Xuan Xiao

List of Publications by Year in Descending Order

48 papers	5,391 citations	39 h-index	55 g-index
55 ext. papers	5,839 ext. citations	3.7 avg, IF	6.4 L-index

#	Paper	IF	Citations
48	iPTT(2 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, 6636350	2.8	1
47	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	6.8	1
46	Identifying GPCR-drug interaction based on wordbook learning from sequences. *BMC Bioinformatics*, **2020**, 21, 150	3.6	5
45	pLoc_bal-mGpos: Predict subcellular localization of Gram-positive bacterial proteins by quasi-balancing training dataset and PseAAC. *Genomics*, **2019**, 111, 886-892	4.3	75
44	pLoc_bal-mAnimal: predict subcellular localization of animal proteins by balancing training dataset and PseAAC. *Bioinformatics*, **2019**, 35, 398-406	7.2	76
43	Computational Prediction of Ubiquitination Proteins Using Evolutionary Profiles and Functional Domain Annotation. *Current Genomics*, **2019**, 20, 389-399	2.6	5
42	pLoc_bal-mVirus: Predict Subcellular Localization of Multi-Label Virus Proteins by ChouŴGeneral PseAAC and IHTS Treatment to Balance Training Dataset. *Medicinal Chemistry*, **2019**, 15, 496-509	1.8	41
41	pLoc_bal-mHum: Predict subcellular localization of human proteins by PseAAC and quasi-balancing training dataset. *Genomics*, **2019**, 111, 1274-1282	4.3	53
40	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	4.3	30
39	iPPI-PseAAC(CGR): Identify protein-protein interactions by incorporating chaos game representation into PseAAC. *Journal of Theoretical Biology*, **2019**, 460, 195-203	2.3	73
38	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	7.2	124
37	pLoc-mEuk: Predict subcellular localization of multi-label eukaryotic proteins by extracting the key GO information into general PseAAC. *Genomics*, **2018**, 110, 50-58	4.3	176
36	pLoc_bal-mPlant: Predict Subcellular Localization of Plant Proteins by General PseAAC and Balancing Training Dataset. *Current Pharmaceutical Design*, **2018**, 24, 4013-4022	3.3	41
35	iKcr-PseEns: Identify lysine crotonylation sites in histone proteins with pseudo components and ensemble classifier. *Genomics*, **2018**, 110, 239-246	4.3	109
34	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	2.3	62
33	iPhos-PseEvo: Identifying Human Phosphorylated Proteins by Incorporating Evolutionary Information into General PseAAC via Grey System Theory. *Molecular Informatics*, **2017**, 36, 1600010	3.8	82
32	Multi-label Learning for Predicting the Activities of Antimicrobial Peptides. *Scientific Reports*, **2017**, 7, 2202	4.9	8

31	iRNAm5C-PseDNC: identifying RNA 5-methylcytosine sites by incorporating physical-chemical properties into pseudo dinucleotide composition. *Oncotarget*, **2017**, 8, 41178-41188	3.3	148
30	iATC-mISF: a multi-label classifier for predicting the classes of anatomical therapeutic chemicals. *Bioinformatics*, **2017**, 33, 341-346	7.2	59
29	pLoc-mVirus: Predict subcellular localization of multi-location virus proteins via incorporating the optimal GO information into general PseAAC. *Gene*, **2017**, 628, 315-321	3.8	131
28	pLoc-mAnimal: predict subcellular localization of animal proteins with both single and multiple sites. *Bioinformatics*, **2017**, 33, 3524-3531	7.2	163
27	Rectified-Linear-Unit-Based Deep Learning for Biomedical Multi-label Data. *Interdisciplinary Sciences, Computational Life Sciences*, **2017**, 9, 419-422	3.5	12
26	Multi-iPPseEvo: A Multi-label Classifier for Identifying Human Phosphorylated Proteins by Incorporating Evolutionary Information into Chou's General PseAAC via Grey System Theory. *Molecular Informatics*, **2017**, 36, 1600085	3.8	26
25	iATC-mHyb: a hybrid multi-label classifier for predicting the classification of anatomical therapeutic chemicals. *Oncotarget*, **2017**, 8, 58494-58503	3.3	98
24	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	1.8	93
23	pLoc-mGneg: Predict subcellular localization of Gram-negative bacterial proteins by deep gene ontology learning via general PseAAC. *Genomics*, **2017**, 110, 231-231	4.3	115
22	iPTM-mLys: identifying multiple lysine PTM sites and their different types. *Bioinformatics*, **2016**, 32, 3116-3123	7.3	212
21	pSuc-Lys: Predict lysine succinylation sites in proteins with PseAAC and ensemble random forest approach. *Journal of Theoretical Biology*, **2016**, 394, 223-230	2.3	252
20	pRNAm-PC: Predicting N(6)-methyladenosine sites in RNA sequences via physical-chemical properties. *Analytical Biochemistry*, **2016**, 497, 60-7	3.1	213
19	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	3.1	218
18	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, 1946-61	3.6	111
17	iPhos-PseEn: identifying phosphorylation sites in proteins by fusing different pseudo components into an ensemble classifier. *Oncotarget*, **2016**, 7, 51270-51283	3.3	133
16	iROS-gPseKNC: Predicting replication origin sites in DNA by incorporating dinucleotide position-specific propensity into general pseudo nucleotide composition. *Oncotarget*, **2016**, 7, 34180-9	3.3	103
15	iPPBS-Opt: A Sequence-Based Ensemble Classifier for Identifying Protein-Protein Binding Sites by Optimizing Imbalanced Training Datasets. *Molecules*, **2016**, 21, E95	4.8	131
14	iHyd-PseCp: Identify hydroxyproline and hydroxylysine in proteins by incorporating sequence-coupled effects into general PseAAC. *Oncotarget*, **2016**, 7, 44310-44321	3.3	138

13	iCar-PseCp: identify carbonylation sites in proteins by Monte Carlo sampling and incorporating sequence coupled effects into general PseAAC. *Oncotarget*, **2016**, 7, 34558-70	3.3	161
12	iDNA-Methyl: identifying DNA methylation sites via pseudo trinucleotide composition. *Analytical Biochemistry*, **2015**, 474, 69-77	3.1	226
11	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	2.3	243
10	Benchmark data for identifying DNA methylation sites via pseudo trinucleotide composition. *Data in Brief*, **2015**, 4, 87-9	1.2	8
9	iMethyl-PseAAC: identification of protein methylation sites via a pseudo amino acid composition approach. *BioMed Research International*, **2014**, 2014, 947416	3	126
8	iLoc-Animal: a multi-label learning classifier for predicting subcellular localization of animal proteins. *Molecular BioSystems*, **2013**, 9, 634-44		213
7	iAMP-2L: a two-level multi-label classifier for identifying antimicrobial peptides and their functional types. *Analytical Biochemistry*, **2013**, 436, 168-77	3.1	334
6	iCDI-PseFpt: identify the channel-drug interaction in cellular networking with PseAAC and molecular fingerprints. *Journal of Theoretical Biology*, **2013**, 337, 71-9	2.3	101
5	iEzy-drug: a web server for identifying the interaction between enzymes and drugs in cellular networking. *BioMed Research International*, **2013**, 2013, 701317	3	65
4	iGPCR-drug: a web server for predicting interaction between GPCRs and drugs in cellular networking. *PLoS ONE*, **2013**, 8, e72234	3.7	88
3	iLoc-Hum: using the accumulation-label scale to predict subcellular locations of human proteins with both single and multiple sites. *Molecular BioSystems*, **2012**, 8, 629-41		316
2	iNR-PhysChem: a sequence-based predictor for identifying nuclear receptors and their subfamilies via physical-chemical property matrix. *PLoS ONE*, **2012**, 7, e30869	3.7	66
1	GPCR-2L: predicting G protein-coupled receptors and their types by hybridizing two different modes of pseudo amino acid compositions. *Molecular BioSystems*, **2011**, 7, 911-9		121