Saman Zeeshan

List of Publications by Year in Descending Order

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	RNA-seq driven expression and enrichment analysis to investigate CVD genes with associated phenotypes among high-risk heart failure patients. *Human Genomics*, **2021**, 15, 67	6.8	1
21	Targeting the immune microenvironment during immunotherapy for solid tumors. *Molecular and Cellular Oncology*, **2021**, 8, 1994327	1.2	1
20	Advancing clinical genomics and precision medicine with GVViZ: FAIR bioinformatics platform for variable gene-disease annotation, visualization, and expression analysis. *Human Genomics*, **2021**, 15, 37	6.8	5
19	Integrative clinical, genomics and metabolomics data analysis for mainstream precision medicine to investigate COVID-19. *BMJ Innovations*, **2021**, 7, 6-10	1.8	9
18	Genomics pipelines to investigate susceptibility in whole genome and exome sequenced data for variant discovery, annotation, prediction and genotyping. *PeerJ*, **2021**, 9, e11724	3.1	3
17	JWES: a new pipeline for whole genome/exome sequence data processing, management, and gene-variant discovery, annotation, prediction, and genotyping. *FEBS Open Bio*, **2021**, 11, 2441-2452	2.7	1
16	Human gene and disease associations for clinical-genomics and precision medicine research. *Clinical and Translational Medicine*, **2020**, 10, 297-318	5.7	13
15	Artificial intelligence with multi-functional machine learning platform development for better healthcare and precision medicine. *Database: the Journal of Biological Databases and Curation*, **2020**, 2020,	5	108
14	100 Years of evolving gene-disease complexities and scientific debutants. *Briefings in Bioinformatics*, **2020**, 21, 885-905	13.4	14
13	Bioinformatics Tools for PacBio Sequenced Amplicon Data Pre-processing and Target Sequence Extraction. *Lecture Notes in Networks and Systems*, **2020**, 326-340	0.5	
12	Debutant iOS app and gene-disease complexities in clinical genomics and precision medicine. *Clinical and Translational Medicine*, **2019**, 8, 26	5.7	7
11	Mining biomedical images towards valuable information retrieval in biomedical and life sciences. *Database: the Journal of Biological Databases and Curation*, **2016**, 2016,	5	15
10	Lipid-Pro: a computational lipid identification solution for untargeted lipidomics on data-independent acquisition tandem mass spectrometry platforms. *Bioinformatics*, **2015**, 31, 1150-3	7.2	24
9	Software applications toward quantitative metabolic flux analysis and modeling. *Briefings in Bioinformatics*, **2014**, 15, 91-107	13.4	45
8	Applying WEKA towards Machine Learning With Genetic Algorithm and Back-propagation Neural Networks. *Journal of Data Mining in Genomics & Proteomics*, **2014**, 05,		1
7	Cultivating Software Solutions Development in the Scientific Academia. *Recent Patents on Computer Science*, **2014**, 7, 54-66	1	11
6	IsotopoW a database application for facile analysis and management of mass isotopomer data. *Database: the Journal of Biological Databases and Curation*, **2014**, 2014,	5	14

LIST OF PUBLICATIONS

5	Developing sustainable software solutions for bioinformatics by the " Butterfly" paradigm. *F1000Research*, **2014**, 3, 71	3.6	12
4	Ant-App-DB: a smart solution for monitoring arthropods activities, experimental data management and solar calculations without GPS in behavioral field studies. *F1000Research*, **2014**, 3, 311	3.6	3
3	Software LS-MIDA for efficient mass isotopomer distribution analysis in metabolic modelling. *BMC Bioinformatics*, **2013**, 14, 218	3.6	17
2	Computational Feature Performance and Domain Specific Architecture Evaluation of Software Applications Towards Metabolic Flux Analysis. *Recent Patents on Computer Science*, **2012**, 5, 165-176	1	2
1	Ant-App-DB: a smart solution for monitoring arthropods activities, experimental data management and solar calculations without GPS in behavioral field studies. *F1000Research*,3, 311	3.6	1