Kuo-Chen Chou

List of Publications by Year
in descending order

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296	49,061	439	2072
papers	citations	135 h-index	211 g-index

306	306	306	11755
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Using CHOU'S 5-Steps Rule to Predict O-Linked Serine Glycosylation Sites by Blending Position Relative Features and Statistical Moment. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2045-2056.	1.9	30
2	iPhosH-PseAAC: Identify Phosphohistidine Sites in Proteins by Blending Statistical Moments and Position Relative Features According to the Chou's 5-Step Rule and General Pseudo Amino Acid Composition. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 596-610.	1.9	70
3	The Remarkable Impacts of Gordon Life Science Institute. Natural Science, 2021, 13, 43-75.	0.2	2
4	Proposing Pseudo Amino Acid Components is an Important Milestone for Proteome and Genome Analyses. International Journal of Peptide Research and Therapeutics, 2020, 26, 1085-1098.	0.9	19
5	A Two-Level Computation Model Based on Deep Learning Algorithm for Identification of piRNA and Their Functions via Chouâ€™s 5-Steps Rule. International Journal of Peptide Research and Therapeutics, 2020, 26, 795-809.	0.9	62
6	Progresses in Predicting Post-translational Modification. International Journal of Peptide Research and Therapeutics, 2020, 26, 873-888.	0.9	52
7	Glioma stages prediction based on machine learning algorithm combined with protein-protein interaction networks. Genomics, 2020, 112, 837-847.	1.3	31
8	iProtease-PseAAC(2L): A two-layer predictor for identifying proteases and their types using Chou's 5-step-rule and general PseAAC. Analytical Biochemistry, 2020, 588, 113477.	1.1	36
9	Some illuminating remarks on molecular genetics and genomics as well as drug development. Molecular Genetics and Genomics, 2020, 295, 261-274.	1.0	4
10	An Insightful 10-year Recollection Since the Emergence of the 5-steps Rule. Current Pharmaceutical Design, 2020, 25, 4223-4234.	0.9	10
11	iHyd-LysSite (EPSV): Identifying Hydroxylysine Sites in Protein Using Statistical Formulation by Extracting Enhanced Position and Sequence Variant Feature Technique. Current Genomics, 2020, 21, 536-545.	0.7	37
12	Distorted Key Theory and its Implication for Drug Development. Current Proteomics, 2020, 17, 311-323.	0.1	7
13	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
14	Computational analysis and prediction of lysine malonylation sites by exploiting informative features in an integrative machine-learning framework. Briefings in Bioinformatics, 2019, 20, 2185-2199.	3.2	82
15	pLoc_bal-mAnimal: predict subcellular localization of animal proteins by balancing training dataset and PseAAC. Bioinformatics, 2019, 35, 398-406.	1.8	89
16	MULTiPly: a novel multi-layer predictor for discovering general and specific types of promoters. Bioinformatics, 2019, 35, 2957-2965.	1.8	109
17	Positive-unlabelled learning of glycosylation sites in the human proteome. BMC Bioinformatics, 2019, 20, 112.	1.2	60
18	The preliminary efficacy evaluation of the CTLA-4-Ig treatment against Lupus nephritis through in-silico analyses. Journal of Theoretical Biology, 2019, 471, 74-81.	0.8	5

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19	SPrenylC-PseAAC: A sequence-based model developed via Chou's 5-steps rule and general PseAAC for identifying S-prenylation sites in proteins. Journal of Theoretical Biology, 2019, 468, 1-11.	0.8	115
20	pLoc_bal-mHum: Predict subcellular localization of human proteins by PseAAC and quasi-balancing training dataset. Genomics, 2019, 111, 1274-1282.	1.3	63
21	Twenty years of bioinformatics research for protease-specific substrate and cleavage site prediction: a comprehensive revisit and benchmarking of existing methods. Briefings in Bioinformatics, 2019, 20, 2150-2166.	3.2	70
22	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
23	SPalmitoylC-PseAAC: A sequence-based model developed via Chou's 5-steps rule and general PseAAC for identifying S-palmitoylation sites in proteins. Analytical Biochemistry, 2019, 568, 14-23.	1.1	105
24	pSSbond-PseAAC: Prediction of disulfide bonding sites by integration of PseAAC and statistical moments. Journal of Theoretical Biology, 2019, 463, 47-55.	0.8	68
25	Bastion3: a two-layer ensemble predictor of type III secreted effectors. Bioinformatics, 2019, 35, 2017-2028.	1.8	69
26	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
27	Large-scale comparative assessment of computational predictors for lysine post-translational modification sites. Briefings in Bioinformatics, 2019, 20, 2267-2290.	3.2	99
28	iDNA6mA-PseKNC: Identifying DNA N6-methyladenosine sites by incorporating nucleotide physicochemical properties into PseKNC. Genomics, 2019, 111, 96-102.	1.3	234
29	iProt-Sub: a comprehensive package for accurately mapping and predicting protease-specific substrates and cleavage sites. Briefings in Bioinformatics, 2019, 20, 638-658.	3.2	166
30	Advances in Predicting Subcellular Localization of Multi-label Proteins and its Implication for Developing Multi-target Drugs. Current Medicinal Chemistry, 2019, 26, 4918-4943.	1.2	86
31	Simulated Protein Thermal Detection (SPTD) for Enzyme Thermostability Study and an Application Example for Pullulanase from Bacillus deramificans. Current Pharmaceutical Design, 2019, 24, 4023-4033.	0.9	20
32	pLoc_bal-mPlant: Predict Subcellular Localization of Plant Proteins by General PseAAC and Balancing Training Dataset. Current Pharmaceutical Design, 2019, 24, 4013-4022.	0.9	46
33	pNitro-Tyr-PseAAC: Predict Nitrotyrosine Sites in Proteins by Incorporating Five Features into Chouâ€™s General PseAAC. Current Pharmaceutical Design, 2019, 24, 4034-4043.	0.9	45
34	iHyd-PseAAC (EPSV): Identifying Hydroxylation Sites in Proteins by Extracting Enhanced Position and Sequence Variant Feature via Chou's 5- Step Rule and General Pseudo Amino Acid Composition. Current Genomics, 2019, 20, 124-133.	0.7	46
35	iMethylK-PseAAC: Improving Accuracy of Lysine Methylation Sites Identification by Incorporating Statistical Moments and Position Relative Features into General PseAAC via Chouâ€™s 5-steps Rule. Current Genomics, 2019, 20, 275-292.	0.7	42
36	iSulfoTyr-PseAAC: Identify Tyrosine Sulfation Sites by Incorporating Statistical Moments via Chouâ€™s 5-steps Rule and Pseudo Components. Current Genomics, 2019, 20, 306-320.	0.7	45

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37	Impacts of Pseudo Amino Acid Components and 5-steps Rule to Proteomics and Proteome Analysis. Current Topics in Medicinal Chemistry, 2019, 19, 2283-2300.	1.0	30
38	An Epidemic Avian Influenza Prediction Model Based on Google Trends. Letters in Organic Chemistry, 2019, 16, 303-310.	0.2	34
39	Prediction of Nitrosocysteine Sites Using Position and Composition Variant Features. Letters in Organic Chemistry, 2019, 16, 283-293.	0.2	34
40	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
41	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
42	An insightful recollection since the birth of Gordon Life Science Institute about 17 years ago. Advancement in Scientific and Engineering Research, 2019, 4, 31-36.	5.0	8
43	iFeature: a Python package and web server for features extraction and selection from protein and peptide sequences. Bioinformatics, 2018, 34, 2499-2502.	1.8	481
44	PREvaIL, an integrative approach for inferring catalytic residues using sequence, structural, and network features in a machine-learning framework. Journal of Theoretical Biology, 2018, 443, 125-137.	0.8	124
45	A Novel Modeling in Mathematical Biology for Classification of Signal Peptides. Scientific Reports, 2018, 8, 1039.	1.6	70
46	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.	1.8	139
47	iPhosT-PseAAC: Identify phosphothreonine sites by incorporating sequence statistical moments into PseAAC. Analytical Biochemistry, 2018, 550, 109-116.	1.1	111
48	Bastion6: a bioinformatics approach for accurate prediction of type VI secreted effectors. Bioinformatics, 2018, 34, 2546-2555.	1.8	108
49	iPromoter-2L: a two-layer predictor for identifying promoters and their types by multi-window-based PseKNC. Bioinformatics, 2018, 34, 33-40.	1.8	277
50	PROSPERous: high-throughput prediction of substrate cleavage sites for 90 proteases with improved accuracy. Bioinformatics, 2018, 34, 684-687.	1.8	131
51	pLoc-mEuk: Predict subcellular localization of multi-label eukaryotic proteins by extracting the key GO information into general PseAAC. Genomics, 2018, 110, 50-58.	1.3	193
52	pLoc-mGneg: Predict subcellular localization of Gram-negative bacterial proteins by deep gene ontology learning via general PseAAC. Genomics, 2018, 110, 231-239.	1.3	130
53	iKcr-PseEns: Identify lysine crotonylation sites in histone proteins with pseudo components and ensemble classifier. Genomics, 2018, 110, 239-246.	1.3	127
54	PhoglyStruct: Prediction of phosphoglycerylated lysine residues using structural properties of amino acids. Scientific Reports, 2018, 8, 17923.	1.6	31

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55	iPhosY-PseAAC: identify phosphotyrosine sites by incorporating sequence statistical moments into PseAAC. Molecular Biology Reports, 2018, 45, 2501-2509.	1.0	57
56	iRNA(m6A)-PseDNC: Identifying N6-methyladenosine sites using pseudo dinucleotide composition. Analytical Biochemistry, 2018, 561-562, 59-65.	1.1	162
57	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
58	iRO-3wPseKNC: identify DNA replication origins by three-window-based PseKNC. Bioinformatics, 2018, 34, 3086-3093.	1.8	108
59	Quokka: a comprehensive tool for rapid and accurate prediction of kinase family-specific phosphorylation sites in the human proteome. Bioinformatics, 2018, 34, 4223-4231.	1.8	151
60	iRNA-3typeA: Identifying Three Types of Modification at RNAâ€™s Adenosine Sites. Molecular Therapy - Nucleic Acids, 2018, 11, 468-474.	2.3	173
61	iRSpot-Pse6NC: Identifying recombination spots in Saccharomyces cerevisiae by incorporating hexamer composition into general PseKNC. International Journal of Biological Sciences, 2018, 14, 883-891.	2.6	145
62	iLoc-lncRNA: predict the subcellular location of lncRNAs by incorporating octamer composition into general PseKNC. Bioinformatics, 2018, 34, 4196-4204.	1.8	227
63	Implications of Newly Identified Brain eQTL Genes and Their Interactors in Schizophrenia. Molecular Therapy - Nucleic Acids, 2018, 12, 433-442.	2.3	63
64	iEnhancer-EL: identifying enhancers and their strength with ensemble learning approach. Bioinformatics, 2018, 34, 3835-3842.	1.8	172
65	iATC-mISF: a multi-label classifier for predicting the classes of anatomical therapeutic chemicals. Bioinformatics, 2017, 33, 341-346.	1.8	139
66	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
67	2L-piRNA: A Two-Layer Ensemble Classifier for Identifying Piwi-Interacting RNAs and Their Function. Molecular Therapy - Nucleic Acids, 2017, 7, 267-277.	2.3	226
68	iRNA-PseColl: Identifying the Occurrence Sites of Different RNA Modifications by Incorporating Collective Effects of Nucleotides into PseKNC. Molecular Therapy - Nucleic Acids, 2017, 7, 155-163.	2.3	259
69	pLoc-mVirus: Predict subcellular localization of multi-location virus proteins via incorporating the optimal GO information into general PseAAC. Gene, 2017, 628, 315-321.	1.0	138
70	pLoc-mAnimal: predict subcellular localization of animal proteins with both single and multiple sites. Bioinformatics, 2017, 33, 3524-3531.	1.8	175
71	pLoc-mPlant: predict subcellular localization of multi-location plant proteins by incorporating the optimal GO information into general PseAAC. Molecular BioSystems, 2017, 13, 1722-1727.	2.9	178
72	iRSpot-EL: identify recombination spots with an ensemble learning approach. Bioinformatics, 2017, 33, 35-41.	1.8	280

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73	Prediction of the aquatic toxicity of aromatic compounds to tetrahymena pyriformis through support vector regression. Oncotarget, 2017, 8, 49359-49369.	0.8	53
74	iATC-mHyb: a hybrid multi-label classifier for predicting the classification of anatomical therapeutic chemicals. Oncotarget, 2017, 8, 58494-58503.	0.8	118
75	Pse-Analysis: a python package for DNA/RNA and protein/peptide sequence analysis based on pseudo components and kernel methods. Oncotarget, 2017, 8, 13338-13343.	0.8	119
76	iRNA-AI: identifying the adenosine to inosine editing sites in RNA sequences. Oncotarget, 2017, 8, 4208-4217.	0.8	209
77	iRNAm5C-PseDNC: identifying RNA 5-methylcytosine sites by incorporating physical-chemical properties into pseudo dinucleotide composition. Oncotarget, 2017, 8, 41178-41188.	0.8	191
78	Small molecular floribundiquinone B derived from medicinal plants inhibits acetylcholinesterase activity. Oncotarget, 2017, 8, 57149-57162.	0.8	21
79	2L-PCA: a two-level principal component analyzer for quantitative drug design and its applications. Oncotarget, 2017, 8, 70564-70578.	0.8	17
80	An Unprecedented Revolution in Medicinal Chemistry Driven by the Progress of Biological Science. Current Topics in Medicinal Chemistry, 2017, 17, 2337-2358.	1.0	252
81	iPreny-PseAAC: Identify C-terminal Cysteine Prenylation Sites in Proteins by Incorporating Two Tiers of Sequence Couplings into PseAAC. Medicinal Chemistry, 2017, 13, 544-551.	0.7	125
82	Chlorella vulgaris Induces Apoptosis of Human Non-Small Cell Lung Carcinoma (NSCLC) Cells. Medicinal Chemistry, 2017, 13, 560-568.	0.7	15
83	iPGK-PseAAC: Identify Lysine Phosphoglycerylation Sites in Proteins by Incorporating Four Different Tiers of Amino Acid Pairwise Coupling Information into the General PseAAC. Medicinal Chemistry, 2017, 13, 552-559.	0.7	128
84	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.	0.7	104
85	Pse-in-One 2.0: An Improved Package of Web Servers for Generating Various Modes of Pseudo Components of DNA, RNA, and Protein Sequences. Natural Science, 2017, 09, 67-91.	0.2	115
86	pLoc-mGpos: Incorporate Key Gene Ontology Information into General PseAAC for Predicting Subcellular Localization of Gram-Positive Bacterial Proteins. Natural Science, 2017, 09, 330-349.	0.2	51
87	iOri-Human: identify human origin of replication by incorporating dinucleotide physicochemical properties into pseudo nucleotide composition. Oncotarget, 2016, 7, 69783-69793.	0.8	166
88	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
89	iACP: a sequence-based tool for identifying anticancer peptides. Oncotarget, 2016, 7, 16895-16909.	0.8	354
90	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

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91	iHyd-PseCp: Identify hydroxyproline and hydroxylysine in proteins by incorporating sequence-coupled effects into general PseAAC. Oncotarget, 2016, 7, 44310-44321.	0.8	150
92	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
93	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
94	iDHS-EL: identifying DNase I hypersensitive sites by fusing three different modes of pseudo nucleotide composition into an ensemble learning framework. Bioinformatics, 2016, 32, 2411-2418.	1.8	196
95	iPTM-mLys: identifying multiple lysine PTM sites and their different types. Bioinformatics, 2016, 32, 3116-3123.	1.8	236
96	iMiRNA-PseDPC: microRNA precursor identification with a pseudo distance-pair composition approach. Journal of Biomolecular Structure and Dynamics, 2016, 34, 223-235.	2.0	120
97	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
98	pRNAm-PC: Predicting N6-methyladenosine sites in RNA sequences via physicalâ€“chemical properties. Analytical Biochemistry, 2016, 497, 60-67.	1.1	247
99	Using deformation energy to analyze nucleosome positioning in genomes. Genomics, 2016, 107, 69-75.	1.3	104
100	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
101	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
102	iEnhancer-2L: a two-layer predictor for identifying enhancers and their strength by pseudo k-tuple nucleotide composition. Bioinformatics, 2016, 32, 362-369.	1.8	323
103	repRNA: a web server for generating various feature vectors of RNA sequences. Molecular Genetics and Genomics, 2016, 291, 473-481.	1.0	122
104	iRNA-PseU: Identifying RNA pseudouridine sites. Molecular Therapy - Nucleic Acids, 2016, 5, e332.	2.3	172
105	iPhos-PseEn: Identifying phosphorylation sites in proteins by fusing different pseudo components into an ensemble classifier. Oncotarget, 2016, 7, 51270-51283.	0.8	142
106	Recent Novel High-Tech Researches in Molecular Biology. BioMed Research International, 2015, 2015, 1-3.	0.9	2
107	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.	0.8	265
108	Benchmark data for identifying DNA methylation sites via pseudo trinucleotide composition. Data in Brief, 2015, 4, 87-89.	0.5	8

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109	iDNA-Methyl: Identifying DNA methylation sites via pseudo trinucleotide composition. Analytical Biochemistry, 2015, 474, 69-77.	1.1	246
110	repDNA: a Python package to generate various modes of feature vectors for DNA sequences by incorporating user-defined physicochemical properties and sequence-order effects. Bioinformatics, 2015, 31, 1307-1309.	1.8	242
111	PseKNC-General: a cross-platform package for generating various modes of pseudo nucleotide compositions. Bioinformatics, 2015, 31, 119-120.	1.8	210
112	Pseudo nucleotide composition or PseKNC: an effective formulation for analyzing genomic sequences. Molecular BioSystems, 2015, 11, 2620-2634.	2.9	289
113	Pse-in-One: a web server for generating various modes of pseudo components of DNA, RNA, and protein sequences. Nucleic Acids Research, 2015, 43, W65-W71.	6.5	664
114	Benchmark data for identifying N 6 -methyladenosine sites in the Saccharomyces cerevisiae genome. Data in Brief, 2015, 5, 376-378.	0.5	9
115	iRNA-Methyl: Identifying N6-methyladenosine sites using pseudo nucleotide composition. Analytical Biochemistry, 2015, 490, 26-33.	1.1	350
116	Identification of microRNA precursor with the degenerate K-tuple or Kmer strategy. Journal of Theoretical Biology, 2015, 385, 153-159.	0.8	159
117	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
118	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
119	Identification of DNA-binding proteins by incorporating evolutionary information into pseudo amino acid composition via the top-n-gram approach. Journal of Biomolecular Structure and Dynamics, 2015, 33, 1720-1730.	2.0	80
120	Identification of Real MicroRNA Precursors with a Pseudo Structure Status Composition Approach. PLoS ONE, 2015, 10, e0121501.	1.1	193
121	Recent Progress in Predicting Posttranslational Modification Sites in Proteins. Current Topics in Medicinal Chemistry, 2015, 16, 591-603.	1.0	91
122	Impacts of Bioinformatics to Medicinal Chemistry. Medicinal Chemistry, 2015, 11, 218-234.	0.7	496
123	Gestational Influenza Increases the Risk of Psychosis in Adults. Medicinal Chemistry, 2015, 11, 676-682.	0.7	17
124	iNitro-Tyr: Prediction of Nitrotyrosine Sites in Proteins with General Pseudo Amino Acid Composition. PLoS ONE, 2014, 9, e105018.	1.1	178
125	iMethyl-PseAAC: Identification of Protein Methylation Sites via a Pseudo Amino Acid Composition Approach. BioMed Research International, 2014, 2014, 1-12.	0.9	152
126	iSS-PseDNC: Identifying Splicing Sites Using Pseudo Dinucleotide Composition. BioMed Research International, 2014, 2014, 1-12.	0.9	144

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127	iPro54-PseKNC: a sequence-based predictor for identifying sigma-54 promoters in prokaryote with pseudo k-tuple nucleotide composition. Nucleic Acids Research, 2014, 42, 12961-12972.	6.5	467
128	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
129	iHyd-PseAAC: Predicting Hydroxyproline and Hydroxylysine in Proteins by Incorporating Dipeptide Position-Specific Propensity into Pseudo Amino Acid Composition. International Journal of Molecular Sciences, 2014, 15, 7594-7610.	1.8	190
130	iCTX-Type: A Sequence-Based Predictor for Identifying the Types of Conotoxins in Targeting Ion Channels. BioMed Research International, 2014, 2014, 1-10.	0.9	185
131	Combining evolutionary information extracted from frequency profiles with sequence-based kernels for protein remote homology detection. Bioinformatics, 2014, 30, 472-479.	1.8	266
132	iTIS-PseTNC: A sequence-based predictor for identifying translation initiation site in human genes using pseudo trinucleotide composition. Analytical Biochemistry, 2014, 462, 76-83.	1.1	245
133	iNuc-PseKNC: a sequence-based predictor for predicting nucleosome positioning in genomes with pseudo k-tuple nucleotide composition. Bioinformatics, 2014, 30, 1522-1529.	1.8	349
134	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
135	PseKNC: A flexible web server for generating pseudo K-tuple nucleotide composition. Analytical Biochemistry, 2014, 456, 53-60.	1.1	409
136	iDNA-Prot|dis: Identifying DNA-Binding Proteins by Incorporating Amino Acid Distance-Pairs and Reduced Alphabet Profile into the General Pseudo Amino Acid Composition. PLoS ONE, 2014, 9, e106691.	1.1	242
137	Research/Review: Structure and Linkage Disequilibrium Analysis of Adamantane Resistant Mutations in Influenza Virus M2 Proton Channel. Current Drug Metabolism, 2014, 15, 526-534.	0.7	1
138	Research/Review: Insights into the Mutation-Induced Dysfunction of Arachidonic Acid Metabolism from Modeling of Human CYP2J2. Current Drug Metabolism, 2014, 15, 502-513.	0.7	13
139	iLoc-Animal: a multi-label learning classifier for predicting subcellular localization of animal proteins. Molecular BioSystems, 2013, 9, 634.	2.9	245
140	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
141	iHSP-PseRAAAC: Identifying the heat shock protein families using pseudo reduced amino acid alphabet composition. Analytical Biochemistry, 2013, 442, 118-125.	1.1	287
142	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
143	Some remarks on predicting multi-label attributes in molecular biosystems. Molecular BioSystems, 2013, 9, 1092.	2.9	393
144	iRSpot-PseDNC: identify recombination spots with pseudo dinucleotide composition. Nucleic Acids Research, 2013, 41, e68-e68.	6.5	562

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145	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
146	Metallo-β-Lactamases: Structural Features, Antibiotic Recognition, Inhibition, and Inhibitor Design. Current Topics in Medicinal Chemistry, 2013, 13, 1242-1253.	1.0	31
147	Recent Advances in Predicting Protein Classification and Their Applications to Drug Development. Current Topics in Medicinal Chemistry, 2013, 13, 1622-1635.	1.0	22
148	iSNO-PseAAC: Predict Cysteine S-Nitrosylation Sites in Proteins by Incorporating Position Specific Amino Acid Propensity into Pseudo Amino Acid Composition. PLoS ONE, 2013, 8, e55844.	1.1	333
149	iGPCR-Drug: A Web Server for Predicting Interaction between GPCRs and Drugs in Cellular Networking. PLoS ONE, 2013, 8, e72234.	1.1	106
150	Recent Progresses in Identifying Nuclear Receptors and Their Families. Current Topics in Medicinal Chemistry, 2013, 13, 1192-1200.	1.0	28
151	Predict Drug-Protein Interaction in Cellular Networking. Current Topics in Medicinal Chemistry, 2013, 13, 1707-1712.	1.0	29
152	iSNO-AAPair: incorporating amino acid pairwise coupling into PseAAC for predicting cysteineS-nitrosylation sites in proteins. PeerJ, 2013, 1, e171.	0.9	259
153	Recent Advances in Computational Studies on Influenza A Virus M2 Proton Channel. Mini-Reviews in Medicinal Chemistry, 2012, 12, 971-978.	1.1	16
154	Predicting Anatomical Therapeutic Chemical (ATC) Classification of Drugs by Integrating Chemical-Chemical Interactions and Similarities. PLoS ONE, 2012, 7, e35254.	1.1	159
155	Deciphering the effects of gene deletion on yeast longevity using network and machine learning approaches. Biochimie, 2012, 94, 1017-1025.	1.3	67
156	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
157	Hepatitis C Virus Network Based Classification of Hepatocellular Cirrhosis and Carcinoma. PLoS ONE, 2012, 7, e34460.	1.1	52
158	Design Novel Dual Agonists for Treating Type-2 Diabetes by Targeting Peroxisome Proliferator-Activated Receptors with Core Hopping Approach. PLoS ONE, 2012, 7, e38546.	1.1	91
159	iNuc-PhysChem: A Sequence-Based Predictor for Identifying Nucleosomes via Physicochemical Properties. PLoS ONE, 2012, 7, e47843.	1.1	181
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