List of Publications by Year in descending order

68 papers	7,101 citations	61984 43 h-index	110387 64 g-index
69 all docs	69 docs citations	69 times ranked	2639 citing authors

#	Article	IF	Citations
1	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
2	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
3	iLoc-Euk: A Multi-Label Classifier for Predicting the Subcellular Localization of Singleplex and Multiplex Eukaryotic Proteins. PLoS ONE, 2011, 6, e18258.	2.5	298
4	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
5	iDNA-Prot: Identification of DNA Binding Proteins Using Random Forest with Grey Model. PLoS ONE, 2011, 6, e24756.	2.5	255
6	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
7	iLoc-Virus: A multi-label learning classifier for identifying the subcellular localization of virus proteins with both single and multiple sites. Journal of Theoretical Biology, 2011, 284, 42-51.	1.7	252
8	pRNAm-PC: Predicting N6-methyladenosine sites in RNA sequences via physicalâ€“chemical properties. Analytical Biochemistry, 2016, 497, 60-67.	2.4	247
9	iLoc-Animal: a multi-label learning classifier for predicting subcellular localization of animal proteins. Molecular BioSystems, 2013, 9, 634.	2.9	245
10	A Multi-Label Classifier for Predicting the Subcellular Localization of Gram-Negative Bacterial Proteins with Both Single and Multiple Sites. PLoS ONE, 2011, 6, e20592.	2.5	235
11	iRSpot-TNCPseAAC: Identify Recombination Spots with Trinucleotide Composition and Pseudo Amino Acid Components. International Journal of Molecular Sciences, 2014, 15, 1746-1766.	4.1	227
12	iLoc-Plant: a multi-label classifier for predicting the subcellular localization of plant proteins with both single and multiple sites. Molecular BioSystems, 2011, 7, 3287.	2.9	198
13	iRNAm5C-PseDNC: identifying RNA 5-methylcytosine sites by incorporating physical-chemical properties into pseudo dinucleotide composition. Oncotarget, 2017, 8, 41178-41188.	1.8	191
14	iDrug-Target: predicting the interactions between drug compounds and target proteins in cellular networking via benchmark dataset optimization approach. Journal of Biomolecular Structure and Dynamics, 2015, 33, 2221-2233.	3.5	185
15	pSumo-CD: predicting sumoylation sites in proteins with covariance discriminant algorithm by incorporating sequence-coupled effects into general PseAAC. Bioinformatics, 2016, 32, 3133-3141.	4.1	177
16	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
17	iHyd-PseCp: Identify hydroxyproline and hydroxylysine in proteins by incorporating sequence-coupled effects into general PseAAC. Oncotarget, 2016, 7, 44310-44321.	1.8	150
18	iUbiq-Lys: prediction of lysine ubiquitination sites in proteins by extracting sequence evolution information via a gray system model. Journal of Biomolecular Structure and Dynamics, 2015, 33, 1731-1742.	3.5	149

#	Article	IF	Citations
19	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
20	iPhos-PseEn: Identifying phosphorylation sites in proteins by fusing different pseudo components into an ensemble classifier. Oncotarget, 2016, 7, 51270-51283.	1.8	142
21	iATC-mISF: a multi-label classifier for predicting the classes of anatomical therapeutic chemicals. Bioinformatics, 2017, 33, 341-346.	4.1	139
22	iLoc-Gpos: A Multi-Layer Classifier for Predicting the Subcellular Localization of Singleplex and Multiplex Gram-Positive Bacterial Proteins. Protein and Peptide Letters, 2012, 19, 4-14.	0.9	138
23	iKcr-PseEns: Identify lysine crotonylation sites in histone proteins with pseudo components and ensemble classifier. Genomics, 2018, 110, 239-246.	2.9	127
24	Predicting protein structural classes with pseudo amino acid composition: An approach using geometric moments of cellular automaton image. Journal of Theoretical Biology, 2008, 254, 691-696.	1.7	126
25	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
26	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
27	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
28	iGPCR-Drug: A Web Server for Predicting Interaction between GPCRs and Drugs in Cellular Networking. PLoS ONE, 2013, 8, e72234.	2.5	106
29	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
30	pLoc_bal-mAnimal: predict subcellular localization of animal proteins by balancing training dataset and PseAAC. Bioinformatics, 2019, 35, 398-406.	4.1	89
31	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
32	NR-2L: A Two-Level Predictor for Identifying Nuclear Receptor Subfamilies Based on Sequence-Derived Features. PLoS ONE, 2011, 6, e23505.	2.5	88
33	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
34	Bagging-based spectral clustering ensemble selection. Pattern Recognition Letters, 2011, 32, 1456-1467.	4.2	86
35	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
36	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

#	Article	IF	Citations
37	iNR-Drug: Predicting the Interaction of Drugs with Nuclear Receptors in Cellular Networking. International Journal of Molecular Sciences, 2014, 15, 4915-4937.	4.1	71
38	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
39	pLoc_bal-mHum: Predict subcellular localization of human proteins by PseAAC and quasi-balancing training dataset. Genomics, 2019, 111, 1274-1282.	2.9	63
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.	2.9	60
41	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
42	Quat-2L: a web-server for predicting protein quaternary structural attributes. Molecular Diversity, 2011, 15, 149-155.	3.9	49
43	An improved multilevel thresholding approach based modified bacterial foraging optimization. Applied Intelligence, 2017, 46, 214-226.	5.3	45
44	pLoc_bal-mEuk: Predict Subcellular Localization of Eukaryotic Proteins by General PseAAC and Quasi-balancing Training Dataset. Medicinal Chemistry, 2019, 15, 472-485.	1.5	44
45	Classifying Multifunctional Enzymes by Incorporating Three Different Models into Chouâ€™s General Pseudo Amino Acid Composition. Journal of Membrane Biology, 2016, 249, 551-557.	2.1	32
46	Predict Drug-Protein Interaction in Cellular Networking. Current Topics in Medicinal Chemistry, 2013, 13, 1707-1712.	2.1	29
47	iAFP-Ense: An Ensemble Classifier for Identifying Antifreeze Protein by Incorporating Grey Model and PSSM into PseAAC. Journal of Membrane Biology, 2016, 249, 845-854.	2.1	25
48	Predicting the Functional Types of Singleplex and Multiplex Eukaryotic Membrane Proteins via Different Models of Chouâ€™s Pseudo Amino Acid Compositions. Journal of Membrane Biology, 2016, 249, 23-29.	2.1	24
49	Similarity-based spectral clustering ensemble selection. , 2012, , .		21
50	iSS-PC: Identifying Splicing Sites via Physical-Chemical Properties Using Deep Sparse Auto-Encoder. Scientific Reports, 2017, 7, 8222.	3.3	21
51	iMem-Seq: A Multi-label Learning Classifier for Predicting Membrane Proteins Types. Journal of Membrane Biology, 2015, 248, 745-752.	2.1	19
52	BOW-GBDT: A GBDT Classifier Combining With Artificial Neural Network for Identifying GPCRâ€“Drug Interaction Based on Wordbook Learning From Sequences. Frontiers in Cell and Developmental Biology, 2020, 8, 623858.	3.7	16
53	Prediction of Proteinâ€“Protein Interactions with Physicochemical Descriptors and Wavelet Transform via Random Forests. Journal of the Association for Laboratory Automation, 2016, 21, 368-377.	2.8	13
54	iDHSs-PseTNC: Identifying DNase I Hypersensitive Sites with Pseuo Trinucleotide Component by Deep Sparse Auto-encoder. Letters in Organic Chemistry, 2017, 14, .	0.5	12

#	Article	IF	Citations
55	HGDTI: predicting drugâ€“target interaction by using information aggregation based on heterogeneous graph neural network. BMC Bioinformatics, 2022, 23, 126.	2.6	11
56	iCataly-PseAAC: Identification of Enzymes Catalytic Sites Using Sequence Evolution Information with Grey Model GM (2,1). Journal of Membrane Biology, 2015, 248, 1033-1041.	2.1	10
57	Identifying Acetylation Protein by Fusing Its PseAAC and Functional Domain Annotation. Frontiers in Bioengineering and Biotechnology, 2019, 7, 311.	4.1	10
58	Identifying GPCR-drug interaction based on wordbook learning from sequences. BMC Bioinformatics, 2020, 21, 150.	2.6	10
59	Benchmark data for identifying DNA methylation sites via pseudo trinucleotide composition. Data in Brief, 2015, 4, 87-89.	1.0	8
60	DTI-BERT: Identifying Drug-Target Interactions in Cellular Networking Based on BERT and Deep Learning Method. Frontiers in Genetics, 0, 13, .	2.3	7
61	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
62	iCDI-W2vCom: Identifying the Ion Channelâ€“Drug Interaction in Cellular Networking Based on word2vec and node2vec. Frontiers in Genetics, 2021, 12, 738274.	2.3	6
63	PAI-SAE: Predicting Adenosine To Inosine Editing Sites Based On Hybrid Features By Using Spare Auto-Encoder. IOP Conference Series: Earth and Environmental Science, 2018, 170, 052018.	0.3	3
64	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
65	iAI-DSAE: A Computational Method for Adenosine to Inosine Editing Site Prediction. Letters in Organic Chemistry, 2019, 16, 347-355.	0.5	1
66	Identifying Pupylation Proteins and Sites by Incorporating Multiple Methods. Frontiers in Endocrinology, 2022, 13, 849549.	3.5	1
67	Using AdaboostSVM to Predict the GPCR Functional Classes. International Conference on Bioinformatics and Biomedical Engineering: [proceedings] International Conference on Bioinformatics and Biomedical Engineering, 2010, , .	0.0	0
68	Boundary Focal Loss for Class Imbalanced Learning. , 2021, , .		0