Jelili Oyelade

List of Publications by Year
in descending order

27 papers	594 citations	840776 11 h-index	752698 20 g-index
28 all docs	28 docs citations	28 times ranked	938 citing authors

#	Article	IF	Citations
1	Predicting host dependency factors of pathogens in Drosophila melanogaster using machine learning. Computational and Structural Biotechnology Journal, 2021, 19, 4581-4592.	4.1	4
2	Machine learning approach to gene essentiality prediction: a review. Briefings in Bioinformatics, 2021, 22, .	6.5	47
3	Essential gene prediction in Drosophila melanogaster using machine learning approaches based on sequence and functional features. Computational and Structural Biotechnology Journal, 2020, 18, 612-621.	4.1	30
4	Overview of the human genome. , 2020, , 9-26.		0
5	Gene Expression Profiling Analysis Reveals Putative Phytochemotherapeutic Target for Castration-Resistant Prostate Cancer. Frontiers in Oncology, 2019, 9, 714.	2.8	5
6	Epidemiology of Plasmodium falciparum infection and drug resistance markers in Ota Area, Southwestern Nigeria . Infection and Drug Resistance, 2019, Volume 12, 1941-1949.	2.7	3
7	Computational Identification of Metabolic Pathways of<i>Plasmodium falciparum</i>using the<mml:math xmlns:mml="http://www.w3.org/1998/Math/MathML" id="M1"><mml:mi>k</mml:mi></mml:math>-Shortest Path Algorithm. International Journal of Genomics, 2019, 2019, 1-13.	1.6	9
8	Data Clustering: Algorithms and Its Applications. , 2019, , .		41
9	Potential Anti-Cancer Flavonoids Isolated From <i>Caesalpinia bonduc</i> Young Twigs and Leaves: Molecular Docking and In Silico Studies. Bioinformatics and Biology Insights, 2019, 13, 117793221882137.	2.0	40
10	Genomic Interventions in Medicine. Bioinformatics and Biology Insights, 2018, 12, 117793221881610.	2.0	5
11	In Silico Knockout Screening of<i> Plasmodium falciparum</i> Reactions and Prediction of Novel Essential Reactions by Analysing the Metabolic Network. BioMed Research International, 2018, 2018, 1-11.	1.9	8
12	Inter-Species/Host-Parasite Protein Interaction Predictions Reviewed. Current Bioinformatics, 2018, 13, 396-406.	1.5	24
13	Functional enrichment of human protein complexes in malaria parasites. , 2017, , .		0
14	Modeling of Metabolic Pathways Using Petri Net. , 2017, , .		1
15	Extreme Pathway Analysis of Mycobacterium Tuberculosis. , 2017, , .		0
16	Development of Bioinformatics Infrastructure for Genomics Research. Global Heart, 2017, 12, 91.	2.3	47
17	Modeling of the Glycolysis Pathway inPlasmodium falciparumusing Petri Nets. Bioinformatics and Biology Insights, 2016, 10, BBI.S37296.	2.0	11
18	Clustering Algorithms: Their Application to Gene Expression Data. Bioinformatics and Biology Insights, 2016, 10, BBI.S38316.	2.0	139

#	Article	IF	Citations
19	H3ABioNet, a sustainable pan-African bioinformatics network for human heredity and health in Africa. Genome Research, 2016, 26, 271-277.	5.5	94
20	Cluster analysis of Plasmodium RNA-seq time-course data identifies stage-specific co-regulated biological processes and regulatory elements. F1000Research, 2016, 5, 1932.	1.6	2
21	In Silico Gene Regulatory Network of the Maurer's Cleft Pathway in Plasmodium falciparum. Evolutionary Bioinformatics, 2015, 11, EBO.S25585.	1.2	2
22	Bioinformatics, Healthcare Informatics and Analytics: An Imperative for Improved Healthcare System. International Journal of Applied Information Systems, 2015, 8, 1-6.	0.1	18
23	Design and Implementation of Text To Speech Conversion for Visually Impaired People. International Journal of Applied Information Systems, 2014, 7, 25-30.	0.1	31
24	Reducing the Time Requirement of k-Means Algorithm. PLoS ONE, 2012, 7, e49946.	2.5	18
25	Computational identification of signalling pathways in Plasmodium falciparum. Infection, Genetics and Evolution, 2011, 11, 755-764.	2.3	15
26	Effectiveness of model-based clustering in analyzing Plasmodium falciparum RNA-seq time-course data. F1000Research, 0, 6, 1706.	1.6	0
27	Effectiveness of model-based clustering in analyzing Plasmodium falciparum RNA-seq time-course data. F1000Research, 0, 6, 1706.	1.6	0