Niema Moshiri

List of Publications by Year
in descending order

15 papers	**507** citations	1307594 **7** h-index	1281871 **11** g-index
28 all docs	**28** docs citations	**28** times ranked	**698** citing authors

#	Article	IF	Citations
1	An Evaluation of Phylogenetic Workflows in Viral Molecular Epidemiology. Viruses, 2022, 14, 774.	3.3	2
2	Accelerators for Classical Molecular Dynamics Simulations of Biomolecules. Journal of Chemical Theory and Computation, 2022, 18, 4047-4069.	5.3	15
3	ViralMSA: massively scalable reference-guided multiple sequence alignment of viral genomes. Bioinformatics, 2021, 37, 714-716.	4.1	55
4	FPGA Acceleration of Protein Back-Translation and Alignment. , 2021, , .		1
5	Timing the SARS-CoV-2 index case in Hubei province. Science, 2021, 372, 412-417.	12.6	109
6	HIV Care Prioritization Using Phylogenetic Branch Length. Journal of Acquired Immune Deficiency Syndromes (1999), 2021, 86, 626-637.	2.1	5
7	SEPIA: simulation-based evaluation of prioritization algorithms. BMC Medical Informatics and Decision Making, 2021, 21, 177.	3.0	0
8	Ten simple rules for attending your first conference. PLoS Computational Biology, 2021, 17, e1009133.	3.2	1
9	TreeSwift: A massively scalable Python tree package. SoftwareX, 2020, 11, 100436.	2.6	23
10	GenieHD: Efficient DNA Pattern Matching Accelerator Using Hyperdimensional Computing. , 2020, , .		34
11	Ten simple rules for writing and sharing computational analyses in Jupyter Notebooks. PLoS Computational Biology, 2019, 15, e1007007.	3.2	86
12	TreeCluster: Clustering biological sequences using phylogenetic trees. PLoS ONE, 2019, 14, e0221068.	2.5	99
13	FAVITES: simultaneous simulation of transmission networks, phylogenetic trees and sequences. Bioinformatics, 2019, 35, 1852-1861.	4.1	45
14	A Two-State Model of Tree Evolution and Its Applications to Alu Retrotransposition. Systematic Biology, 2018, 67, 475-489.	5.6	5
15	NiemaGraphGen: A memory-efficient global-scale contact network simulation toolkit. GigaByte, 0, 2022, 1-11.	0.0	2