Abdoulaye Banire Diallo

List of Publications by Year
in descending order

15 papers	204 citations	1163117 8 h-index	1281871 11 g-index
19 all docs	19 docs citations	19 times ranked	326 citing authors

#	Article	IF	Citations
1	Improving candidate Biosynthetic Gene Clusters in fungi through reinforcement learning. Bioinformatics, 2022, 38, 3984-3991.	4.1	2
2	TOUCAN: a framework for fungal biosynthetic gene cluster discovery. NAR Genomics and Bioinformatics, 2020, 2, lqaa098.	3.2	13
3	Selected Papers from the Workshop on Computational Biology: Joint with the International Joint Conference on Artificial Intelligence and the International Conference on Machine Learning, 2018. Journal of Computational Biology, 2019, 26, 507-508.	1.6	2
4	Toward an Alignment-Free Method for Feature Extraction and Accurate Classification of Viral Sequences. Journal of Computational Biology, 2019, 26, 519-535.	1.6	20
5	Statistical Linear Models in Virus Genomic Alignment-free Classification: Application to Hepatitis C Viruses. , 2019, , .		4
6	Subtle differences in selective pressures applied on the envelope gene of HIV-1 in pregnant versus non-pregnant women. Infection, Genetics and Evolution, 2018, 62, 141-150.	2.3	0
7	T-GOWler: Discovering Generalized Process Models Within Texts. Journal of Computational Biology, 2017, 24, 799-808.	1.6	0
8	A machine learning approach for viral genome classification. BMC Bioinformatics, 2017, 18, 208.	2.6	47
9	Preface: Selected Papers from the Workshop Bioinformatics and Artificial Intelligence Joined with the International Joint Conference on Artificial Intelligence. Journal of Computational Biology, 2017, 24, 733-733.	1.6	0
10	A novel comprehensive wheat miRNA database, including related bioinformatics software. Current Plant Biology, 2016, 7-8, 31-33.	4.7	19
11	ProtNN: fast and accurate protein 3D-structure classification in structural and topological space. BioData Mining, 2016, 9, 30.	4.0	9
12	Classification of bioinformatics workflows using weighted versions of partitioning and hierarchical clustering algorithms. BMC Bioinformatics, 2015, 16, 68.	2.6	13
13	An integrative approach to identify hexaploid wheat miRNAome associated with development and tolerance to abiotic stress. BMC Genomics, 2015, 16, 339.	2.8	25
14	Ancestors 1.0: a web server for ancestral sequence reconstruction. Bioinformatics, 2010, 26, 130-131.	4.1	38
15	A Whole Genome Study and Identification of Specific Carcinogenic Regions of the Human Papilloma Viruses. Journal of Computational Biology, 2009, 16, 1461-1473.	1.6	6