

Ling-Hong Hung

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4889597/publications.pdf>

Version: 2024-02-01

20
papers

914
citations

933447

10
h-index

940533

16
g-index

30
all docs

30
docs citations

30
times ranked

1852
citing authors

#	ARTICLE	IF	CITATIONS
1	Data access for the 1,000 Plants (1KP) project. GigaScience, 2014, 3, 17.	6.4	582
2	PROTINFO: new algorithms for enhanced protein structure predictions. Nucleic Acids Research, 2005, 33, W77-W80.	14.5	60
3	Accurate and automated classification of protein secondary structure with PsiCSI. Protein Science, 2003, 12, 288-295.	7.6	44
4	GUIDock: Using Docker Containers with a Common Graphics User Interface to Address the Reproducibility of Research. PLoS ONE, 2016, 11, e0152686.	2.5	40
5	PROTINFO: secondary and tertiary protein structure prediction. Nucleic Acids Research, 2003, 31, 3296-3299.	14.5	38
6	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
7	Building Containerized Workflows Using the BioDepot-Workflow-Builder. Cell Systems, 2019, 9, 508-514.e3.	6.2	18
8	fast_protein_cluster: parallel and optimized clustering of large-scale protein modeling data. Bioinformatics, 2014, 30, 1774-1776.	4.1	16
9	Accelerated protein structure comparison using TM-score-GPU. Bioinformatics, 2012, 28, 2191-2192.	4.1	15
10	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
11	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
12	Hot-starting software containers for STAR aligner. GigaScience, 2018, 7, .	6.4	9
13	Integration of Multiple Data Sources for Gene Network Inference Using Genetic Perturbation Data. Journal of Computational Biology, 2019, 26, 1113-1129.	1.6	7
14	A graphical, interactive and GPU-enabled workflow to process long-read sequencing data. BMC Genomics, 2021, 22, 626.	2.8	7
15	De Novo Protein Structure Prediction. Biological and Medical Physics Series, 2007, , 43-63.	0.4	7
16	Holistic optimization of an RNA-seq workflow for multi-threaded environments. Bioinformatics, 2019, 35, 4173-4175.	4.1	4
17	An Investigation on Public Cloud Performance Variation for an RNA Sequencing Workflow. , 2020, , .		2
18	Characterizing Performance Variation of Genomic Data Analysis Workflows on the Public Cloud. , 2020, , .		1

#	ARTICLE	IF	CITATIONS
19	Using BioDepot-workflow-Builder to Create and Execute Reproducible Bioinformatics Workflows. , 2018, , .		0
20	Using BioDepot-workflow-builder to Access Public Databases in a Containerized Environment. , 2019, , .		0