List of Publications by Year in descending order

68 papers	7,101 citations	61857 43 h-index	110170 64 g-index
69 all docs	69 docs citations	69 times ranked	2639 citing authors

#	Article	IF	Citations
1	HGDTI: predicting drugâ€“target interaction by using information aggregation based on heterogeneous graph neural network. BMC Bioinformatics, 2022, 23, 126.	1.2	11
2	Identifying Pupylation Proteins and Sites by Incorporating Multiple Methods. Frontiers in Endocrinology, 2022, 13, 849549.	1.5	1
3	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.	0.7	3
4	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.	1.9	6
5	iCDI-W2vCom: Identifying the Ion Channelâ€“Drug Interaction in Cellular Networking Based on word2vec and node2vec. Frontiers in Genetics, 2021, 12, 738274.	1.1	6
6	Boundary Focal Loss for Class Imbalanced Learning. , 2021, , .		0
7	Identifying GPCR-drug interaction based on wordbook learning from sequences. BMC Bioinformatics, 2020, 21, 150.	1.2	10
8	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.	1.8	16
9	pLoc_bal-mGpos: Predict subcellular localization of Gram-positive bacterial proteins by quasi-balancing training dataset and PseAAC. Genomics, 2019, 111, 886-892.	1.3	87
10	pLoc_bal-mAnimal: predict subcellular localization of animal proteins by balancing training dataset and PseAAC. Bioinformatics, 2019, 35, 398-406.	1.8	89
11	Identifying Acetylation Protein by Fusing Its PseAAC and Functional Domain Annotation. Frontiers in Bioengineering and Biotechnology, 2019, 7, 311.	2.0	10
12	pLoc_bal-mHum: Predict subcellular localization of human proteins by PseAAC and quasi-balancing training dataset. Genomics, 2019, 111, 1274-1282.	1.3	63
13	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.	1.3	60
14	iPPI-PseAAC(CGR): Identify protein-protein interactions by incorporating chaos game representation into PseAAC. Journal of Theoretical Biology, 2019, 460, 195-203.	0.8	88
15	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.	0.7	50
16	pLoc_bal-mEuk: Predict Subcellular Localization of Eukaryotic Proteins by General PseAAC and Quasi-balancing Training Dataset. Medicinal Chemistry, 2019, 15, 472-485.	0.7	44
17	iAI-DSAE: A Computational Method for Adenosine to Inosine Editing Site Prediction. Letters in Organic Chemistry, 2019, 16, 347-355.	0.2	1
18	iKcr-PseEns: Identify lysine crotonylation sites in histone proteins with pseudo components and ensemble classifier. Genomics, 2018, 110, 239-246.	1.3	127

#	Article	IF	Citations
19	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.	0.8	71
20	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.	0.2	3
21	iATC-mISF: a multi-label classifier for predicting the classes of anatomical therapeutic chemicals. Bioinformatics, 2017, 33, 341-346.	1.8	139
22	iPhosâ€PseEvo: Identifying Human Phosphorylated Proteins by Incorporating Evolutionary Information into General PseAAC via Grey System Theory. Molecular Informatics, 2017, 36, 1600010.	1.4	94
23	iSS-PC: Identifying Splicing Sites via Physical-Chemical Properties Using Deep Sparse Auto-Encoder. Scientific Reports, 2017, 7, 8222.	1.6	21
24	An improved multilevel thresholding approach based modified bacterial foraging optimization. Applied Intelligence, 2017, 46, 214-226.	3.3	45
25	iRNAm5C-PseDNC: identifying RNA 5-methylcytosine sites by incorporating physical-chemical properties into pseudo dinucleotide composition. Oncotarget, 2017, 8, 41178-41188.	0.8	191
26	iDHSs-PseTNC: Identifying DNase I Hypersensitive Sites with Pseuo Trinucleotide Component by Deep Sparse Auto-encoder. Letters in Organic Chemistry, 2017, 14, .	0.2	12
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.	0.8	118
28	iPPBS-Opt: A Sequence-Based Ensemble Classifier for Identifying Protein-Protein Binding Sites by Optimizing Imbalanced Training Datasets. Molecules, 2016, 21, 95.	1.7	142
29	iHyd-PseCp: Identify hydroxyproline and hydroxylysine in proteins by incorporating sequence-coupled effects into general PseAAC. Oncotarget, 2016, 7, 44310-44321.	0.8	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.	0.8	176
31	pSumo-CD: predicting sumoylation sites in proteins with covariance discriminant algorithm by incorporating sequence-coupled effects into general PseAAC. Bioinformatics, 2016, 32, 3133-3141.	1.8	177
32	Classifying Multifunctional Enzymes by Incorporating Three Different Models into Chouâ€™s General Pseudo Amino Acid Composition. Journal of Membrane Biology, 2016, 249, 551-557.	1.0	32
33	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.	1.0	25
34	pSuc-Lys: Predict lysine succinylation sites in proteins with PseAAC and ensemble random forest approach. Journal of Theoretical Biology, 2016, 394, 223-230.	0.8	297
35	pRNAm-PC: Predicting N6-methyladenosine sites in RNA sequences via physicalâ€“chemical properties. Analytical Biochemistry, 2016, 497, 60-67.	1.1	247
36	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.	1.1	254

#	Article	IF	Citations
37	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.	2.0	120
38	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.	1.0	24
39	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
40	iPhos-PseEn: Identifying phosphorylation sites in proteins by fusing different pseudo components into an ensemble classifier. Oncotarget, 2016, 7, 51270-51283.	0.8	142
41	Benchmark data for identifying DNA methylation sites via pseudo trinucleotide composition. Data in Brief, 2015, 4, 87-89.	0.5	8
42	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.	1.0	10
43	iMem-Seq: A Multi-label Learning Classifier for Predicting Membrane Proteins Types. Journal of Membrane Biology, 2015, 248, 745-752.	1.0	19
44	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.	2.0	149
45	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.	2.0	185
46	iRSpot-TNCPseAAC: Identify Recombination Spots with Trinucleotide Composition and Pseudo Amino Acid Components. International Journal of Molecular Sciences, 2014, 15, 1746-1766.	1.8	227
47	iNR-Drug: Predicting the Interaction of Drugs with Nuclear Receptors in Cellular Networking. International Journal of Molecular Sciences, 2014, 15, 4915-4937.	1.8	71
48	iLoc-Animal: a multi-label learning classifier for predicting subcellular localization of animal proteins. Molecular BioSystems, 2013, 9, 634.	2.9	245
49	iAMP-2L: A two-level multi-label classifier for identifying antimicrobial peptides and their functional types. Analytical Biochemistry, 2013, 436, 168-177.	1.1	442
50	iCDI-PseFpt: Identify the channelâ€“drug interaction in cellular networking with PseAAC and molecular fingerprints. Journal of Theoretical Biology, 2013, 337, 71-79.	0.8	113
51	iEzy-Drug: A Web Server for Identifying the Interaction between Enzymes and Drugs in Cellular Networking. BioMed Research International, 2013, 2013, 1-13.	0.9	73
52	iGPCR-Drug: A Web Server for Predicting Interaction between GPCRs and Drugs in Cellular Networking. PLoS ONE, 2013, 8, e72234.	1.1	106
53	Predict Drug-Protein Interaction in Cellular Networking. Current Topics in Medicinal Chemistry, 2013, 13, 1707-1712.	1.0	29
54	Similarity-based spectral clustering ensemble selection. , 2012, , .		21

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55	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
56	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.	0.4	138
57	iNR-PhysChem: A Sequence-Based Predictor for Identifying Nuclear Receptors and Their Subfamilies via Physical-Chemical Property Matrix. PLoS ONE, 2012, 7, e30869.	1.1	81
58	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
59	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.	1.1	235
60	iDNA-Prot: Identification of DNA Binding Proteins Using Random Forest with Grey Model. PLoS ONE, 2011, 6, e24756.	1.1	255
61	Quat-2L: a web-server for predicting protein quaternary structural attributes. Molecular Diversity, 2011, 15, 149-155.	2.1	49
62	Bagging-based spectral clustering ensemble selection. Pattern Recognition Letters, 2011, 32, 1456-1467.	2.6	86
63	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.	0.8	252
64	iLoc-Euk: A Multi-Label Classifier for Predicting the Subcellular Localization of Singleplex and Multiplex Eukaryotic Proteins. PLoS ONE, 2011, 6, e18258.	1.1	298
65	NR-2L: A Two-Level Predictor for Identifying Nuclear Receptor Subfamilies Based on Sequence-Derived Features. PLoS ONE, 2011, 6, e23505.	1.1	88
66	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
67	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.	0.8	126
68	DTI-BERT: Identifying Drug-Target Interactions in Cellular Networking Based on BERT and Deep Learning Method. Frontiers in Genetics, 0, 13, .	1.1	7