

Muhammad Tahir

List of Publications by Year in descending order

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Version: 2024-02-01

20
papers

713
citations

759233

12
h-index

888059

17
g-index

22
all docs

22
docs citations

22
times ranked

400
citing authors

#	ARTICLE	IF	CITATIONS
1	iNuc-STNC: a sequence-based predictor for identification of nucleosome positioning in genomes by extending the concept of SAAC and Chou's PseAAC. <i>Molecular BioSystems</i> , 2016, 12, 2587-2593.	2.9	94
2	iRNA-PseKNC(2methyl): Identify RNA 2'-O-methylation sites by convolution neural network and Chou's pseudo components. <i>Journal of Theoretical Biology</i> , 2019, 465, 1-6.	1.7	90
3	iN6-Methyl (5-step): Identifying RNA N6-methyladenosine sites using deep learning mode via Chou's 5-step rules and Chou's general PseKNC. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2019, 193, 103811.	3.5	83
4	Early and accurate detection and diagnosis of heart disease using intelligent computational model. <i>Scientific Reports</i> , 2020, 10, 19747.	3.3	73
5	iPseU-CNN: Identifying RNA Pseudouridine Sites Using Convolutional Neural Networks. <i>Molecular Therapy - Nucleic Acids</i> , 2019, 16, 463-470.	5.1	72
6	iNuc-ext-PseTNC: an efficient ensemble model for identification of nucleosome positioning by extending the concept of Chou's PseAAC to pseudo-tri-nucleotide composition. <i>Molecular Genetics and Genomics</i> , 2019, 294, 199-210.	2.1	52
7	Sequence based predictor for discrimination of enhancer and their types by applying general form of Chou's trinucleotide composition. <i>Computer Methods and Programs in Biomedicine</i> , 2017, 146, 69-75.	4.7	47
8	Identification of prokaryotic promoters and their strength by integrating heterogeneous features. <i>Genomics</i> , 2020, 112, 1396-1403.	2.9	41
9	Machine learning based identification of protein-protein interactions using derived features of physiochemical properties and evolutionary profiles. <i>Artificial Intelligence in Medicine</i> , 2017, 78, 61-71.	6.5	35
10	iRNA-PseTNC: identification of RNA 5-methylcytosine sites using hybrid vector space of pseudo nucleotide composition. <i>Frontiers of Computer Science</i> , 2020, 14, 451-460.	2.4	29
11	Prediction of N6-methyladenosine sites using convolution neural network model based on distributed feature representations. <i>Neural Networks</i> , 2020, 129, 385-391.	5.9	27
12	A Two-Layer Computational Model for Discrimination of Enhancer and Their Types Using Hybrid Features Pace of Pseudo K-Tuple Nucleotide Composition. <i>Arabian Journal for Science and Engineering</i> , 2018, 43, 6719-6727.	3.0	18
13	Precision Measurement for Industry 4.0 Standards towards Solid Waste Classification through Enhanced Imaging Sensors and Deep Learning Model. <i>Wireless Communications and Mobile Computing</i> , 2021, 2021, 1-10.	1.2	13
14	Applications, limitations, and improvements in visible light communication systems. , 2015, , .		12
15	iEnhancer-Deep: A Computational Predictor for Enhancer Sites and Their Strength Using Deep Learning. <i>Applied Sciences (Switzerland)</i> , 2022, 12, 2120.	2.5	11
16	Efficient computational model for classification of protein localization images using Extended Threshold Adjacency Statistics and Support Vector Machines. <i>Computer Methods and Programs in Biomedicine</i> , 2018, 157, 205-215.	4.7	10
17	Prediction of Piwi-Interacting RNAs and Their Functions via Convolutional Neural Network. <i>IEEE Access</i> , 2021, 9, 54233-54240.	4.2	2
18	An effective machine learning-based model for the prediction of protein-protein interaction sites in health systems. <i>Neural Computing and Applications</i> , 2024, 36, 65-75.	5.6	2

#	ARTICLE	IF	CITATIONS
19	Multimedia sensor networks: Recent trends, research challenges and future directions. , 2017, , .		1
20	An Effective Deep Learning-Based Architecture for Prediction of N7-Methylguanosine Sites in Health Systems. Electronics (Switzerland), 2022, 11, 1917.	3.1	1