

Xuan Xiao

List of Publications by Year in descending order

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Version: 2024-02-01

52
papers

6,276
citations

76196

40
h-index

197535

49
g-index

55
all docs

55
docs citations

55
times ranked

2083
citing authors

#	ARTICLE	IF	CITATIONS
1	iAMP-2L: A two-level multi-label classifier for identifying antimicrobial peptides and their functional types. <i>Analytical Biochemistry</i> , 2013, 436, 168-177.	1.1	442
2	iLoc-Hum: using the accumulation-label scale to predict subcellular locations of human proteins with both single and multiple sites. <i>Molecular BioSystems</i> , 2012, 8, 629-641.	2.9	335
3	pSuc-Lys: Predict lysine succinylation sites in proteins with PseAAC and ensemble random forest approach. <i>Journal of Theoretical Biology</i> , 2016, 394, 223-230.	0.8	297
4	iPPI-Esml: An ensemble classifier for identifying the interactions of proteins by incorporating their physicochemical properties and wavelet transforms into PseAAC. <i>Journal of Theoretical Biology</i> , 2015, 377, 47-56.	0.8	265
5	iSuc-PseOpt: Identifying lysine succinylation sites in proteins by incorporating sequence-coupling effects into pseudo components and optimizing imbalanced training dataset. <i>Analytical Biochemistry</i> , 2016, 497, 48-56.	1.1	254
6	pRNAm-PC: Predicting N6-methyladenosine sites in RNA sequences via physical-chemical properties. <i>Analytical Biochemistry</i> , 2016, 497, 60-67.	1.1	247
7	iDNA-Methyl: Identifying DNA methylation sites via pseudo trinucleotide composition. <i>Analytical Biochemistry</i> , 2015, 474, 69-77.	1.1	246
8	iLoc-Animal: a multi-label learning classifier for predicting subcellular localization of animal proteins. <i>Molecular BioSystems</i> , 2013, 9, 634.	2.9	245
9	iPTM-mLys: identifying multiple lysine PTM sites and their different types. <i>Bioinformatics</i> , 2016, 32, 3116-3123.	1.8	236
10	pLoc-mEuk: Predict subcellular localization of multi-label eukaryotic proteins by extracting the key GO information into general PseAAC. <i>Genomics</i> , 2018, 110, 50-58.	1.3	193
11	iRNAm5C-PseDNC: identifying RNA 5-methylcytosine sites by incorporating physical-chemical properties into pseudo dinucleotide composition. <i>Oncotarget</i> , 2017, 8, 41178-41188.	0.8	191
12	iCar-PseCp: identify carbonylation sites in proteins by Monte Carlo sampling and incorporating sequence coupled effects into general PseAAC. <i>Oncotarget</i> , 2016, 7, 34558-34570.	0.8	176
13	pLoc-mAnimal: predict subcellular localization of animal proteins with both single and multiple sites. <i>Bioinformatics</i> , 2017, 33, 3524-3531.	1.8	175
14	iMethyl-PseAAC: Identification of Protein Methylation Sites via a Pseudo Amino Acid Composition Approach. <i>BioMed Research International</i> , 2014, 2014, 1-12.	0.9	152
15	iHyd-PseCp: Identify hydroxyproline and hydroxylysine in proteins by incorporating sequence-coupled effects into general PseAAC. <i>Oncotarget</i> , 2016, 7, 44310-44321.	0.8	150
16	iPPBS-Opt: A Sequence-Based Ensemble Classifier for Identifying Protein-Protein Binding Sites by Optimizing Imbalanced Training Datasets. <i>Molecules</i> , 2016, 21, 95.	1.7	142
17	iPhos-PseEn: Identifying phosphorylation sites in proteins by fusing different pseudo components into an ensemble classifier. <i>Oncotarget</i> , 2016, 7, 51270-51283.	0.8	142
18	iATC-mISF: a multi-label classifier for predicting the classes of anatomical therapeutic chemicals. <i>Bioinformatics</i> , 2017, 33, 341-346.	1.8	139

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19	pLoc-mHum: predict subcellular localization of multi-location human proteins via general PseAAC to winnow out the crucial GO information. <i>Bioinformatics</i> , 2018, 34, 1448-1456.	1.8	139
20	pLoc-mVirus: Predict subcellular localization of multi-location virus proteins via incorporating the optimal GO information into general PseAAC. <i>Gene</i> , 2017, 628, 315-321.	1.0	138
21	GPCR-2L: predicting G protein-coupled receptors and their types by hybridizing two different modes of pseudo amino acid compositions. <i>Molecular BioSystems</i> , 2011, 7, 911-919.	2.9	136
22	pLoc-mGneg: Predict subcellular localization of Gram-negative bacterial proteins by deep gene ontology learning via general PseAAC. <i>Genomics</i> , 2018, 110, 231-239.	1.3	130
23	iKcr-PseEns: Identify lysine crotonylation sites in histone proteins with pseudo components and ensemble classifier. <i>Genomics</i> , 2018, 110, 239-246.	1.3	127
24	Identification of protein-protein binding sites by incorporating the physicochemical properties and stationary wavelet transforms into pseudo amino acid composition. <i>Journal of Biomolecular Structure and Dynamics</i> , 2016, 34, 1946-1961.	2.0	120
25	iROS-gPseKNC: Predicting replication origin sites in DNA by incorporating dinucleotide position-specific propensity into general pseudo nucleotide composition. <i>Oncotarget</i> , 2016, 7, 34180-34189.	0.8	118
26	iATC-mHyb: a hybrid multi-label classifier for predicting the classification of anatomical therapeutic chemicals. <i>Oncotarget</i> , 2017, 8, 58494-58503.	0.8	118
27	iCDI-PseFpt: Identify the channel-drug interaction in cellular networking with PseAAC and molecular fingerprints. <i>Journal of Theoretical Biology</i> , 2013, 337, 71-79.	0.8	113
28	iGPCR-Drug: A Web Server for Predicting Interaction between GPCRs and Drugs in Cellular Networking. <i>PLoS ONE</i> , 2013, 8, e72234.	1.1	106
29	iRNA-2methyl: Identify RNA 2'-O-methylation Sites by Incorporating Sequence-Coupled Effects into General PseKNC and Ensemble Classifier. <i>Medicinal Chemistry</i> , 2017, 13, 734-743.	0.7	104
30	iPhos-PseEvo: Identifying Human Phosphorylated Proteins by Incorporating Evolutionary Information into General PseAAC via Grey System Theory. <i>Molecular Informatics</i> , 2017, 36, 1600010.	1.4	94
31	pLoc_bal-mAnimal: predict subcellular localization of animal proteins by balancing training dataset and PseAAC. <i>Bioinformatics</i> , 2019, 35, 398-406.	1.8	89
32	iPPI-PseAAC(CGR): Identify protein-protein interactions by incorporating chaos game representation into PseAAC. <i>Journal of Theoretical Biology</i> , 2019, 460, 195-203.	0.8	88
33	pLoc_bal-mGpos: Predict subcellular localization of Gram-positive bacterial proteins by quasi-balancing training dataset and PseAAC. <i>Genomics</i> , 2019, 111, 886-892.	1.3	87
34	iNR-PhysChem: A Sequence-Based Predictor for Identifying Nuclear Receptors and Their Subfamilies via Physical-Chemical Property Matrix. <i>PLoS ONE</i> , 2012, 7, e30869.	1.1	81
35	iEzy-Drug: A Web Server for Identifying the Interaction between Enzymes and Drugs in Cellular Networking. <i>BioMed Research International</i> , 2013, 2013, 1-13.	0.9	73
36	pLoc_bal-mGneg: Predict subcellular localization of Gram-negative bacterial proteins by quasi-balancing training dataset and general PseAAC. <i>Journal of Theoretical Biology</i> , 2018, 458, 92-102.	0.8	71

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37	pLoc_bal-mHum: Predict subcellular localization of human proteins by PseAAC and quasi-balancing training dataset. <i>Genomics</i> , 2019, 111, 1274-1282.	1.3	63
38	iPSW(2L)-PseKNC: A two-layer predictor for identifying promoters and their strength by hybrid features via pseudo K-tuple nucleotide composition. <i>Genomics</i> , 2019, 111, 1785-1793.	1.3	60
39	pLoc_bal-mVirus: Predict Subcellular Localization of Multi-Label Virus Proteins by Chou's General PseAAC and IHTS Treatment to Balance Training Dataset. <i>Medicinal Chemistry</i> , 2019, 15, 496-509.	0.7	50
40	pLoc_bal-mPlant: Predict Subcellular Localization of Plant Proteins by General PseAAC and Balancing Training Dataset. <i>Current Pharmaceutical Design</i> , 2019, 24, 4013-4022.	0.9	46
41	Multi-PPseEvo: A Multi-label Classifier for Identifying Human Phosphorylated Proteins by Incorporating Evolutionary Information into Chou's General PseAAC via Grey System Theory. <i>Molecular Informatics</i> , 2017, 36, 1600085.	1.4	29
42	Rectified-Linear-Unit-Based Deep Learning for Biomedical Multi-label Data. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2017, 9, 419-422.	2.2	18
43	Computational Prediction of Ubiquitination Proteins Using Evolutionary Profiles and Functional Domain Annotation. <i>Current Genomics</i> , 2019, 20, 389-399.	0.7	11
44	Identifying GPCR-drug interaction based on wordbook learning from sequences. <i>BMC Bioinformatics</i> , 2020, 21, 150.	1.2	10
45	Benchmark data for identifying DNA methylation sites via pseudo trinucleotide composition. <i>Data in Brief</i> , 2015, 4, 87-89.	0.5	8
46	Multi-label Learning for Predicting the Activities of Antimicrobial Peptides. <i>Scientific Reports</i> , 2017, 7, 2202.	1.6	8
47	EMCBOW-GPCR: A method for identifying G-protein coupled receptors based on word embedding and wordbooks. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 4961-4969.	1.9	6
48	iPTT(2L)-CNN: A Two-Layer Predictor for Identifying Promoters and Their Types in Plant Genomes by Convolutional Neural Network. <i>Computational and Mathematical Methods in Medicine</i> , 2021, 2021, 1-9.	0.7	3
49	Application of protein Hasse matrix image to predict protein structural classes. , 2010, , .		0
50	Predicting G-Protein-Coupled Receptor classes based on adaptive K-nearest neighbor algorithm. , 2010, , .		0
51	Predicting protein structural classes with pseudo amino acid composition: A new approach using geometric moments of distance matrix image. , 2010, , .		0
52	A new approach using geometric moments of distance matrix image for risk type prediction of human papillomaviruses. , 2011, , .		0