Qiao Ning

List of Publications by Year
in descending order

18 papers	365 citations	1040018 9 h-index	940516 16 g-index
18 all docs	18 docs citations	18 times ranked	515 citing authors

#	Article	IF	Citations
1	Bioinformatics Resources and Tools for Conformational B-Cell Epitope Prediction. Computational and Mathematical Methods in Medicine, 2013, 2013, 1-11.	1.3	89
2	dForml(KNN)-PseAAC: Detecting formylation sites from protein sequences using K-nearest neighbor algorithm via Chou's 5-step rule and pseudo components. Journal of Theoretical Biology, 2019, 470, 43-49.	1.7	55
3	Accurate in silico identification of protein succinylation sites using an iterative semi-supervised learning technique. Journal of Theoretical Biology, 2015, 374, 60-65.	1.7	40
4	Detecting Succinylation sites from protein sequences using ensemble support vector machine. BMC Bioinformatics, 2018, 19, 237.	2.6	37
5	Position-Specific Analysis and Prediction of Protein Pupylation Sites Based on Multiple Features. BioMed Research International, 2013, 2013, 1-9.	1.9	28
6	Identifying N6-methyladenosine sites using extreme gradient boosting system optimized by particle swarm optimizer. Journal of Theoretical Biology, 2019, 467, 39-47.	1.7	21
7	PGluS: prediction of protein S-glutathionylation sites with multiple features and analysis. Molecular BioSystems, 2015, 11, 923-929.	2.9	20
8	Analysis and prediction of human acetylation using a cascade classifier based on support vector machine. BMC Bioinformatics, 2019, 20, 346.	2.6	12
9	Identifying drug–target interactions via heterogeneous graph attention networks combined with cross-modal similarities. Briefings in Bioinformatics, 2022, 23, .	6.5	12
10	PGlcS: Prediction of protein O-GlcNAcylation sites with multiple features and analysis. Journal of Theoretical Biology, 2015, 380, 524-529.	1.7	11
11	SSKM_Succ: A Novel Succinylation Sites Prediction Method Incorporating K-Means Clustering With a New Semi-Supervised Learning Algorithm. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 643-652.	3.0	11
12	Identification of Protein Pupylation Sites Using Bi-Profile Bayes Feature Extraction and Ensemble Learning. Mathematical Problems in Engineering, 2013, 2013, 1-7.	1.1	9
13	Identification of S-glutathionylation sites in species-specific proteins by incorporating five sequence-derived features into the general pseudo-amino acid composition. Journal of Theoretical Biology, 2016, 398, 96-102.	1.7	8
14	A Novel Framework Based on ACO and PSO for RNA Secondary Structure Prediction. Mathematical Problems in Engineering, 2013, 2013, 1-8.	1.1	4
15	m7G-DLSTM: Intergrating directional Double-LSTM and fully connected network for RNA N7-methlguanosine sites prediction in human. Chemometrics and Intelligent Laboratory Systems, 2021, 217, 104398.	3.5	4
16	ABC-Gly: Identifying Protein Lysine Glycation Sites with Artificial Bee Colony Algorithm. Current Proteomics, 2021, 18, 18-26.	0.3	2
17	Heterogeneous Graph Convolutional Network integrates Multi-modal Similarities for Drug-Target Interaction Prediction. , 2021, , .		2
18	pQLyCar: Peptide-based dynamic query-driven sample rescaling strategy for identifying carboxylation sites combined with KNN and SVM. Analytical Biochemistry, 2021, 633, 114386.	2.4	0