Zhijun Liao

List of Publications by Year
in descending order

17 papers	543 citations	933447 10 h-index	940533 16 g-index
17 all docs	17 docs citations	17 times ranked	640 citing authors

#	Article	IF	Citations
1	Identification of DNA-Binding Proteins via Hypergraph Based Laplacian Support Vector Machine. Current Bioinformatics, 2022, 17, 108-117.	1.5	22
2	Identification of Methicillin-Resistant Staphylococcus Aureus From Methicillin-Sensitive Staphylococcus Aureus and Molecular Characterization in Quanzhou, China. Frontiers in Cell and Developmental Biology, 2021, 9, 629681.	3.7	15
3	Predicting subcellular location of protein with evolution information and sequence-based deep learning. BMC Bioinformatics, 2021, 22, 515.	2.6	11
4	RCGA-Net: An Improved Multi-hybrid Attention Mechanism Network in Biomedical Image Segmentation. , 2021, , .		4
5	Iterative feature representations improve N4-methylcytosine site prediction. Bioinformatics, 2019, 35, 4930-4937.	4.1	113
6	Ubiquitin-Specific Protease USP6 Regulates the Stability of the c-Jun Protein. Molecular and Cellular Biology, 2018, 38, .	2.3	24
7	Cancer Diagnosis Through IsomiR Expression with Machine Learning Method. Current Bioinformatics, 2018, 13, 57-63.	1.5	138
8	MiR-93-5p Promotes Cell Proliferation through Down-Regulating PPARGC1A in Hepatocellular Carcinoma Cells by Bioinformatics Analysis and Experimental Verification. Genes, 2018, 9, 51.	2.4	31
9	Classification of Small GTPases with Hybrid Protein Features and Advanced Machine Learning Techniques. Current Bioinformatics, 2018, 13, 492-500.	1.5	43
10	Construction and Identification of the RNAi Recombinant Lentiviral Vector Targeting Human DEPDC7 Gene. Interdisciplinary Sciences, Computational Life Sciences, 2017, 9, 350-356.	3.6	9
11	DEPDC7 inhibits cell proliferation, migration and invasion in hepatoma cells. Oncology Letters, 2017, 14, 7332-7338.	1.8	5
12	Prediction and Identification of KrÃ¼ppel-Like Transcription Factors by Machine Learning Method. Combinatorial Chemistry and High Throughput Screening, 2017, 20, 594-602.	1.1	8
13	Prediction of G Protein-Coupled Receptors with SVM-Prot Features and Random Forest. Scientifica, 2016, 2016, 1-10.	1.7	38
14	<i>In Silico</i> Prediction of Gamma-Aminobutyric Acid Type-A Receptors Using Novel Machine-Learning-Based SVM and GBDT Approaches. BioMed Research International, 2016, 2016, 1-12.	1.9	26
15	Resistance gene identification from Larimichthys crocea with machine learning techniques. Scientific Reports, 2016, 6, 38367.	3.3	3
16	Identification of DEP domain-containing proteins by a machine learning method and experimental analysis of their expression in human HCC tissues. Scientific Reports, 2016, 6, 39655.	3.3	16
17	Which statistical significance test best detects oncomiRNAs in cancer tissues? An exploratory analysis. Oncotarget, 2016, 7, 85613-85623.	1.8	37