

Jelili Oyelade

List of Publications by Year in descending order

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Version: 2024-02-01

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	Clustering Algorithms: Their Application to Gene Expression Data. <i>Bioinformatics and Biology Insights</i> , 2016, 10, BBI.S38316.	2.0	139
2	H3ABioNet, a sustainable pan-African bioinformatics network for human heredity and health in Africa. <i>Genome Research</i> , 2016, 26, 271-277.	5.5	94
3	Development of Bioinformatics Infrastructure for Genomics Research. <i>Global Heart</i> , 2017, 12, 91.	2.3	47
4	Machine learning approach to gene essentiality prediction: a review. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	47
5	Data Clustering: Algorithms and Its Applications. , 2019, , .		41
6	Potential Anti-Cancer Flavonoids Isolated From <i>Caesalpinia bonduca</i> Young Twigs and Leaves: Molecular Docking and In Silico Studies. <i>Bioinformatics and Biology Insights</i> , 2019, 13, 117793221882137.	2.0	40
7	Design and Implementation of Text To Speech Conversion for Visually Impaired People. <i>International Journal of Applied Information Systems</i> , 2014, 7, 25-30.	0.1	31
8	Essential gene prediction in <i>Drosophila melanogaster</i> using machine learning approaches based on sequence and functional features. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 612-621.	4.1	30
9	Inter-Species/Host-Parasite Protein Interaction Predictions Reviewed. <i>Current Bioinformatics</i> , 2018, 13, 396-406.	1.5	24
10	Reducing the Time Requirement of k-Means Algorithm. <i>PLoS ONE</i> , 2012, 7, e49946.	2.5	18
11	Bioinformatics, Healthcare Informatics and Analytics: An Imperative for Improved Healthcare System. <i>International Journal of Applied Information Systems</i> , 2015, 8, 1-6.	0.1	18
12	Computational identification of signalling pathways in <i>Plasmodium falciparum</i> . <i>Infection, Genetics and Evolution</i> , 2011, 11, 755-764.	2.3	15
13	Modeling of the Glycolysis Pathway in <i>Plasmodium falciparum</i> using Petri Nets. <i>Bioinformatics and Biology Insights</i> , 2016, 10, BBI.S37296.	2.0	11
14	Computational Identification of Metabolic Pathways of <i>Plasmodium falciparum</i> using the $\langle \text{mml:math xmlns:mml="http://www.w3.org/1998/Math/MathML" id="M1"} \rangle \langle \text{mml:mi} \rangle k \langle \text{mml:mi} \rangle \langle \text{mml:math} \rangle$ -Shortest Path Algorithm. <i>International Journal of Genomics</i> , 2019, 2019, 1-13.	1.6	9
15	In Silico Knockout Screening of <i>Plasmodium falciparum</i> Reactions and Prediction of Novel Essential Reactions by Analysing the Metabolic Network. <i>BioMed Research International</i> , 2018, 2018, 1-11.	1.9	8
16	Genomic Interventions in Medicine. <i>Bioinformatics and Biology Insights</i> , 2018, 12, 117793221881610.	2.0	5
17	Gene Expression Profiling Analysis Reveals Putative Phytochemotherapeutic Target for Castration-Resistant Prostate Cancer. <i>Frontiers in Oncology</i> , 2019, 9, 714.	2.8	5
18	Predicting host dependency factors of pathogens in <i>Drosophila melanogaster</i> using machine learning. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 4581-4592.	4.1	4

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19	<p><p>Epidemiology of Plasmodium falciparum infection and drug resistance markers in Ota Area, Southwestern Nigeria</p>. Infection and Drug Resistance, 2019, Volume 12, 1941-1949.</p>	2.7	3
20	<p>In Silico Gene Regulatory Network of the Maurer's Cleft Pathway in Plasmodium falciparum. Evolutionary Bioinformatics, 2015, 11, EBO.S25585.</p>	1.2	2
21	<p>Cluster analysis of Plasmodium RNA-seq time-course data identifies stage-specific co-regulated biological processes and regulatory elements. F1000Research, 2016, 5, 1932.</p>	1.6	2
22	<p>Modeling of Metabolic Pathways Using Petri Net. , 2017, , .</p>		1
23	<p>Functional enrichment of human protein complexes in malaria parasites. , 2017, , .</p>		0
24	<p>Extreme Pathway Analysis of Mycobacterium Tuberculosis. , 2017, , .</p>		0
25	<p>Overview of the human genome. , 2020, , 9-26.</p>		0
26	<p>Effectiveness of model-based clustering in analyzing Plasmodium falciparum RNA-seq time-course data. F1000Research, 0, 6, 1706.</p>	1.6	0
27	<p>Effectiveness of model-based clustering in analyzing Plasmodium falciparum RNA-seq time-course data. F1000Research, 0, 6, 1706.</p>	1.6	0