Xuan Xiao

List of Publications by Year
in descending order

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		76326	197818
52	6,276	40	49
papers	citations	h-index	g-index

55	55	55	2083
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	iPTT(2â€‰L)-CNN: A Two-Layer Predictor for Identifying Promoters and Their Types in Plant Genomes by Convolutional Neural Network. Computational and Mathematical Methods in Medicine, 2021, 2021, 1-9.	1.3	3
2	EMCBOW-GPCR: A method for identifying G-protein coupled receptors based on word embedding and wordbooks. Computational and Structural Biotechnology Journal, 2021, 19, 4961-4969.	4.1	6
3	Identifying GPCR-drug interaction based on wordbook learning from sequences. BMC Bioinformatics, 2020, 21, 150.	2.6	10
4	pLoc_bal-mGpos: Predict subcellular localization of Gram-positive bacterial proteins by quasi-balancing training dataset and PseAAC. Genomics, 2019, 111, 886-892.	2.9	87
5	pLoc_bal-mAnimal: predict subcellular localization of animal proteins by balancing training dataset and PseAAC. Bioinformatics, 2019, 35, 398-406.	4.1	89
6	pLoc_bal-mHum: Predict subcellular localization of human proteins by PseAAC and quasi-balancing training dataset. Genomics, 2019, 111, 1274-1282.	2.9	63
7	iPSW(2L)-PseKNC: A two-layer predictor for identifying promoters and their strength by hybrid features via pseudo K-tuple nucleotide composition. Genomics, 2019, 111, 1785-1793.	2.9	60
8	iPPI-PseAAC(CGR): Identify protein-protein interactions by incorporating chaos game representation into PseAAC. Journal of Theoretical Biology, 2019, 460, 195-203.	1.7	88
9	pLoc_bal-mPlant: Predict Subcellular Localization of Plant Proteins by General PseAAC and Balancing Training Dataset. Current Pharmaceutical Design, 2019, 24, 4013-4022.	1.9	46
10	Computational Prediction of Ubiquitination Proteins Using Evolutionary Profiles and Functional Domain Annotation. Current Genomics, 2019, 20, 389-399.	1.6	11
11	pLoc_bal-mVirus: Predict Subcellular Localization of Multi-Label Virus Proteins by Chou's General PseAAC and IHTS Treatment to Balance Training Dataset. Medicinal Chemistry, 2019, 15, 496-509.	1.5	50
12	pLoc-mHum: predict subcellular localization of multi-location human proteins via general PseAAC to winnow out the crucial GO information. Bioinformatics, 2018, 34, 1448-1456.	4.1	139
13	pLoc-mEuk: Predict subcellular localization of multi-label eukaryotic proteins by extracting the key GO information into general PseAAC. Genomics, 2018, 110, 50-58.	2.9	193
14	pLoc-mGneg: Predict subcellular localization of Gram-negative bacterial proteins by deep gene ontology learning via general PseAAC. Genomics, 2018, 110, 231-239.	2.9	130
15	iKcr-PseEns: Identify lysine crotonylation sites in histone proteins with pseudo components and ensemble classifier. Genomics, 2018, 110, 239-246.	2.9	127
16	pLoc_bal-mGneg: Predict subcellular localization of Gram-negative bacterial proteins by quasi-balancing training dataset and general PseAAC. Journal of Theoretical Biology, 2018, 458, 92-102.	1.7	71
17	iATC-mISF: a multi-label classifier for predicting the classes of anatomical therapeutic chemicals. Bioinformatics, 2017, 33, 341-346.	4.1	139
18	iPhosâ€PseEvo: Identifying Human Phosphorylated Proteins by Incorporating Evolutionary Information into General PseAAC via Grey System Theory. Molecular Informatics, 2017, 36, 1600010.	2.5	94

#	Article	IF	Citations
19	Multi-label Learning for Predicting the Activities of Antimicrobial Peptides. Scientific Reports, 2017, 7, 2202.	3.3	8
20	pLoc-mVirus: Predict subcellular localization of multi-location virus proteins via incorporating the optimal GO information into general PseAAC. Gene, 2017, 628, 315-321.	2.2	138
21	pLoc-mAnimal: predict subcellular localization of animal proteins with both single and multiple sites. Bioinformatics, 2017, 33, 3524-3531.	4.1	175
22	Rectified-Linear-Unit-Based Deep Learning for Biomedical Multi-label Data. Interdisciplinary Sciences, Computational Life Sciences, 2017, 9, 419-422.	3.6	18
23	Multiâ€‐PPseEvo: A Multiâ€‐label Classifier for Identifying Human Phosphorylated Proteins by Incorporating Evolutionary Information into Chouâ€²s General PseAAC via Grey System Theory. Molecular Informatics, 2017, 36, 1600085.	2.5	29
24	iATC-mHyb: a hybrid multi-label classifier for predicting the classification of anatomical therapeutic chemicals. Oncotarget, 2017, 8, 58494-58503.	1.8	118
25	iRNAm5C-PseDNC: identifying RNA 5-methylcytosine sites by incorporating physical-chemical properties into pseudo dinucleotide composition. Oncotarget, 2017, 8, 41178-41188.	1.8	191
26	iRNA-2methyl: Identify RNA 2'-O-methylation Sites by Incorporating Sequence-Coupled Effects into General PseKNC and Ensemble Classifier. Medicinal Chemistry, 2017, 13, 734-743.	1.5	104
27	iROS-gPseKNC: Predicting replication origin sites in DNA by incorporating dinucleotide position-specific propensity into general pseudo nucleotide composition. Oncotarget, 2016, 7, 34180-34189.	1.8	118
28	iPPBS-Opt: A Sequence-Based Ensemble Classifier for Identifying Protein-Protein Binding Sites by Optimizing Imbalanced Training Datasets. Molecules, 2016, 21, 95.	3.8	142
29	iHyd-PseCp: Identify hydroxyproline and hydroxylysine in proteins by incorporating sequence-coupled effects into general PseAAC. Oncotarget, 2016, 7, 44310-44321.	1.8	150
30	iCar-PseCp: identify carbonylation sites in proteins by Monte Carlo sampling and incorporating sequence coupled effects into general PseAAC. Oncotarget, 2016, 7, 34558-34570.	1.8	176
31	iPTM-mLys: identifying multiple lysine PTM sites and their different types. Bioinformatics, 2016, 32, 3116-3123.	4.1	236
32	pSuc-Lys: Predict lysine succinylation sites in proteins with PseAAC and ensemble random forest approach. Journal of Theoretical Biology, 2016, 394, 223-230.	1.7	297
33	pRNAm-PC: Predicting N6-methyladenosine sites in RNA sequences via physicalâ€“chemical properties. Analytical Biochemistry, 2016, 497, 60-67.	2.4	247
34	iSuc-PseOpt: Identifying lysine succinylation sites in proteins by incorporating sequence-coupling effects into pseudo components and optimizing imbalanced training dataset. Analytical Biochemistry, 2016, 497, 48-56.	2.4	254
35	Identification of protein-protein binding sites by incorporating the physicochemical properties and stationary wavelet transforms into pseudo amino acid composition. Journal of Biomolecular Structure and Dynamics, 2016, 34, 1946-1961.	3.5	120
36	iPhos-PseEn: Identifying phosphorylation sites in proteins by fusing different pseudo components into an ensemble classifier. Oncotarget, 2016, 7, 51270-51283.	1.8	142

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37	iPPI-Esml: An ensemble classifier for identifying the interactions of proteins by incorporating their physicochemical properties and wavelet transforms into PseAAC. Journal of Theoretical Biology, 2015, 377, 47-56.	1.7	265
38	Benchmark data for identifying DNA methylation sites via pseudo trinucleotide composition. Data in Brief, 2015, 4, 87-89.	1.0	8
39	iDNA-Methyl: Identifying DNA methylation sites via pseudo trinucleotide composition. Analytical Biochemistry, 2015, 474, 69-77.	2.4	246
40	iMethyl-PseAAC: Identification of Protein Methylation Sites via a Pseudo Amino Acid Composition Approach. BioMed Research International, 2014, 2014, 1-12.	1.9	152
41	iLoc-Animal: a multi-label learning classifier for predicting subcellular localization of animal proteins. Molecular BioSystems, 2013, 9, 634.	2.9	245
42	iAMP-2L: A two-level multi-label classifier for identifying antimicrobial peptides and their functional types. Analytical Biochemistry, 2013, 436, 168-177.	2.4	442
43	iCDI-PseFpt: Identify the channelâ€“drug interaction in cellular networking with PseAAC and molecular fingerprints. Journal of Theoretical Biology, 2013, 337, 71-79.	1.7	113
44	iEzy-Drug: A Web Server for Identifying the Interaction between Enzymes and Drugs in Cellular Networking. BioMed Research International, 2013, 2013, 1-13.	1.9	73
45	iGPCR-Drug: A Web Server for Predicting Interaction between GPCRs and Drugs in Cellular Networking. PLoS ONE, 2013, 8, e72234.	2.5	106
46	iLoc-Hum: using the accumulation-label scale to predict subcellular locations of human proteins with both single and multiple sites. Molecular BioSystems, 2012, 8, 629-641.	2.9	335
47	iNR-PhysChem: A Sequence-Based Predictor for Identifying Nuclear Receptors and Their Subfamilies via Physical-Chemical Property Matrix. PLoS ONE, 2012, 7, e30869.	2.5	81
48	GPCR-2L: predicting G protein-coupled receptors and their types by hybridizing two different modes of pseudo amino acid compositions. Molecular BioSystems, 2011, 7, 911-919.	2.9	136
49	A new approach using geometric moments of distance matrix image for risk type prediction of human papillomaviruses. , 2011, , .		0
50	Application of protein Hasse matrix image to predict protein structural classes. , 2010, , .		0
51	Predicting G-Protein-Coupled Receptor classes based on adaptive K-nearest neighbor algorithm. , 2010, , .		0
52	Predicting protein structural classes with pseudo amino acid composition: A new approach using geometric moments of distance matrix image. , 2010, , .		0