

Xuan Xiao

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	iAMP-2L: a two-level multi-label classifier for identifying antimicrobial peptides and their functional types. <i>Analytical Biochemistry</i> , 2013 , 436, 168-77	3.1	334
47	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, 629-41		316
46	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	2.3	252
45	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	2.3	243
44	iDNA-Methyl: identifying DNA methylation sites via pseudo trinucleotide composition. <i>Analytical Biochemistry</i> , 2015 , 474, 69-77	3.1	226
43	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	3.1	218
42	pRNAm-PC: Predicting N(6)-methyladenosine sites in RNA sequences via physical-chemical properties. <i>Analytical Biochemistry</i> , 2016 , 497, 60-7	3.1	213
41	iLoc-Animal: a multi-label learning classifier for predicting subcellular localization of animal proteins. <i>Molecular BioSystems</i> , 2013 , 9, 634-44		213
40	iPTM-mLys: identifying multiple lysine PTM sites and their different types. <i>Bioinformatics</i> , 2016 , 32, 3116-3123	3.1	212
39	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	4.3	176
38	pLoc-mAnimal: predict subcellular localization of animal proteins with both single and multiple sites. <i>Bioinformatics</i> , 2017 , 33, 3524-3531	7.2	163
37	iCar-PseCp: identify carbonylation sites in proteins by Monte Carlo sampling and incorporating sequence coupled effects into general PseAAC. <i>Oncotarget</i> , 2016 , 7, 34558-70	3.3	161
36	iRNAm5C-PseDNC: identifying RNA 5-methylcytosine sites by incorporating physical-chemical properties into pseudo dinucleotide composition. <i>Oncotarget</i> , 2017 , 8, 41178-41188	3.3	148
35	iHyd-PseCp: Identify hydroxyproline and hydroxylysine in proteins by incorporating sequence-coupled effects into general PseAAC. <i>Oncotarget</i> , 2016 , 7, 44310-44321	3.3	138
34	iPhos-PseEn: identifying phosphorylation sites in proteins by fusing different pseudo components into an ensemble classifier. <i>Oncotarget</i> , 2016 , 7, 51270-51283	3.3	133
33	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	3.8	131
32	iPPBS-Opt: A Sequence-Based Ensemble Classifier for Identifying Protein-Protein Binding Sites by Optimizing Imbalanced Training Datasets. <i>Molecules</i> , 2016 , 21, E95	4.8	131

31	iMethyl-PseAAC: identification of protein methylation sites via a pseudo amino acid composition approach. <i>BioMed Research International</i> , 2014 , 2014, 947416	3	126
30	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	7.2	124
29	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, 911-9		121
28	pLoc-mGneg: Predict subcellular localization of Gram-negative bacterial proteins by deep gene ontology learning via general PseAAC. <i>Genomics</i> , 2017 , 110, 231-231	4.3	115
27	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, 1946-61	3.6	111
26	iKcr-PseEns: Identify lysine crotonylation sites in histone proteins with pseudo components and ensemble classifier. <i>Genomics</i> , 2018 , 110, 239-246	4.3	109
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, 34180-9	3.3	103
24	iCDI-PseFpt: identify the channel-drug interaction in cellular networking with PseAAC and molecular fingerprints. <i>Journal of Theoretical Biology</i> , 2013 , 337, 71-9	2.3	101
23	iATC-mHyb: a hybrid multi-label classifier for predicting the classification of anatomical therapeutic chemicals. <i>Oncotarget</i> , 2017 , 8, 58494-58503	3.3	98
22	iRNA-2methyl: Identify RNA 2 nd -methylation Sites by Incorporating Sequence-Coupled Effects into General PseKNC and Ensemble Classifier. <i>Medicinal Chemistry</i> , 2017 , 13, 734-743	1.8	93
21	iGPCR-drug: a web server for predicting interaction between GPCRs and drugs in cellular networking. <i>PLoS ONE</i> , 2013 , 8, e72234	3.7	88
20	iPhos-PseEvo: Identifying Human Phosphorylated Proteins by Incorporating Evolutionary Information into General PseAAC via Grey System Theory. <i>Molecular Informatics</i> , 2017 , 36, 1600010	3.8	82
19	pLoc_bal-mAnimal: predict subcellular localization of animal proteins by balancing training dataset and PseAAC. <i>Bioinformatics</i> , 2019 , 35, 398-406	7.2	76
18	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	4.3	75
17	iPPI-PseAAC(CGR): Identify protein-protein interactions by incorporating chaos game representation into PseAAC. <i>Journal of Theoretical Biology</i> , 2019 , 460, 195-203	2.3	73
16	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	3.7	66
15	iEzy-drug: a web server for identifying the interaction between enzymes and drugs in cellular networking. <i>BioMed Research International</i> , 2013 , 2013, 701317	3	65
14	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	2.3	62

13	iATC-mISF: a multi-label classifier for predicting the classes of anatomical therapeutic chemicals. <i>Bioinformatics</i> , 2017 , 33, 341-346	7.2	59
12	pLoc_bal-mHum: Predict subcellular localization of human proteins by PseAAC and quasi-balancing training dataset. <i>Genomics</i> , 2019 , 111, 1274-1282	4.3	53
11	pLoc_bal-mPlant: Predict Subcellular Localization of Plant Proteins by General PseAAC and Balancing Training Dataset. <i>Current Pharmaceutical Design</i> , 2018 , 24, 4013-4022	3.3	41
10	pLoc_bal-mVirus: Predict Subcellular Localization of Multi-Label Virus Proteins by ChouW/General PseAAC and IHTS Treatment to Balance Training Dataset. <i>Medicinal Chemistry</i> , 2019 , 15, 496-509	1.8	41
9	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	4.3	30
8	Multi-iPPseEvo: A Multi-label Classifier for Identifying Human Phosphorylated Proteins by Incorporating Evolutionary Information into ChouW/General PseAAC via Grey System Theory. <i>Molecular Informatics</i> , 2017 , 36, 1600085	3.8	26
7	Rectified-Linear-Unit-Based Deep Learning for Biomedical Multi-label Data. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2017 , 9, 419-422	3.5	12
6	Multi-label Learning for Predicting the Activities of Antimicrobial Peptides. <i>Scientific Reports</i> , 2017 , 7, 2202	4.9	8
5	Benchmark data for identifying DNA methylation sites via pseudo trinucleotide composition. <i>Data in Brief</i> , 2015 , 4, 87-9	1.2	8
4	Identifying GPCR-drug interaction based on wordbook learning from sequences. <i>BMC Bioinformatics</i> , 2020 , 21, 150	3.6	5
3	Computational Prediction of Ubiquitination Proteins Using Evolutionary Profiles and Functional Domain Annotation. <i>Current Genomics</i> , 2019 , 20, 389-399	2.6	5
2	iPTT(2 L)-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, 6636350	2.8	1
1	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	6.8	1