Zhuo Wang

List of Publications by Year
in descending order

18 papers	351 citations	933447 10 h-index	888059 17 g-index
19 all docs	19 docs citations	19 times ranked	236 citing authors

#	ARTICLE	IF	CITATIONS
1	dbPTM in 2022: an updated database for exploring regulatory networks and functional associations of protein post-translational modifications. Nucleic Acids Research, 2022, 50, D471-D479.	14.5	59
2	dbAMP 2.0: updated resource for antimicrobial peptides with an enhanced scanning method for genomic and proteomic data. Nucleic Acids Research, 2022, 50, D460-D470.	14.5	49
3	Characterization and Identification of Natural Antimicrobial Peptides on Different Organisms. International Journal of Molecular Sciences, 2020, 21, 986.	4.1	45
4	AVPIden: a new scheme for identification and functional prediction of antiviral peptides based on machine learning approaches. Briefings in Bioinformatics, 2021, 22, .	6.5	35
5	Identifying anti-coronavirus peptides by incorporating different negative datasets and imbalanced learning strategies. Briefings in Bioinformatics, 2021, 22, 1085-1095.	6.5	32
6	CircNet 2.0: an updated database for exploring circular RNA regulatory networks in cancers. Nucleic Acids Research, 2022, 50, D93-D101.	14.5	27
7	A large-scale investigation and identification of methicillin-resistant Staphylococcus aureus based on peaks binning of matrix-assisted laser desorption ionization-time of flight MS spectra. Briefings in Bioinformatics, 2021, 22, .	6.5	24
8	Incorporating Deep Learning With Word Embedding to Identify Plant Ubiquitylation Sites. Frontiers in Cell and Developmental Biology, 2020, 8, 572195.	3.7	16
9	Incorporating support vector machine with sequential minimal optimization to identify anticancer peptides. BMC Bioinformatics, 2021, 22, 286.	2.6	13
10	Characterization and identification of lysine crotonylation sites based on machine learning method on both plant and mammalian. Scientific Reports, 2020, 10, 20447.	3.3	12
11	DTWscore: differential expression and cell clustering analysis for time-series single-cell RNA-seq data. BMC Bioinformatics, 2017, 18, 270.	2.6	11
12	Large-scale mass spectrometry data combined with demographics analysis rapidly predicts methicillin resistance in Staphylococcus aureus. Briefings in Bioinformatics, 2020, 22, .	6.5	11
13	Rapid Antibiotic Resistance Serial Prediction in Staphylococcus aureus Based on Large-Scale MALDI-TOF Data by Applying XGBoost in Multi-Label Learning. Frontiers in Microbiology, 2022, 13, 853775.	3.5	6
14	MDRSA: A Web Based-Tool for Rapid Identification of Multidrug Resistant Staphylococcus aureus Based on Matrix-Assisted Laser Desorption Ionization-Time of Flight Mass Spectrometry. Frontiers in Microbiology, 2021, 12, 766206.	3.5	4
15	Large-Scale Samples Based Rapid Detection of Ciprofloxacin Resistance in Klebsiella pneumoniae Using Machine Learning Methods. Frontiers in Microbiology, 2022, 13, 827451.	3.5	4
16	A Method Based on Differential Entropy-Like Function for Detecting Differentially Expressed Genes Across Multiple Conditions in RNA-Seq Studies. Entropy, 2019, 21, 242.	2.2	1
17	The Complexity of Promoter Regions Based on a Vector Topological Entropy. Current Bioinformatics, 2017, 12, .	1.5	1
18	Residue–Residue Contact Can Be a Potential Feature for the Prediction of Lysine Crotonylation Sites. Frontiers in Genetics, 2021, 12, 788467.	2.3	1