

Saman Zeeshan

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

22
papers

310
citations

10
h-index

17
g-index

29
ext. papers

478
ext. citations

4.5
avg, IF

4.26
L-index

#	Paper	IF	Citations
22	Artificial intelligence with multi-functional machine learning platform development for better healthcare and precision medicine. <i>Database: the Journal of Biological Databases and Curation</i> , 2020 , 2020,	5	108
21	Software applications toward quantitative metabolic flux analysis and modeling. <i>Briefings in Bioinformatics</i> , 2014 , 15, 91-107	13.4	45
20	Lipid-Pro: a computational lipid identification solution for untargeted lipidomics on data-independent acquisition tandem mass spectrometry platforms. <i>Bioinformatics</i> , 2015 , 31, 1150-3	7.2	24
19	Software LS-MIDA for efficient mass isotopomer distribution analysis in metabolic modelling. <i>BMC Bioinformatics</i> , 2013 , 14, 218	3.6	17
18	Mining biomedical images towards valuable information retrieval in biomedical and life sciences. <i>Database: the Journal of Biological Databases and Curation</i> , 2016 , 2016,	5	15
17	Isotopova database application for facile analysis and management of mass isotopomer data. <i>Database: the Journal of Biological Databases and Curation</i> , 2014 , 2014,	5	14
16	100 Years of evolving gene-disease complexities and scientific debutants. <i>Briefings in Bioinformatics</i> , 2020 , 21, 885-905	13.4	14
15	Human gene and disease associations for clinical-genomics and precision medicine research. <i>Clinical and Translational Medicine</i> , 2020 , 10, 297-318	5.7	13
14	Developing sustainable software solutions for bioinformatics by the " Butterfly" paradigm. <i>F1000Research</i> , 2014 , 3, 71	3.6	12
13	Cultivating Software Solutions Development in the Scientific Academia. <i>Recent Patents on Computer Science</i> , 2014 , 7, 54-66	1	11
12	Integrative clinical, genomics and metabolomics data analysis for mainstream precision medicine to investigate COVID-19. <i>BMJ Innovations</i> , 2021 , 7, 6-10	1.8	9
11	Debutant iOS app and gene-disease complexities in clinical genomics and precision medicine. <i>Clinical and Translational Medicine</i> , 2019 , 8, 26	5.7	7
10	Advancing clinical genomics and precision medicine with GViZ: FAIR bioinformatics platform for variable gene-disease annotation, visualization, and expression analysis. <i>Human Genomics</i> , 2021 , 15, 37	6.8	5
9	Ant-App-DB: a smart solution for monitoring arthropods activities, experimental data management and solar calculations without GPS in behavioral field studies. <i>F1000Research</i> , 2014 , 3, 311	3.6	3
8	Genomics pipelines to investigate susceptibility in whole genome and exome sequenced data for variant discovery, annotation, prediction and genotyping. <i>PeerJ</i> , 2021 , 9, e11724	3.1	3
7	Computational Feature Performance and Domain Specific Architecture Evaluation of Software Applications Towards Metabolic Flux Analysis. <i>Recent Patents on Computer Science</i> , 2012 , 5, 165-176	1	2
6	Applying WEKA towards Machine Learning With Genetic Algorithm and Back-propagation Neural Networks. <i>Journal of Data Mining in Genomics & Proteomics</i> , 2014 , 05,		1

5	Ant-App-DB: a smart solution for monitoring arthropods activities, experimental data management and solar calculations without GPS in behavioral field studies. <i>F1000Research</i> ,3, 311	3.6	1
4	RNA-seq driven expression and enrichment analysis to investigate CVD genes with associated phenotypes among high-risk heart failure patients. <i>Human Genomics</i> , 2021 , 15, 67	6.8	1
3	Targeting the immune microenvironment during immunotherapy for solid tumors. <i>Molecular and Cellular Oncology</i> , 2021 , 8, 1994327	1.2	1
2	JWES: a new pipeline for whole genome/exome sequence data processing, management, and gene-variant discovery, annotation, prediction, and genotyping. <i>FEBS Open Bio</i> , 2021 , 11, 2441-2452	2.7	1
1	Bioinformatics Tools for PacBio Sequenced Amplicon Data Pre-processing and Target Sequence Extraction. <i>Lecture Notes in Networks and Systems</i> , 2020 , 326-340	0.5	