

Zhijun Liao

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4493285/publications.pdf>

Version: 2024-02-01

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