

Zhuo Wang

List of Publications by Year in descending order

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Version: 2024-02-01

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