducibility of Research. PLoS ONE, 2016, 11, e0152686.	2.5	40
12	fast_protein_cluster: parallel and optimized clustering of large-scale protein modeling data. Bioinformatics, 2014, 30, 1774-1776.	4.1	16
13	Data access for the 1,000 Plants (1KP) project. GigaScience, 2014, 3, 17.	6.4	582
14	Accelerated protein structure comparison using TM-score-GPU. Bioinformatics, 2012, 28, 2191-2192.	4.1	15
15	GPU-Q-J, a fast method for calculating root mean square deviation (RMSD) after optimal superposition. BMC Research Notes, 2011, 4, 97.	1.4	11
16	De Novo Protein Structure Prediction. Biological and Medical Physics Series, 2007, , 43-63.	0.4	7
17	An automated assignment-free Bayesian approach for accurately identifying proton contacts from NOESY data. Journal of Biomolecular NMR, 2006, 36, 189-198.	2.8	14
18	PROTINFO: new algorithms for enhanced protein structure predictions. Nucleic Acids Research, 2005, 33, W77-W80.	14.5	60

#	Article	IF	Citations
19	Accurate and automated classification of protein secondary structure with PsiCSI. Protein Science, 2003, 12, 288-295.	7.6	44
20	PROTINFO: secondary and tertiary protein structure prediction. Nucleic Acids Research, 2003, 31, 3296-3299.	14.5	38