

iRSpot-PseDNC: identify recombination spots with pse

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Citation Report

#	ARTICLE	IF	CITATIONS
1	A Multilabel Model Based on Chou's Pseudo-Amino Acid Composition for Identifying Membrane Proteins with Both Single and Multiple Functional Types. <i>Journal of Membrane Biology</i> , 2013, 246, 327-334.	1.0	65
2	Analysis of codon use features of stearyl-acyl carrier protein desaturase gene in <i>Camellia sinensis</i> . <i>Journal of Theoretical Biology</i> , 2013, 334, 80-86.	0.8	18
3	Predicting the heats of combustion of polynitro arene, polynitro heteroarene, acyclic and cyclic nitramine, nitrate ester and nitroaliphatic compounds using bee algorithm and adaptive neuro-fuzzy inference system. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2013, 128, 37-48.	1.8	16
4	iLoc-Animal: a multi-label learning classifier for predicting subcellular localization of animal proteins. <i>Molecular BioSystems</i> , 2013, 9, 634.	2.9	245
5	iAMP-2L: A two-level multi-label classifier for identifying antimicrobial peptides and their functional types. <i>Analytical Biochemistry</i> , 2013, 436, 168-177.	1.1	442
6	iHSP-PseRAAAC: Identifying the heat shock protein families using pseudo reduced amino acid alphabet composition. <i>Analytical Biochemistry</i> , 2013, 442, 118-125.	1.1	287
7	Efficacy of function specific 3D-motifs in enzyme classification according to their EC-numbers. <i>Journal of Theoretical Biology</i> , 2013, 336, 36-43.	0.8	5
8	Predicting acidic and alkaline enzymes by incorporating the average chemical shift and gene ontology informations into the general form of Chou's PseAAC. <i>Process Biochemistry</i> , 2013, 48, 1048-1053.	1.8	38
9	Alignment free comparison: k word voting model and its applications. <i>Journal of Theoretical Biology</i> , 2013, 335, 276-282.	0.8	4
10	Discriminating bioluminescent proteins by incorporating average chemical shift and evolutionary information into the general form of Chou's pseudo amino acid composition. <i>Journal of Theoretical Biology</i> , 2013, 334, 45-51.	0.8	60
11	Support vector machine with a Pearson VII function kernel for discriminating halophilic and non-halophilic proteins. <i>Computational Biology and Chemistry</i> , 2013, 46, 16-22.	1.1	33
12	Linear regression model of short k-word: a similarity distance suitable for biological sequences with various lengths. <i>Journal of Theoretical Biology</i> , 2013, 337, 61-70.	0.8	19
13	iCDI-PseFpt: Identify the channel-drug interaction in cellular networking with PseAAC and molecular fingerprints. <i>Journal of Theoretical Biology</i> , 2013, 337, 71-79.	0.8	113
14	Using radial basis function on the general form of Chou's pseudo amino acid composition and PSSM to predict subcellular locations of proteins with both single and multiple sites. <i>BioSystems</i> , 2013, 113, 50-57.	0.9	79
15	Some remarks on predicting multi-label attributes in molecular biosystems. <i>Molecular BioSystems</i> , 2013, 9, 1092.	2.9	393
16	A soft sensor based on adaptive fuzzy neural network and support vector regression for industrial melt index prediction. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2013, 126, 83-90.	1.8	38
17	Predict Subcellular Locations of Singleplex and Multiplex Proteins by Semi-Supervised Learning and Dimension-Reducing General Mode of Chou's PseAAC. <i>IEEE Transactions on Nanobioscience</i> , 2013, 12, 311-320.	2.2	64
18	Comparison between the Repression Potency of siRNA Targeting the Coding Region and the 3'-Untranslated Region of mRNA. <i>BioMed Research International</i> , 2013, 2013, 1-5.	0.9	7

#	ARTICLE	IF	CITATIONS
19	iEzy-Drug: A Web Server for Identifying the Interaction between Enzymes and Drugs in Cellular Networking. <i>BioMed Research International</i> , 2013, 2013, 1-13.	0.9	73
20	SubMito-PSPCP: Predicting Protein Submitochondrial Locations by Hybridizing Positional Specific Physicochemical Properties with Pseudoamino Acid Compositions. <i>BioMed Research International</i> , 2013, 2013, 1-7.	0.9	31
21	Protein Remote Homology Detection by Combining Chou's Pseudo Amino Acid Composition and Profile-Based Protein Representation. <i>Molecular Informatics</i> , 2013, 32, 775-782.	1.4	103
22	Metallo-β-Lactamases: Structural Features, Antibiotic Recognition, Inhibition, and Inhibitor Design. <i>Current Topics in Medicinal Chemistry</i> , 2013, 13, 1242-1253.	1.0	31
23	iSNO-PseAAC: Predict Cysteine S-Nitrosylation Sites in Proteins by Incorporating Position Specific Amino Acid Propensity into Pseudo Amino Acid Composition. <i>PLoS ONE</i> , 2013, 8, e55844.	1.1	333
24	iGPCR-Drug: A Web Server for Predicting Interaction between GPCRs and Drugs in Cellular Networking. <i>PLoS ONE</i> , 2013, 8, e72234.	1.1	106
25	AcalPred: A Sequence-Based Tool for Discriminating between Acidic and Alkaline Enzymes. <i>PLoS ONE</i> , 2013, 8, e75726.	1.1	92
26	Naïve Bayes Classifier with Feature Selection to Identify Phage Virion Proteins. <i>Computational and Mathematical Methods in Medicine</i> , 2013, 2013, 1-6.	0.7	145
27	Identification of Antioxidants from Sequence Information Using Naïve Bayes. <i>Computational and Mathematical Methods in Medicine</i> , 2013, 2013, 1-5.	0.7	102
28	iNitro-Tyr: Prediction of Nitrotyrosine Sites in Proteins with General Pseudo Amino Acid Composition. <i>PLoS ONE</i> , 2014, 9, e105018.	1.1	178
29	iMethyl-PseAAC: Identification of Protein Methylation Sites via a Pseudo Amino Acid Composition Approach. <i>BioMed Research International</i> , 2014, 2014, 1-12.	0.9	152
30	Protein Binding Site Prediction by Combining Hidden Markov Support Vector Machine and Profile-Based Propensities. <i>Scientific World Journal, The</i> , 2014, 2014, 1-6.	0.8	9
31	Prediction of DNase I Hypersensitive Sites by Using Pseudo Nucleotide Compositions. <i>Scientific World Journal, The</i> , 2014, 2014, 1-4.	0.8	26
32	iSS-PseDNC: Identifying Splicing Sites Using Pseudo Dinucleotide Composition. <i>BioMed Research International</i> , 2014, 2014, 1-12.	0.9	144
33	Prediction of Four Kinds of Simple Supersecondary Structures in Protein by Using Chemical Shifts. <i>Scientific World Journal, The</i> , 2014, 2014, 1-5.	0.8	2
34	iPro54-PseKNC: a sequence-based predictor for identifying sigma-54 promoters in prokaryote with pseudo k-tuple nucleotide composition. <i>Nucleic Acids Research</i> , 2014, 42, 12961-12972.	6.5	467
35	Sequence-based identification of recombination spots using pseudo nucleic acid representation and recursive feature extraction by linear kernel SVM. <i>BMC Bioinformatics</i> , 2014, 15, 340.	1.2	25
36	SPoRE: a mathematical model to predict double strand breaks and axis protein sites in meiosis. <i>BMC Bioinformatics</i> , 2014, 15, 391.	1.2	2

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37	Predicting the Types of J-Proteins Using Clustered Amino Acids. BioMed Research International, 2014, 2014, 1-8.	0.9	30
38	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
39	PseAAC-General: Fast Building Various Modes of General Form of Chou's Pseudo-Amino Acid Composition for Large-Scale Protein Datasets. International Journal of Molecular Sciences, 2014, 15, 3495-3506.	1.8	275
40	Prediction of Protein-Protein Interaction with Pairwise Kernel Support Vector Machine. International Journal of Molecular Sciences, 2014, 15, 3220-3233.	1.8	51
41	enDNA-Prot: Identification of DNA-Binding Proteins by Applying Ensemble Learning. BioMed Research International, 2014, 2014, 1-10.	0.9	32
42	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
43	Prediction of Protein S-Nitrosylation Sites Based on Adapted Normal Distribution Bi-Profile Bayes and Chou's Pseudo Amino Acid Composition. International Journal of Molecular Sciences, 2014, 15, 10410-10423.	1.8	94
44	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
45	Combining evolutionary information extracted from frequency profiles with sequence-based kernels for protein remote homology detection. Bioinformatics, 2014, 30, 472-479.	1.8	266
46	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
47	Prediction of Signal Peptide Cleavage Sites with Subsite-Coupled and Template Matching Fusion Algorithm. Molecular Informatics, 2014, 33, 230-239.	1.4	7
48	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
49	Multi-Label Learning With Fuzzy Hypergraph Regularization for Protein Subcellular Location Prediction. IEEE Transactions on Nanobioscience, 2014, 13, 438-447.	2.2	12
50	Potential non homologous protein targets of mycobacterium tuberculosis H37Rv identified from protein-protein interaction network. Journal of Theoretical Biology, 2014, 361, 152-158.	0.8	9
51	k-mer Sparse matrix model for genetic sequence and its applications in sequence comparison. Journal of Theoretical Biology, 2014, 363, 145-150.	0.8	8
52	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
53	Quad-PRE: A Hybrid Method to Predict Protein Quaternary Structure Attributes. Computational and Mathematical Methods in Medicine, 2014, 2014, 1-9.	0.7	3
54	Predicting anticancer peptides with Chou's pseudo amino acid composition and investigating their mutagenicity via Ames test. Journal of Theoretical Biology, 2014, 341, 34-40.	0.8	237

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55	A two-stage SVM method to predict membrane protein types by incorporating amino acid classifications and physicochemical properties into a general form of Chou's PseAAC. <i>Journal of Theoretical Biology</i> , 2014, 344, 31-39.	0.8	82
56	A protein structural classes prediction method based on PSI-BLAST profile. <i>Journal of Theoretical Biology</i> , 2014, 353, 19-23.	0.8	32
57	Screening drug target proteins based on sequence information. <i>Journal of Biomedical Informatics</i> , 2014, 49, 269-274.	2.5	7
58	Accurate prediction of protein structural classes by incorporating predicted secondary structure information into the general form of Chou's pseudo amino acid composition. <i>Journal of Theoretical Biology</i> , 2014, 344, 12-18.	0.8	79
59	Chou's pseudo amino acid composition improves sequence-based antifreeze protein prediction. <i>Journal of Theoretical Biology</i> , 2014, 356, 30-35.	0.8	126
60	Sequence-specific flexibility organization of splicing flanking sequence and prediction of splice sites in the human genome. <i>Chromosome Research</i> , 2014, 22, 321-334.	1.0	4
61	Neural network and SVM classifiers accurately predict lipid binding proteins, irrespective of sequence homology. <i>Journal of Theoretical Biology</i> , 2014, 356, 213-222.	0.8	61
62	Signal peptide discrimination and cleavage site identification using SVM and NN. <i>Computers in Biology and Medicine</i> , 2014, 45, 98-110.	3.9	5
63	Protein subcellular localization in human and hamster cell lines: Employing local ternary patterns of fluorescence microscopy images. <i>Journal of Theoretical Biology</i> , 2014, 340, 85-95.	0.8	14
64	Prediction of posttranslational modification sites from amino acid sequences with kernel methods. <i>Journal of Theoretical Biology</i> , 2014, 344, 78-87.	0.8	42
65	Exon skipping event prediction based on histone modifications. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2014, 6, 241-249.	2.2	10
66	Genome-wide characterization and prediction of <i>Arabidopsis thaliana</i> replication origins. <i>BioSystems</i> , 2014, 124, 1-6.	0.9	11
67	Identifying ion channel genes related to cardiomyopathy using a novel decision forest strategy. <i>Molecular BioSystems</i> , 2014, 10, 2407.	2.9	5
68	Transmission of intra-cellular genetic information: A system proposal. <i>Journal of Theoretical Biology</i> , 2014, 358, 208-231.	0.8	12
69	Prediction of CpG island methylation status by integrating DNA physicochemical properties. <i>Genomics</i> , 2014, 104, 229-233.	1.3	33
70	Prediction of protein structure classes by incorporating different protein descriptors into general Chou's pseudo amino acid composition. <i>Journal of Theoretical Biology</i> , 2014, 360, 109-116.	0.8	111
71	Prediction of bacterial protein subcellular localization by incorporating various features into Chou's PseAAC and a backward feature selection approach. <i>Biochimie</i> , 2014, 104, 100-107.	1.3	63
72	R3P-Loc: A compact multi-label predictor using ridge regression and random projection for protein subcellular localization. <i>Journal of Theoretical Biology</i> , 2014, 360, 34-45.	0.8	30

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73	A set of descriptors for identifying the protein-drug interaction in cellular networking. <i>Journal of Theoretical Biology</i> , 2014, 359, 120-128.	0.8	22
74	Prediction of Protein Secondary Structure Using Feature Selection and Analysis Approach. <i>Acta Biotheoretica</i> , 2014, 62, 1-14.	0.7	12
75	Discriminating protein structure classes by incorporating Pseudo Average Chemical Shift to Chou's general PseAAC and Support Vector Machine. <i>Computer Methods and Programs in Biomedicine</i> , 2014, 116, 184-192.	2.6	66
76	GPCRserver: an accurate and novel G protein-coupled receptor predictor. <i>Molecular BioSystems</i> , 2014, 10, 2495-2504.	2.9	10
77	LECTINPred: web Server that Uses Complex Networks of Protein Structure for Prediction of Lectins with Potential Use as Cancer Biomarkers or in Parasite Vaccine Design. <i>Molecular Informatics</i> , 2014, 33, 276-285.	1.4	10
78	Protein fold recognition by alignment of amino acid residues using kernelized dynamic time warping. <i>Journal of Theoretical Biology</i> , 2014, 354, 137-145.	0.8	30
79	TIBS: A web database to browse gene expression in irritable bowel syndrome. <i>Journal of Theoretical Biology</i> , 2014, 354, 48-53.	0.8	2
80	PseKNC: A flexible web server for generating pseudo K-tuple nucleotide composition. <i>Analytical Biochemistry</i> , 2014, 456, 53-60.	1.1	409
81	Constructing a linear QSAR for some metabolizable drugs by human or pig flavin-containing monooxygenases using some molecular features selected by a genetic algorithm trained SVM. <i>Journal of Theoretical Biology</i> , 2014, 356, 85-97.	0.8	2
82	Human proteins characterization with subcellular localizations. <i>Journal of Theoretical Biology</i> , 2014, 358, 61-73.	0.8	11
83	An effective haplotype assembly algorithm based on hypergraph partitioning. <i>Journal of Theoretical Biology</i> , 2014, 358, 85-92.	0.8	11
84	Prediction of the determinants of thermal stability by linear discriminant analysis: The case of the glutamate dehydrogenase protein family. <i>Journal of Theoretical Biology</i> , 2014, 357, 160-168.	0.8	2
85	Predicting DNA binding proteins using support vector machine with hybrid fractal features. <i>Journal of Theoretical Biology</i> , 2014, 343, 186-192.	0.8	21
86	Identification and analysis of the N6-methyladenosine in the <i>Saccharomyces cerevisiae</i> transcriptome. <i>Scientific Reports</i> , 2015, 5, 13859.	1.6	96
87	The pattern of DNA cleavage intensity around indels. <i>Scientific Reports</i> , 2015, 5, 8333.	1.6	11
88	NRfamPred: A proteome-scale two level method for prediction of nuclear receptor proteins and their sub-families. <i>Scientific Reports</i> , 2014, 4, 6810.	1.6	15
89	iSuc-PseAAC: predicting lysine succinylation in proteins by incorporating peptide position-specific propensity. <i>Scientific Reports</i> , 2015, 5, 10184.	1.6	75
90	PseDNA-Pro: DNA-Binding Protein Identification by Combining Chou's PseAAC and Physicochemical Distance Transformation. <i>Molecular Informatics</i> , 2015, 34, 8-17.	1.4	152

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91	Identifying DNA-binding proteins by combining support vector machine and PSSM distance transformation. <i>BMC Systems Biology</i> , 2015, 9, S10.	3.0	85
92	DSPMP: Discriminating secretory proteins of malaria parasite by hybridizing different descriptors of <scp>C</scp>hou's pseudo amino acid patterns. <i>Journal of Computational Chemistry</i> , 2015, 36, 2317-2327.	1.5	40
93	Reverse Engineering of Genome-wide Gene Regulatory Networks from Gene Expression Data. <i>Current Genomics</i> , 2015, 16, 3-22.	0.7	79
94	Detecting Protein-Protein Interactions with a Novel Matrix-Based Protein Sequence Representation and Support Vector Machines. <i>BioMed Research International</i> , 2015, 2015, 1-9.	0.9	45
95	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.	0.8	265
96	Novel 3D bio-macromolecular bilinear descriptors for protein science: Predicting protein structural classes. <i>Journal of Theoretical Biology</i> , 2015, 374, 125-137.	0.8	20
97	Predict Gram-Positive and Gram-Negative Subcellular Localization via Incorporating Evolutionary Information and Physicochemical Features Into Chou's General PseAAC. <i>IEEE Transactions on Nanobioscience</i> , 2015, 14, 915-926.	2.2	72
98	Surveying and benchmarking techniques to analyse DNA gel fingerprint images. <i>Briefings in Bioinformatics</i> , 2015, 17, bbv102.	3.2	4
99	A Novel Cylindrical Representation for Characterizing Intrinsic Properties of Protein Sequences. <i>Journal of Chemical Information and Modeling</i> , 2015, 55, 1261-1270.	2.5	6
100	A method to distinguish between lysine acetylation and lysine ubiquitination with feature selection and analysis. <i>Journal of Biomolecular Structure and Dynamics</i> , 2015, 33, 2479-2490.	2.0	33
101	Identification of protein-interacting nucleotides in a RNA sequence using composition profile of tri-nucleotides. <i>Genomics</i> , 2015, 105, 197-203.	1.3	24
102	Prediction of success for polymerase chain reactions using the Markov maximal order model and support vector machine. <i>Journal of Theoretical Biology</i> , 2015, 369, 51-58.	0.8	1
103	Accurate prediction of protein structural classes by incorporating PSSS and PSSM into Chou's general PseAAC. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2015, 142, 28-35.	1.8	45
104	Protein submitochondrial localization from integrated sequence representation and SVM-based backward feature extraction. <i>Molecular BioSystems</i> , 2015, 11, 170-177.	2.9	13
105	iORI-PseKNC: A predictor for identifying origin of replication with pseudo k-tuple nucleotide composition. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2015, 141, 100-106.	1.8	76
106	iDNA-Methyl: Identifying DNA methylation sites via pseudo trinucleotide composition. <i>Analytical Biochemistry</i> , 2015, 474, 69-77.	1.1	246
107	Predicting the subcellular localization of mycobacterial proteins by incorporating the optimal tripeptides into the general form of pseudo amino acid composition. <i>Molecular BioSystems</i> , 2015, 11, 558-563.	2.9	106
108	Discrimination of membrane transporter protein types using K-nearest neighbor method derived from the similarity distance of total diversity measure. <i>Molecular BioSystems</i> , 2015, 11, 950-957.	2.9	36

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109	Environmental genes and genomes: understanding the differences and challenges in the approaches and software for their analyses. <i>Briefings in Bioinformatics</i> , 2015, 16, 745-758.	3.2	66
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. <i>Bioinformatics</i> , 2015, 31, 1307-1309.	1.8	242
111	PseKNC-General: a cross-platform package for generating various modes of pseudo nucleotide compositions. <i>Bioinformatics</i> , 2015, 31, 119-120.	1.8	210
112	Probabilistic expression of spatially varied amino acid dimers into general form of Chou's pseudo amino acid composition for protein fold recognition. <i>Journal of Theoretical Biology</i> , 2015, 380, 291-298.	0.8	22
113	Predicting industrial polymer melt index via incorporating chaotic characters into Chou's general PseAAC. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2015, 146, 232-240.	1.8	23
114	iLM-2L: A two-level predictor for identifying protein lysine methylation sites and their methylation degrees by incorporating K-gap amino acid pairs into Chou's general PseAAC. <i>Journal of Theoretical Biology</i> , 2015, 385, 50-57.	0.8	24
115	Protein cold adaptation: Role of physico-chemical parameters in adaptation of proteins to low temperatures. <i>Journal of Theoretical Biology</i> , 2015, 383, 130-137.	0.8	8
116	Pseudo nucleotide composition or PseKNC: an effective formulation for analyzing genomic sequences. <i>Molecular BioSystems</i> , 2015, 11, 2620-2634.	2.9	289
117	Identify five kinds of simple super-secondary structures with quadratic discriminant algorithm based on the chemical shifts. <i>Journal of Theoretical Biology</i> , 2015, 380, 392-398.	0.8	13
118	Pse-in-One: a web server for generating various modes of pseudo components of DNA, RNA, and protein sequences. <i>Nucleic Acids Research</i> , 2015, 43, W65-W71.	6.5	664
119	TargetFreeze: Identifying Antifreeze Proteins via a Combination of Weights using Sequence Evolutionary Information and Pseudo Amino Acid Composition. <i>Journal of Membrane Biology</i> , 2015, 248, 1005-1014.	1.0	36
120	iCataly-PseAAC: Identification of Enzymes Catalytic Sites Using Sequence Evolution Information with Grey Model GM (2,1). <i>Journal of Membrane Biology</i> , 2015, 248, 1033-1041.	1.0	10
121	Using weighted features to predict recombination hotspots in <i>Saccharomyces cerevisiae</i> . <i>Journal of Theoretical Biology</i> , 2015, 382, 15-22.	0.8	16
122	PGlcS: Prediction of protein O-GlcNAcylation sites with multiple features and analysis. <i>Journal of Theoretical Biology</i> , 2015, 380, 524-529.	0.8	11
123	VR-BFDT: A variance reduction based binary fuzzy decision tree induction method for protein function prediction. <i>Journal of Theoretical Biology</i> , 2015, 377, 10-24.	0.8	2
124	Protein remote homology detection by combining Chou's distance-pair pseudo amino acid composition and principal component analysis. <i>Molecular Genetics and Genomics</i> , 2015, 290, 1919-1931.	1.0	62
125	Analysis of the multi-copied genes and the impact of the redundant protein coding sequences on gene annotation in prokaryotic genomes. <i>Journal of Theoretical Biology</i> , 2015, 376, 8-14.	0.8	30
126	miRNA-dis: microRNA precursor identification based on distance structure status pairs. <i>Molecular BioSystems</i> , 2015, 11, 1194-1204.	2.9	66

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127	The small-molecule inhibitor selectivity between IKK α and IKK β kinases in NF- κ B signaling pathway. <i>Journal of Receptor and Signal Transduction Research</i> , 2015, 35, 307-318.	1.3	25
128	Characterization of proteins in <i>S. cerevisiae</i> with subcellular localizations. <i>Molecular BioSystems</i> , 2015, 11, 1360-1369.	2.9	2
129	iTIS-PseKNC: Identification of Translation Initiation Site in human genes using pseudo k-tuple nucleotides composition. <i>Computers in Biology and Medicine</i> , 2015, 66, 252-257.	3.9	32
130	3D model for Cancerous Inhibitor of Protein Phosphatase 2A armadillo domain unveils highly conserved protein-protein interaction characteristics. <i>Journal of Theoretical Biology</i> , 2015, 386, 78-88.	0.8	6
131	Benchmark data for identifying N ⁶ -methyladenosine sites in the <i>Saccharomyces cerevisiae</i> genome. <i>Data in Brief</i> , 2015, 5, 376-378.	0.5	9
132	Prediction of drug's Anatomical Therapeutic Chemical (ATC) code by integrating drug's domain network. <i>Journal of Biomedical Informatics</i> , 2015, 58, 80-88.	2.5	15
133	iRNA-Methyl: Identifying N ⁶ -methyladenosine sites using pseudo nucleotide composition. <i>Analytical Biochemistry</i> , 2015, 490, 26-33.	1.1	350
134	Classification of membrane protein types using Voting Feature Interval in combination with Chou's Pseudo Amino Acid Composition. <i>Journal of Theoretical Biology</i> , 2015, 384, 78-83.	0.8	137
135	Identifying new targets in leukemogenesis using computational approaches. <i>Saudi Journal of Biological Sciences</i> , 2015, 22, 610-622.	1.8	8
136	Identification of microRNA precursor with the degenerate K-tuple or Kmer strategy. <i>Journal of Theoretical Biology</i> , 2015, 385, 153-159.	0.8	159
137	Improved prediction of accessible surface area results in efficient energy function application. <i>Journal of Theoretical Biology</i> , 2015, 380, 380-391.	0.8	30
138	Rare k-mer DNA: Identification of sequence motifs and prediction of CpG island and promoter. <i>Journal of Theoretical Biology</i> , 2015, 387, 88-100.	0.8	13
139	iUbiq-Lys: prediction of lysine ubiquitination sites in proteins by extracting sequence evolution information via a gray system model. <i>Journal of Biomolecular Structure and Dynamics</i> , 2015, 33, 1731-1742.	2.0	149
140	iDrug-Target: predicting the interactions between drug compounds and target proteins in cellular networking via benchmark dataset optimization approach. <i>Journal of Biomolecular Structure and Dynamics</i> , 2015, 33, 2221-2233.	2.0	185
141	A new technique for generating pathogenic barcodes in breast cancer susceptibility analysis. <i>Journal of Theoretical Biology</i> , 2015, 366, 84-90.	0.8	5
142	Using temperature effects to predict the interactions between two RNAs. <i>Journal of Theoretical Biology</i> , 2015, 364, 98-102.	0.8	0
143	A Hook's law-based approach to protein folding rate. <i>Journal of Theoretical Biology</i> , 2015, 364, 407-417.	0.8	9
144	Gram-positive and Gram-negative protein subcellular localization by incorporating evolutionary-based descriptors into Chou's general PseAAC. <i>Journal of Theoretical Biology</i> , 2015, 364, 284-294.	0.8	232

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145	fabp4 is central to eight obesity associated genes: A functional gene network-based polymorphic study. <i>Journal of Theoretical Biology</i> , 2015, 364, 344-354.	0.8	33
146	Distribution bias of the sequence matching between exons and introns in exon joint and EJC binding region in <i>C. elegans</i> . <i>Journal of Theoretical Biology</i> , 2015, 364, 295-304.	0.8	5
147	Identification of DNA-binding proteins by incorporating evolutionary information into pseudo amino acid composition via the top-n-gram approach. <i>Journal of Biomolecular Structure and Dynamics</i> , 2015, 33, 1720-1730.	2.0	80
148	iOri-Human: identify human origin of replication by incorporating dinucleotide physicochemical properties into pseudo nucleotide composition. <i>Oncotarget</i> , 2016, 7, 69783-69793.	0.8	166
149	iROS-gPseKNC: Predicting replication origin sites in DNA by incorporating dinucleotide position-specific propensity into general pseudo nucleotide composition. <i>Oncotarget</i> , 2016, 7, 34180-34189.	0.8	118
150	iACP: a sequence-based tool for identifying anticancer peptides. <i>Oncotarget</i> , 2016, 7, 16895-16909.	0.8	354
151	Predicting Subcellular Localization of Apoptosis Proteins Combining GO Features of Homologous Proteins and Distance Weighted KNN Classifier. <i>BioMed Research International</i> , 2016, 2016, 1-8.	0.9	10
152	Recombination Hotspot/Coldspot Identification Combining Three Different Pseudocomponents via an Ensemble Learning Approach. <i>BioMed Research International</i> , 2016, 2016, 1-7.	0.9	1
153	SABinder: A Web Service for Predicting Streptavidin-Binding Peptides. <i>BioMed Research International</i> , 2016, 2016, 1-8.	0.9	35
154	Numerical Characterization of Protein Sequences Based on the Generalized Chou's Pseudo Amino Acid Composition. <i>Applied Sciences (Switzerland)</i> , 2016, 6, 406.	1.3	10
155	iPPBS-Opt: A Sequence-Based Ensemble Classifier for Identifying Protein-Protein Binding Sites by Optimizing Imbalanced Training Datasets. <i>Molecules</i> , 2016, 21, 95.	1.7	142
156	iHyd-PseCp: Identify hydroxyproline and hydroxylysine in proteins by incorporating sequence-coupled effects into general PseAAC. <i>Oncotarget</i> , 2016, 7, 44310-44321.	0.8	150
157	iCar-PseCp: identify carbonylation sites in proteins by Monte Carlo sampling and incorporating sequence coupled effects into general PseAAC. <i>Oncotarget</i> , 2016, 7, 34558-34570.	0.8	176
158	Identification of thermophilic proteins by incorporating evolutionary and acid dissociation information into Chou's general pseudo amino acid composition. <i>Journal of Theoretical Biology</i> , 2016, 407, 138-142.	0.8	35
159	Combining pseudo dinucleotide composition with the Z curve method to improve the accuracy of predicting DNA elements: a case study in recombination spots. <i>Molecular BioSystems</i> , 2016, 12, 2893-2900.	2.9	19
160	Identification of Damaging ns<sc>SNV</sc>s in Human<i><sc>ERCC</sc>2</i> Gene. <i>Chemical Biology and Drug Design</i> , 2016, 88, 441-450.	1.5	5
161	pSumo-CD: predicting sumoylation sites in proteins with covariance discriminant algorithm by incorporating sequence-coupled effects into general PseAAC. <i>Bioinformatics</i> , 2016, 32, 3133-3141.	1.8	177
162	Predicting protein-protein interactions by weighted pseudo amino acid composition. <i>International Journal of Data Mining and Bioinformatics</i> , 2016, 15, 272.	0.1	6

#	ARTICLE	IF	CITATIONS
163	gDNA-Prot: Predict DNA-binding proteins by employing support vector machine and a novel numerical characterization of protein sequence. <i>Journal of Theoretical Biology</i> , 2016, 406, 8-16.	0.8	13
164	PAI: Predicting adenosine to inosine editing sites by using pseudo nucleotide compositions. <i>Scientific Reports</i> , 2016, 6, 35123.	1.6	32
165	Recombination spot identification Based on gapped k-mers. <i>Scientific Reports</i> , 2016, 6, 23934.	1.6	24
166	Identifying 2â€²-O-methylation sites by integrating nucleotide chemical properties and nucleotide compositions. <i>Genomics</i> , 2016, 107, 255-258.	1.3	55
167	An ensemble distance measure of k-mer and Natural Vector for the phylogenetic analysis of multiple-segmented viruses. <i>Journal of Theoretical Biology</i> , 2016, 398, 136-144.	0.8	10
168	iDHS-EL: identifying DNase I hypersensitive sites by fusing three different modes of pseudo nucleotide composition into an ensemble learning framework. <i>Bioinformatics</i> , 2016, 32, 2411-2418.	1.8	196
169	Diagnosis of patients with chronic kidney disease by using two fuzzy classifiers. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2016, 153, 140-145.	1.8	37
170	Prediction of Golgi-resident protein types using general form of Chou's pseudo-amino acid compositions: Approaches with minimal redundancy maximal relevance feature selection. <i>Journal of Theoretical Biology</i> , 2016, 402, 38-44.	0.8	50
171	Identifying N 6-methyladenosine sites in the <i>Arabidopsis thaliana</i> transcriptome. <i>Molecular Genetics and Genomics</i> , 2016, 291, 2225-2229.	1.0	58
172	Prediction of G-protein coupled receptors and their subfamilies by incorporating various sequence features into Chou's general PseAAC. <i>Computer Methods and Programs in Biomedicine</i> , 2016, 134, 197-213.	2.6	30
173	Endogenous signal peptides in recombinant protein production by <i>Pichia pastoris</i> : From in-silico analysis to fermentation. <i>Journal of Theoretical Biology</i> , 2016, 408, 22-33.	0.8	26
174	Gene expression classification using epigenetic features and DNA sequence composition in the human embryonic stem cell line H1. <i>Gene</i> , 2016, 592, 227-234.	1.0	10
175	Comparison of genomic data via statistical distribution. <i>Journal of Theoretical Biology</i> , 2016, 407, 318-327.	0.8	5
176	Identifying RNA 5-methylcytosine sites via pseudo nucleotide compositions. <i>Molecular BioSystems</i> , 2016, 12, 3307-3311.	2.9	48
177	BioTriangle: a web-accessible platform for generating various molecular representations for chemicals, proteins, DNAs/RNAs and their interactions. <i>Journal of Cheminformatics</i> , 2016, 8, 34.	2.8	39
178	Identifying anticancer peptides by using improved hybrid compositions. <i>Scientific Reports</i> , 2016, 6, 33910.	1.6	44
179	Predicting DNA Methylation State of CpG Dinucleotide Using Genome Topological Features and Deep Networks. <i>Scientific Reports</i> , 2016, 6, 19598.	1.6	75
180	RAMPred: identifying the N1-methyladenosine sites in eukaryotic transcriptomes. <i>Scientific Reports</i> , 2016, 6, 31080.	1.6	50

#	ARTICLE	IF	CITATIONS
181	iRSpot-DACC: a computational predictor for recombination hot/cold spots identification based on dinucleotide-based auto-cross covariance. <i>Scientific Reports</i> , 2016, 6, 33483.	1.6	29
182	iAFP-Ense: An Ensemble Classifier for Identifying Antifreeze Protein by Incorporating Grey Model and PSSM into PseAAC. <i>Journal of Membrane Biology</i> , 2016, 249, 845-854.	1.0	25
183	EnhancerPred: a predictor for discovering enhancers based on the combination and selection of multiple features. <i>Scientific Reports</i> , 2016, 6, 38741.	1.6	80
184	iPTM-mLys: identifying multiple lysine PTM sites and their different types. <i>Bioinformatics</i> , 2016, 32, 3116-3123.	1.8	236
185	Combined sequence and sequence-structure based methods for analyzing FGF23, CYP24A1 and VDR genes. <i>Meta Gene</i> , 2016, 9, 26-36.	0.3	7
186	An estimator for local analysis of genome based on the minimal absent word. <i>Journal of Theoretical Biology</i> , 2016, 395, 23-30.	0.8	4
187	Improving N6-methyladenosine site prediction with heuristic selection of nucleotide physicalâ€œchemical properties. <i>Analytical Biochemistry</i> , 2016, 508, 104-113.	1.1	43
188	tRNAfeature: An algorithm for tRNA features to identify tRNA genes in DNA sequences. <i>Journal of Theoretical Biology</i> , 2016, 404, 251-261.	0.8	3
189	Cellâ€œPeptide Specific Interaction Can Inhibit <i>Mycobacterium tuberculosis</i> H37Rv Infection. <i>Journal of Cellular Biochemistry</i> , 2016, 117, 946-958.	1.2	6
190	Exploring local discriminative information from evolutionary profiles for cytokineâ€œreceptor interaction prediction. <i>Neurocomputing</i> , 2016, 217, 37-45.	3.5	11
191	iMiRNA-PseDPC: microRNA precursor identification with a pseudo distance-pair composition approach. <i>Journal of Biomolecular Structure and Dynamics</i> , 2016, 34, 223-235.	2.0	120
192	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.	0.8	297
193	Analysis on the preference for sequence matching between mRNA sequences and the corresponding introns in ribosomal protein genes. <i>Journal of Theoretical Biology</i> , 2016, 392, 113-121.	0.8	5
194	Protein fold recognition using HMMâ€œHMM alignment and dynamic programming. <i>Journal of Theoretical Biology</i> , 2016, 393, 67-74.	0.8	33
195	Prediction of Proteinâ€œProtein Interaction Sites with Machine-Learning-Based Data-Cleaning and Post-Filtering Procedures. <i>Journal of Membrane Biology</i> , 2016, 249, 141-153.	1.0	34
196	Chemometric approach to fatty acid metabolism-distribution networks and methane production in ruminal microbiome. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2016, 151, 1-8.	1.8	5
197	Predicting Golgi-resident protein types using pseudo amino acid compositions: Approaches with positional specific physicochemical properties. <i>Journal of Theoretical Biology</i> , 2016, 391, 35-42.	0.8	34
198	Inversion of the stereochemical configuration (3S, 5S)-clavaminic acid into (3R, 5R)-clavulanic acid: A computationally-assisted approach based on experimental evidence. <i>Journal of Theoretical Biology</i> , 2016, 395, 40-50.	0.8	10

#	ARTICLE	IF	CITATIONS
199	Predicting lysine phosphoglycerlation with fuzzy SVM by incorporating k-spaced amino acid pairs into Chou's general PseAAC. <i>Journal of Theoretical Biology</i> , 2016, 397, 145-150.	0.8	92
200	pRNAm-PC: Predicting N6-methyladenosine sites in RNA sequences via physical-chemical properties. <i>Analytical Biochemistry</i> , 2016, 497, 60-67.	1.1	247
201	Using deformation energy to analyze nucleosome positioning in genomes. <i>Genomics</i> , 2016, 107, 69-75.	1.3	104
202	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.	1.1	254
203	A New Multi-label Classifier for Identifying the Functional Types of Singleplex and Multiplex Antimicrobial Peptides. <i>International Journal of Peptide Research and Therapeutics</i> , 2016, 22, 281-287.	0.9	7
204	ProTSAV: A protein tertiary structure analysis and validation server. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016, 1864, 11-19.	1.1	69
205	A balanced secondary structure predictor. <i>Journal of Theoretical Biology</i> , 2016, 389, 60-71.	0.8	26
206	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, 1946-1961.	2.0	120
207	iEnhancer-2L: a two-layer predictor for identifying enhancers and their strength by pseudo k-tuple nucleotide composition. <i>Bioinformatics</i> , 2016, 32, 362-369.	1.8	323
208	Identifying Antioxidant Proteins by Using Optimal Dipeptide Compositions. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2016, 8, 186-191.	2.2	42
209	Association analysis between the distributions of histone modifications and gene expression in the human embryonic stem cell. <i>Gene</i> , 2016, 575, 90-100.	1.0	10
210	iRSpot-GAEnsC: identifying recombination spots via ensemble classifier and extending the concept of Chou's PseAAC to formulate DNA samples. <i>Molecular Genetics and Genomics</i> , 2016, 291, 285-296.	1.0	120
211	Identify Secretory Protein of Malaria Parasite with Modified Quadratic Discriminant Algorithm and Amino Acid Composition. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2016, 8, 156-161.	2.2	8
212	repRNA: a web server for generating various feature vectors of RNA sequences. <i>Molecular Genetics and Genomics</i> , 2016, 291, 473-481.	1.0	122
213	MethyRNA: a web server for identification of N ⁶ -methyladenosine sites. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017, 35, 683-687.	2.0	124
214	iPhosPseEvo: Identifying Human Phosphorylated Proteins by Incorporating Evolutionary Information into General PseAAC via Grey System Theory. <i>Molecular Informatics</i> , 2017, 36, 1600010.	1.4	94
215	Application of Takagi-Sugeno fuzzy model optimized with an improved Free Search algorithm to industrial polypropylene melt index prediction. <i>Transactions of the Institute of Measurement and Control</i> , 2017, 39, 1613-1622.	1.1	3
216	PDC-SGB: Prediction of effective drug combinations using a stochastic gradient boosting algorithm. <i>Journal of Theoretical Biology</i> , 2017, 417, 1-7.	0.8	85

#	ARTICLE	IF	CITATIONS
217	EnhancerPred2.0: predicting enhancers and their strength based on position-specific trinucleotide propensity and electronâ€“ion interaction potential feature selection. <i>Molecular BioSystems</i> , 2017, 13, 767-774.	2.9	42
218	Predicting antimicrobial peptides with improved accuracy by incorporating the compositional, physico-chemical and structural features into Chouâ€™s general PseAAC. <i>Scientific Reports</i> , 2017, 7, 42362.	1.6	358
219	Evolutionary mechanism and biological functions of 8-mers containing CG dinucleotide in yeast. <i>Chromosome Research</i> , 2017, 25, 173-189.	1.0	6
220	A novel alignment-free method to classify protein folding types by combining spectral graph clustering with Chou's pseudo amino acid composition. <i>Journal of Theoretical Biology</i> , 2017, 424, 49-54.	0.8	55
221	A computational model for predicting integrase catalytic domain of retrovirus. <i>Journal of Theoretical Biology</i> , 2017, 423, 63-70.	0.8	1
222	2L-â€“iRNA: A Two-Layer Ensemble Classifier for Identifying Piwi-Interacting RNAs and Their Function. <i>Molecular Therapy - Nucleic Acids</i> , 2017, 7, 267-277.	2.3	226
223	Prediction of metastasis in advanced colorectal carcinomas using CGH data. <i>Journal of Theoretical Biology</i> , 2017, 429, 116-123.	0.8	5
224	Recognition of long-range enhancer-promoter interactions by adding genomic signatures of segmented regulatory regions. <i>Genomics</i> , 2017, 109, 341-352.	1.3	15
225	Transmembrane region prediction by using sequence-derived features and machine learning methods. <i>RSC Advances</i> , 2017, 7, 29200-29211.	1.7	3
226	pDHS-SVM: A prediction method for plant DNase I hypersensitive sites based on support vector machine. <i>Journal of Theoretical Biology</i> , 2017, 426, 126-133.	0.8	17
227	iRNA-PseColl: Identifying the Occurrence Sites of Different RNA Modifications by Incorporating Collective Effects of Nucleotides into PseKNC. <i>Molecular Therapy - Nucleic Acids</i> , 2017, 7, 155-163.	2.3	259
228	Predicting membrane protein types using various decision tree classifiers based on various modes of general PseAAC for imbalanced datasets. <i>Journal of Theoretical Biology</i> , 2017, 435, 208-217.	0.8	29
229	A novel nucleic acid sequence encoding strategy for high-performance aptamer identification and the aid of sequence design and optimization. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2017, 170, 32-37.	1.8	5
230	Computational prediction of therapeutic peptides based on graph index. <i>Journal of Biomedical Informatics</i> , 2017, 75, 63-69.	2.5	33
231	iSS-PC: Identifying Splicing Sites via Physical-Chemical Properties Using Deep Sparse Auto-Encoder. <i>Scientific Reports</i> , 2017, 7, 8222.	1.6	21
232	Prediction of lysine crotonylation sites by incorporating the composition of k-spaced amino acid pairs into Chouâ€™s general PseAAC. <i>Journal of Molecular Graphics and Modelling</i> , 2017, 77, 200-204.	1.3	77
233	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.	1.0	138
234	pLoc-mAnimal: predict subcellular localization of animal proteins with both single and multiple sites. <i>Bioinformatics</i> , 2017, 33, 3524-3531.	1.8	175

#	ARTICLE	IF	CITATIONS
235	Prediction of presynaptic and postsynaptic neurotoxins by combining various Chou's pseudo components. <i>Scientific Reports</i> , 2017, 7, 5827.	1.6	35
236	Highly accurate prediction of protein self-interactions by incorporating the average block and PSSM information into the general PseAAC. <i>Journal of Theoretical Biology</i> , 2017, 432, 80-86.	0.8	9
237	DIRProt: a computational approach for discriminating insecticide resistant proteins from non-resistant proteins. <i>BMC Bioinformatics</i> , 2017, 18, 190.	1.2	13
238	Gly-PseAAC: Identifying protein lysine glycation through sequences. <i>Gene</i> , 2017, 602, 1-7.	1.0	37
239	iRSpot-EL: identify recombination spots with an ensemble learning approach. <i>Bioinformatics</i> , 2017, 33, 35-41.	1.8	280
240	Prediction of nucleosome positioning by the incorporation of frequencies and distributions of three different nucleotide segment lengths into a general pseudo k-tuple nucleotide composition. <i>Bioinformatics</i> , 2017, 33, 42-48.	1.8	25
241	Predicting the Organelle Location of Noncoding RNAs Using Pseudo Nucleotide Compositions. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2017, 9, 540-544.	2.2	19
242	A machine-learning approach for predicting palmitoylation sites from integrated sequence-based features. <i>Journal of Bioinformatics and Computational Biology</i> , 2017, 15, 1650025.	0.3	5
243	The Physical and Geometric Properties of Human Transposon Stem-Loop Structures under Natural Selection. <i>Biophysics (Russian Federation)</i> , 2017, 62, 857-864.	0.2	0
244	Detection of Interactions between Proteins by Using Legendre Moments Descriptor to Extract Discriminatory Information Embedded in PSSM. <i>Molecules</i> , 2017, 22, 1366.	1.7	28
245	Prediction of the aquatic toxicity of aromatic compounds to tetrahymena pyriformis through support vector regression. <i>Oncotarget</i> , 2017, 8, 49359-49369.	0.8	53
246	iATC-mHyb: a hybrid multi-label classifier for predicting the classification of anatomical therapeutic chemicals. <i>Oncotarget</i> , 2017, 8, 58494-58503.	0.8	118
247	Taxonomic Classification for Living Organisms Using Convolutional Neural Networks. <i>Genes</i> , 2017, 8, 326.	1.0	16
248	Genome-Wide Prediction of DNA Methylation Using DNA Composition and Sequence Complexity in Human. <i>International Journal of Molecular Sciences</i> , 2017, 18, 420.	1.8	8
249	UltraPse: A Universal and Extensible Software Platform for Representing Biological Sequences. <i>International Journal of Molecular Sciences</i> , 2017, 18, 2400.	1.8	16
250	MLACP: machine-learning-based prediction of anticancer peptides. <i>Oncotarget</i> , 2017, 8, 77121-77136.	0.8	207
251	Pse-Analysis: a python package for DNA/RNA and protein/peptide sequence analysis based on pseudo components and kernel methods. <i>Oncotarget</i> , 2017, 8, 13338-13343.	0.8	119
252	iRNA-AI: identifying the adenosine to inosine editing sites in RNA sequences. <i>Oncotarget</i> , 2017, 8, 4208-4217.	0.8	209

#	ARTICLE	IF	CITATIONS
253	iRNAm5C-PseDNC: identifying RNA 5-methylcytosine sites by incorporating physical-chemical properties into pseudo dinucleotide composition. <i>Oncotarget</i> , 2017, 8, 41178-41188.	0.8	191
254	Enhanced prediction of recombination hotspots using input features extracted by class specific autoencoders. <i>Journal of Theoretical Biology</i> , 2018, 444, 73-82.	0.8	10
255	Recognition of the long range enhancer-promoter interactions by further adding DNA structure properties and transcription factor binding motifs in human cell lines. <i>Journal of Theoretical Biology</i> , 2018, 445, 136-150.	0.8	8
256	Prediction of citrullination sites by incorporating k-spaced amino acid pairs into Chou's general pseudo amino acid composition. <i>Gene</i> , 2018, 664, 78-83.	1.0	83
257	NucPosPred: Predicting species-specific genomic nucleosome positioning via four different modes of general PseKNC. <i>Journal of Theoretical Biology</i> , 2018, 450, 15-21.	0.8	35
258	Predicting protein submitochondrial locations by incorporating the pseudo-position specific scoring matrix into the general Chou's pseudo-amino acid composition. <i>Journal of Theoretical Biology</i> , 2018, 450, 86-103.	0.8	72
259	Prediction of DNase I hypersensitive sites in plant genome using multiple modes of pseudo components. <i>Analytical Biochemistry</i> , 2018, 549, 149-156.	1.1	10
260	Accurate RNA 5-methylcytosine site prediction based on heuristic physical-chemical properties reduction and classifier ensemble. <i>Analytical Biochemistry</i> , 2018, 550, 41-48.	1.1	43
261	DeepEfflux: a 2D convolutional neural network model for identifying families of efflux proteins in transporters. <i>Bioinformatics</i> , 2018, 34, 3111-3117.	1.8	35
262	Efficient computational model for classification of protein localization images using Extended Threshold Adjacency Statistics and Support Vector Machines. <i>Computer Methods and Programs in Biomedicine</i> , 2018, 157, 205-215.	2.6	10
263	EvoStruct-Sub: An accurate Gram-positive protein subcellular localization predictor using evolutionary and structural features. <i>Journal of Theoretical Biology</i> , 2018, 443, 138-146.	0.8	31
264	A Novel Modeling in Mathematical Biology for Classification of Signal Peptides. <i>Scientific Reports</i> , 2018, 8, 1039.	1.6	70
265	Nucleosome Positioning With Fractal Entropy Increment of Diversity in Telemedicine. <i>IEEE Access</i> , 2018, 6, 33451-33459.	2.6	23
266	O-GlcNAcPRED-II: an integrated classification algorithm for identifying O-GlcNAcylation sites based on fuzzy undersampling and a <i>k</i> -means PCA oversampling technique. <i>Bioinformatics</i> , 2018, 34, 2029-2036.	1.8	128
267	iRSpot-ADPM: Identify recombination spots by incorporating the associated dinucleotide product model into Chou's pseudo components. <i>Journal of Theoretical Biology</i> , 2018, 441, 1-8.	0.8	60
268	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.	1.8	139
269	RBSURFpred: Modeling protein accessible surface area in real and binary space using regularized and optimized regression. <i>Journal of Theoretical Biology</i> , 2018, 441, 44-57.	0.8	6
270	PyBioMed: a python library for various molecular representations of chemicals, proteins and DNAs and their interactions. <i>Journal of Cheminformatics</i> , 2018, 10, 16.	2.8	94

#	ARTICLE	IF	CITATIONS
271	iPhosT-PseAAC: Identify phosphothreonine sites by incorporating sequence statistical moments into PseAAC. <i>Analytical Biochemistry</i> , 2018, 550, 109-116.	1.1	111
272	Using Chou's general PseAAC to analyze the evolutionary relationship of receptor associated proteins (RAP) with various folding patterns of protein domains. <i>Journal of Theoretical Biology</i> , 2018, 445, 62-74.	0.8	65
273	iPromoter-2L: a two-layer predictor for identifying promoters and their types by multi-window-based PseKNC. <i>Bioinformatics</i> , 2018, 34, 33-40.	1.8	277
274	A Two-Layer Computational Model for Discrimination of Enhancer and Their Types Using Hybrid Features Pace of Pseudo K-Tuple Nucleotide Composition. <i>Arabian Journal for Science and Engineering</i> , 2018, 43, 6719-6727.	1.7	18
275	pLoc-mGneg: Predict subcellular localization of Gram-negative bacterial proteins by deep gene ontology learning via general PseAAC. <i>Genomics</i> , 2018, 110, 231-239.	1.3	130
276	iKcr-PseEns: Identify lysine crotonylation sites in histone proteins with pseudo components and ensemble classifier. <i>Genomics</i> , 2018, 110, 239-246.	1.3	127
277	DHSpred: support-vector-machine-based human DNase I hypersensitive sites prediction using the optimal features selected by random forest. <i>Oncotarget</i> , 2018, 9, 1944-1956.	0.8	91
278	SFPEL-LPI: Sequence-based feature projection ensemble learning for predicting LncRNA-protein interactions. <i>PLoS Computational Biology</i> , 2018, 14, e1006616.	1.5	164
279	Predicting membrane proteins and their types by extracting various sequence features into Chou's general PseAAC. <i>Molecular Biology Reports</i> , 2018, 45, 2295-2306.	1.0	51
280	iPhosY-PseAAC: identify phosphotyrosine sites by incorporating sequence statistical moments into PseAAC. <i>Molecular Biology Reports</i> , 2018, 45, 2501-2509.	1.0	57
281	iRecSpot-EF: Effective sequence based features for recombination hotspot prediction. <i>Computers in Biology and Medicine</i> , 2018, 103, 17-23.	3.9	19
282	A computational method for prediction of xylanase enzymes activity in strains of <i>Bacillus subtilis</i> based on pseudo amino acid composition features. <i>PLoS ONE</i> , 2018, 13, e0205796.	1.1	23
283	iGHBP: Computational identification of growth hormone binding proteins from sequences using extremely randomised tree. <i>Computational and Structural Biotechnology Journal</i> , 2018, 16, 412-420.	1.9	101
284	Improved DNA-Binding Protein Identification by Incorporating Evolutionary Information Into the Chou's PseAAC. <i>IEEE Access</i> , 2018, 6, 66545-66556.	2.6	47
285	Predicting lysine lipoylation sites using bi-profile bayes feature extraction and fuzzy support vector machine algorithm. <i>Analytical Biochemistry</i> , 2018, 561-562, 11-17.	1.1	8
286	iRNA(m6A)-PseDNC: Identifying N6-methyladenosine sites using pseudo dinucleotide composition. <i>Analytical Biochemistry</i> , 2018, 561-562, 59-65.	1.1	162
287	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.	0.8	71
288	Using Two-dimensional Principal Component Analysis and Rotation Forest for Prediction of Protein-Protein Interactions. <i>Scientific Reports</i> , 2018, 8, 12874.	1.6	27

#	ARTICLE	IF	CITATIONS
289	Predicting apoptosis protein subcellular localization by integrating auto-cross correlation and PSSM into Chou's PseAAC. <i>Journal of Theoretical Biology</i> , 2018, 457, 163-169.	0.8	53
290	PseUI: Pseudouridine sites identification based on RNA sequence information. <i>BMC Bioinformatics</i> , 2018, 19, 306.	1.2	105
291	iRO-3wPseKNC: identify DNA replication origins by three-window-based PseKNC. <i>Bioinformatics</i> , 2018, 34, 3086-3093.	1.8	108
292	DPP-PseAAC: A DNA-binding protein prediction model using Chou's general PseAAC. <i>Journal of Theoretical Biology</i> , 2018, 452, 22-34.	0.8	126
293	Identify Gram-negative bacterial secreted protein types by incorporating different modes of PSSM into Chou's general PseAAC via Kullback-Leibler divergence. <i>Journal of Theoretical Biology</i> , 2018, 454, 22-29.	0.8	36
294	kinPhospho: a comprehensive tool for rapid and accurate prediction of kinase family-specific phosphorylation sites in the human proteome. <i>Bioinformatics</i> , 2018, 34, 4223-4231.	1.8	151
295	iRNA-3typeA: Identifying Three Types of Modification at RNA's Adenosine Sites. <i>Molecular Therapy - Nucleic Acids</i> , 2018, 11, 468-474.	2.3	173
296	PrESOGensis: A two-layer multi-label predictor for identifying fertility-related proteins using support vector machine and pseudo amino acid composition approach. <i>Scientific Reports</i> , 2018, 8, 9025.	1.6	12
297	Predicting membrane protein types by incorporating a novel feature set into Chou's general PseAAC. <i>Journal of Theoretical Biology</i> , 2018, 455, 319-328.	0.8	52
298	Analysis and prediction of ion channel inhibitors by using feature selection and Chou's general pseudo amino acid composition. <i>Journal of Theoretical Biology</i> , 2018, 456, 41-48.	0.8	34
299	AlPpred: Sequence-Based Prediction of Anti-inflammatory Peptides Using Random Forest. <i>Frontiers in Pharmacology</i> , 2018, 9, 276.	1.6	160
300	iRSpot-Pse6NC: Identifying recombination spots in <i>Saccharomyces cerevisiae</i> by incorporating hexamer composition into general PseKNC. <i>International Journal of Biological Sciences</i> , 2018, 14, 883-891.	2.6	145
301	iLoc-lncRNA: predict the subcellular location of lncRNAs by incorporating octamer composition into general PseKNC. <i>Bioinformatics</i> , 2018, 34, 4196-4204.	1.8	227
302	Protein Sequence Comparison and DNA-binding Protein Identification with Generalized PseAAC and Graphical Representation. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2018, 21, 100-110.	0.6	8
303	ir-HSP: Improved Recognition of Heat Shock Proteins, Their Families and Sub-types Based On g-Spaced Di-peptide Features and Support Vector Machine. <i>Frontiers in Genetics</i> , 2017, 8, 235.	1.1	18
304	nifPred: Proteome-Wide Identification and Categorization of Nitrogen-Fixation Proteins of Diazotrophs Based on Composition-Transition-Distribution Features Using Support Vector Machine. <i>Frontiers in Microbiology</i> , 2018, 9, 1100.	1.5	13
305	A Novel Hybrid Sequence-Based Model for Identifying Anticancer Peptides. <i>Genes</i> , 2018, 9, 158.	1.0	95
306	Assessing the Performances of Protein Function Prediction Algorithms from the Perspectives of Identification Accuracy and False Discovery Rate. <i>International Journal of Molecular Sciences</i> , 2018, 19, 183.	1.8	35

#	ARTICLE	IF	CITATIONS
307	SeqSVM: A Sequence-Based Support Vector Machine Method for Identifying Antioxidant Proteins. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1773.	1.8	79
308	Genome-wide analysis of H3K36me3 and its regulations to cancer-related genes expression in human cell lines. <i>BioSystems</i> , 2018, 171, 59-65.	0.9	13
309	70ProPred: a predictor for discovering sigma70 promoters based on combining multiple features. <i>BMC Systems Biology</i> , 2018, 12, 44.	3.0	72
310	iRNA-2OM: A Sequence-Based Predictor for Identifying 2â€²-O-Methylation Sites in <i>Homo sapiens</i> . <i>Journal of Computational Biology</i> , 2018, 25, 1266-1277.	0.8	137
311	Implications of Newly Identified Brain eQTL Genes and Their Interactors in Schizophrenia. <i>Molecular Therapy - Nucleic Acids</i> , 2018, 12, 433-442.	2.3	63
312	PIP-EL: A New Ensemble Learning Method for Improved Proinflammatory Peptide Predictions. <i>Frontiers in Immunology</i> , 2018, 9, 1783.	2.2	100
313	BlaPred: Predicting and classifying β -lactamase using a 3-tier prediction system via Chou's general PseAAC. <i>Journal of Theoretical Biology</i> , 2018, 457, 29-36.	0.8	45
314	Predicting protein lysine methylation sites by incorporating single-residue structural features into Chou's pseudo components. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2018, 179, 31-38.	1.8	13
315	iEnhancer-EL: identifying enhancers and their strength with ensemble learning approach. <i>Bioinformatics</i> , 2018, 34, 3835-3842.	1.8	172
316	iRSpot-SF: Prediction of recombination hotspots by incorporating sequence based features into Chou's Pseudo components. <i>Genomics</i> , 2019, 111, 966-972.	1.3	30
317	pLoc_bal-mAnimal: predict subcellular localization of animal proteins by balancing training dataset and PseAAC. <i>Bioinformatics</i> , 2019, 35, 398-406.	1.8	89
318	Tensor Algebra-based Geometrical (3D) Biomacro-Molecular Descriptors for Protein Research: Theory, Applications and Comparison with other Methods. <i>Scientific Reports</i> , 2019, 9, 11391.	1.6	7
319	PACES: prediction of N4-acetylcytidine (ac4C) modification sites in mRNA. <i>Scientific Reports</i> , 2019, 9, 11112.	1.6	41
320	Identifying DNase I hypersensitive sites using multi-features fusion and F-score features selection via Chou's 5-steps rule. <i>Biophysical Chemistry</i> , 2019, 253, 106227.	1.5	40
321	iN6-Methyl (5-step): Identifying RNA N6-methyladenosine sites using deep learning mode via Chou's 5-step rules and Chou's general PseKNC. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2019, 193, 103811.	1.8	83
322	MsDBP: Exploring DNA-Binding Proteins by Integrating Multiscale Sequence Information via Chou's Five-Step Rule. <i>Journal of Proteome Research</i> , 2019, 18, 3119-3132.	1.8	72
323	RNAm5CPred: Prediction of RNA 5-Methylcytosine Sites Based on Three Different Kinds of Nucleotide Composition. <i>Molecular Therapy - Nucleic Acids</i> , 2019, 18, 739-747.	2.3	49
324	i6mA-DNCP: Computational Identification of DNA N6-Methyladenine Sites in the Rice Genome Using Optimized Dinucleotide-Based Features. <i>Genes</i> , 2019, 10, 828.	1.0	35

#	ARTICLE	IF	CITATIONS
325	FKRR-MVSF: A Fuzzy Kernel Ridge Regression Model for Identifying DNA-Binding Proteins by Multi-View Sequence Features via Chou's Five-Step Rule. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4175.	1.8	26
326	A sequence-based approach for identifying recombination spots in <i>Saccharomyces cerevisiae</i> by using hyper-parameter optimization in FastText and support vector machine. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2019, 194, 103855.	1.8	11
327	EPAI-NC: Enhanced prediction of adenosine to inosine RNA editing sites using nucleotide compositions. <i>Analytical Biochemistry</i> , 2019, 569, 16-21.	1.1	11
328	Identification of D Modification Sites by Integrating Heterogeneous Features in <i>Saccharomyces cerevisiae</i> . <i>Molecules</i> , 2019, 24, 380.	1.7	15
329	Identifying N6-methyladenosine sites using extreme gradient boosting system optimized by particle swarm optimizer. <i>Journal of Theoretical Biology</i> , 2019, 467, 39-47.	0.8	21
330	iDHS-DMCAC: identifying DNase I hypersensitive sites with balanced dinucleotide-based detrending moving-average cross-correlation coefficient. <i>SAR and QSAR in Environmental Research</i> , 2019, 30, 429-445.	1.0	7
331	Analysis and prediction of human acetylation using a cascade classifier based on support vector machine. <i>BMC Bioinformatics</i> , 2019, 20, 346.	1.2	12
332	Meta-4mCpred: A Sequence-Based Meta-Predictor for Accurate DNA 4mC Site Prediction Using Effective Feature Representation. <i>Molecular Therapy - Nucleic Acids</i> , 2019, 16, 733-744.	2.3	182
333	Predicting protein sub-Golgi locations by combining functional domain enrichment scores with pseudo-amino acid compositions. <i>Journal of Theoretical Biology</i> , 2019, 473, 38-43.	0.8	17
334	iRSpot-SPI: Deep learning-based recombination spots prediction by incorporating secondary sequence information coupled with physio-chemical properties via Chou's 5-step rule and pseudo components. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2019, 189, 169-180.	1.8	58
335	iRNAD: a computational tool for identifying D modification sites in RNA sequence. <i>Bioinformatics</i> , 2019, 35, 4922-4929.	1.8	75
336	Recognition of 3'-end L1, Alu, processed pseudogenes, and mRNA stem-loops in the human genome using sequence-based and structure-based machine-learning models. <i>Scientific Reports</i> , 2019, 9, 7211.	1.6	0
337	iDNA6mA (5-step rule): Identification of DNA N6-methyladenine sites in the rice genome by intelligent computational model via Chou's 5-step rule. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2019, 189, 96-101.	1.8	81
338	iN6-methylat (5-step): identifying DNA N6-methyladenine sites in rice genome using continuous bag of nucleobases via Chou's 5-step rule. <i>Molecular Genetics and Genomics</i> , 2019, 294, 1173-1182.	1.0	55
339	iPseU-CNN: Identifying RNA Pseudouridine Sites Using Convolutional Neural Networks. <i>Molecular Therapy - Nucleic Acids</i> , 2019, 16, 463-470.	2.3	72
340	IMKPse: Identification of Protein Malonylation Sites by the Key Features Into General PseAAC. <i>IEEE Access</i> , 2019, 7, 54073-54083.	2.6	25
341	LAIPT: Lysine Acetylation Site Identification with Polynomial Tree. <i>International Journal of Molecular Sciences</i> , 2019, 20, 113.	1.8	14
342	dForml(KNN)-PseAAC: Detecting formylation sites from protein sequences using K-nearest neighbor algorithm via Chou's 5-step rule and pseudo components. <i>Journal of Theoretical Biology</i> , 2019, 470, 43-49.	0.8	55

#	ARTICLE	IF	CITATIONS
343	Deeplon: Deep learning approach for classifying ion transporters and ion channels from membrane proteins. <i>Journal of Computational Chemistry</i> , 2019, 40, 1521-1529.	1.5	12
344	iMotor-CNN: Identifying molecular functions of cytoskeleton motor proteins using 2D convolutional neural network via Chou's 5-step rule. <i>Analytical Biochemistry</i> , 2019, 575, 17-26.	1.1	52
345	iEnhancer-5Step: Identifying enhancers using hidden information of DNA sequences via Chou's 5-step rule and word embedding. <i>Analytical Biochemistry</i> , 2019, 571, 53-61.	1.1	109
346	iEsGene-ZCPseKNC: Identify Essential Genes Based on Z Curve Pseudo k -Tuple Nucleotide Composition. <i>IEEE Access</i> , 2019, 7, 165241-165247.	2.6	7
347	CircSLNN: Identifying RBP-Binding Sites on circRNAs via Sequence Labeling Neural Networks. <i>Frontiers in Genetics</i> , 2019, 10, 1184.	1.1	47
348	RAACBook: a web server of reduced amino acid alphabet for sequence-dependent inference by using Chou's five-step rule. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	51
349	iPro70-FMWin: identifying Sigma70 promoters using multiple windowing and minimal features. <i>Molecular Genetics and Genomics</i> , 2019, 294, 69-84.	1.0	43
350	pLoc_bal-mHum: Predict subcellular localization of human proteins by PseAAC and quasi-balancing training dataset. <i>Genomics</i> , 2019, 111, 1274-1282.	1.3	63
351	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.	1.3	60
352	MFSC: Multi-voting based feature selection for classification of Golgi proteins by adopting the general form of Chou's PseAAC components. <i>Journal of Theoretical Biology</i> , 2019, 463, 99-109.	0.8	46
353	iRNA-PseKNC(2methyl): Identify RNA 2'-O-methylation sites by convolution neural network and Chou's pseudo components. <i>Journal of Theoretical Biology</i> , 2019, 465, 1-6.	0.8	90
354	pSSbond-PseAAC: Prediction of disulfide bonding sites by integration of PseAAC and statistical moments. <i>Journal of Theoretical Biology</i> , 2019, 463, 47-55.	0.8	68
355	Analysis and prediction of animal toxins by various Chou's pseudo components and reduced amino acid compositions. <i>Journal of Theoretical Biology</i> , 2019, 462, 221-229.	0.8	30
356	Predicting protein-protein interactions by fusing various Chou's pseudo components and using wavelet denoising approach. <i>Journal of Theoretical Biology</i> , 2019, 462, 329-346.	0.8	50
357	TargetDBP: Accurate DNA-Binding Protein Prediction via Sequence-based Multi-View Feature Learning. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 17, 1-1.	1.9	28
358	Fu-SulfPred: Identification of Protein S-sulfenylation Sites by Fusing Forests via Chou's General PseAAC. <i>Journal of Theoretical Biology</i> , 2019, 461, 51-58.	0.8	49
359	Prediction and functional analysis of prokaryote lysine acetylation site by incorporating six types of features into Chou's general PseAAC. <i>Journal of Theoretical Biology</i> , 2019, 461, 92-101.	0.8	27
360	iPPI-PseAAC(CGR): Identify protein-protein interactions by incorporating chaos game representation into PseAAC. <i>Journal of Theoretical Biology</i> , 2019, 460, 195-203.	0.8	88

#	ARTICLE	IF	CITATIONS
361	pDHS-DSET: Prediction of DNase I hypersensitive sites in plant genome using DS evidence theory. <i>Analytical Biochemistry</i> , 2019, 564-565, 54-63.	1.1	18
362	iRSpot-DTS: Predict recombination spots by incorporating the dinucleotide-based sparse-cross covariance information into Chou's pseudo components. <i>Genomics</i> , 2019, 111, 1760-1770.	1.3	27
363	Effective DNA binding protein prediction by using key features via Chou's general PseAAC. <i>Journal of Theoretical Biology</i> , 2019, 460, 64-78.	0.8	49
364	iTerm-PseKNC: a sequence-based tool for predicting bacterial transcriptional terminators. <i>Bioinformatics</i> , 2019, 35, 1469-1477.	1.8	173
365	Large-scale comparative assessment of computational predictors for lysine post-translational modification sites. <i>Briefings in Bioinformatics</i> , 2019, 20, 2267-2290.	3.2	99
366	iNuc-ext-PseTNC: an efficient ensemble model for identification of nucleosome positioning by extending the concept of Chou's PseAAC to pseudo-tri-nucleotide composition. <i>Molecular Genetics and Genomics</i> , 2019, 294, 199-210.	1.0	52
367	iRSpot-PDI: Identification of recombination spots by incorporating dinucleotide property diversity information into Chou's pseudo components. <i>Genomics</i> , 2019, 111, 457-464.	1.3	29
368	iDNA6mA-PseKNC: Identifying DNA N6-methyladenosine sites by incorporating nucleotide physicochemical properties into PseKNC. <i>Genomics</i> , 2019, 111, 96-102.	1.3	234
369	iProt-Sub: a comprehensive package for accurately mapping and predicting protease-specific substrates and cleavage sites. <i>Briefings in Bioinformatics</i> , 2019, 20, 638-658.	3.2	166
370	BioSeq-Analysis: a platform for DNA, RNA and protein sequence analysis based on machine learning approaches. <i>Briefings in Bioinformatics</i> , 2019, 20, 1280-1294.	3.2	251
371	iNR-2L: A two-level sequence-based predictor developed via Chou's 5-steps rule and general PseAAC for identifying nuclear receptors and their families. <i>Genomics</i> , 2020, 112, 276-285.	1.3	54
372	Prediction of lysine formylation sites using the composition of k-spaced amino acid pairs via Chou's 5-steps rule and general pseudo components. <i>Genomics</i> , 2020, 112, 859-866.	1.3	70
373	A comprehensive review and performance evaluation of bioinformatics tools for HLA class I peptide-binding prediction. <i>Briefings in Bioinformatics</i> , 2020, 21, 1119-1135.	3.2	127
374	iLearn: an integrated platform and meta-learner for feature engineering, machine-learning analysis and modeling of DNA, RNA and protein sequence data. <i>Briefings in Bioinformatics</i> , 2020, 21, 1047-1057.	3.2	294
375	Prediction of S-Sulfenylation Sites Using Statistical Moments Based Features via CHOU'S 5-Step Rule. <i>International Journal of Peptide Research and Therapeutics</i> , 2020, 26, 1291-1301.	0.9	34
376	A comparison and assessment of computational method for identifying recombination hotspots in <i>Saccharomyces cerevisiae</i> . <i>Briefings in Bioinformatics</i> , 2020, 21, 1568-1580.	3.2	78
377	Physicochemical n-grams Tool: A tool for protein physicochemical descriptor generation via Chou's 5-step rule. <i>Chemical Biology and Drug Design</i> , 2020, 95, 79-86.	1.5	20
378	Proposing Pseudo Amino Acid Components is an Important Milestone for Proteome and Genome Analyses. <i>International Journal of Peptide Research and Therapeutics</i> , 2020, 26, 1085-1098.	0.9	19

#	ARTICLE	IF	CITATIONS
379	A Two-Level Computation Model Based on Deep Learning Algorithm for Identification of piRNA and Their Functions via Chou's 5-Steps Rule. <i>International Journal of Peptide Research and Therapeutics</i> , 2020, 26, 795-809.	0.9	62
380	Progresses in Predicting Post-translational Modification. <i>International Journal of Peptide Research and Therapeutics</i> , 2020, 26, 873-888.	0.9	52
381	Glioma stages prediction based on machine learning algorithm combined with protein-protein interaction networks. <i>Genomics</i> , 2020, 112, 837-847.	1.3	31
382	Identification of prokaryotic promoters and their strength by integrating heterogeneous features. <i>Genomics</i> , 2020, 112, 1396-1403.	1.3	41
383	Identifying FL11 subtype by characterizing tumor immune microenvironment in prostate adenocarcinoma via Chou's 5-steps rule. <i>Genomics</i> , 2020, 112, 1500-1515.	1.3	29
384	Bibliometric analysis of support vector machines research trend: a case study in China. <i>International Journal of Machine Learning and Cybernetics</i> , 2020, 11, 715-728.	2.3	66
385	Convolutional neural network-based annotation of bacterial type IV secretion system effectors with enhanced accuracy and reduced false discovery. <i>Briefings in Bioinformatics</i> , 2020, 21, 1825-1836.	3.2	90
386	Using Chou's General Pseudo Amino Acid Composition to Classify Laccases from Bacterial and Fungal Sources via Chou's Five-Step Rule. <i>Applied Biochemistry and Biotechnology</i> , 2020, 190, 1035-1048.	1.4	20
387	cACP: Classifying anticancer peptides using discriminative intelligent model via Chou's 5-step rules and general pseudo components. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2020, 196, 103912.	1.8	50
388	Is There Any Sequence Feature in the RNA Pseudouridine Modification Prediction Problem?. <i>Molecular Therapy - Nucleic Acids</i> , 2020, 19, 293-303.	2.3	22
389	Detecting antimicrobial peptides by exploring the mutual information of their sequences. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 5037-5043.	2.0	4
390	Accurate prediction of DNA N4-methylcytosine sites via boost-learning various types of sequence features. <i>BMC Genomics</i> , 2020, 21, 627.	1.2	20
391	Prediction of antioxidant proteins using hybrid feature representation method and random forest. <i>Genomics</i> , 2020, 112, 4666-4674.	1.3	46
392	Prediction of Recombination Spots Using Novel Hybrid Feature Extraction Method via Deep Learning Approach. <i>Frontiers in Genetics</i> , 2020, 11, 539227.	1.1	15
393	Prediction of m5C Modifications in RNA Sequences by Combining Multiple Sequence Features. <i>Molecular Therapy - Nucleic Acids</i> , 2020, 21, 332-342.	2.3	33
394	Identification of 4-carboxyglutamate residue sites based on position based statistical feature and multiple classification. <i>Scientific Reports</i> , 2020, 10, 16913.	1.6	49
395	A deep learning-based computational approach for discrimination of DNA N6-methyladenosine sites by fusing heterogeneous features. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2020, 206, 104151.	1.8	9
396	cACP-2LFS: Classification of Anticancer Peptides Using Sequential Discriminative Model of KSAAP and Two-Level Feature Selection Approach. <i>IEEE Access</i> , 2020, 8, 131939-131948.	2.6	29

#	ARTICLE	IF	CITATIONS
397	IncLocPred: Predicting LncRNA Subcellular Localization Using Multiple Sequence Feature Information. IEEE Access, 2020, 8, 124702-124711.	2.6	11
398	i6mA-DNC: Prediction of DNA N6-Methyladenosine sites in rice genome based on dinucleotide representation using deep learning. Chemometrics and Intelligent Laboratory Systems, 2020, 204, 104102.	1.8	17
399	m7GPredictor: An improved machine learning-based model for predicting internal m7G modifications using sequence properties. Analytical Biochemistry, 2020, 609, 113905.	1.1	18
400	miRNALoc: predicting miRNA subcellular localizations based on principal component scores of physico-chemical properties and pseudo compositions of di-nucleotides. Scientific Reports, 2020, 10, 14557.	1.6	12
401	Novel Transformer Networks for Improved Sequence Labeling in genomics. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 97-106.	1.9	15
402	iMethyl-Deep: N6 Methyladenosine Identification of Yeast Genome with Automatic Feature Extraction Technique by Using Deep Learning Algorithm. Genes, 2020, 11, 529.	1.0	23
403	Prediction of N6-methyladenosine sites using convolution neural network model based on distributed feature representations. Neural Networks, 2020, 129, 385-391.	3.3	27
404	iPseU-Layer: Identifying RNA Pseudouridine Sites Using Layered Ensemble Model. Interdisciplinary Sciences, Computational Life Sciences, 2020, 12, 193-203.	2.2	9
405	Predicting lncRNA-Protein Interactions With miRNAs as Mediators in a Heterogeneous Network Model. Frontiers in Genetics, 2019, 10, 1341.	1.1	27
406	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
407	CirRNAPL: A web server for the identification of circRNA based on extreme learning machine. Computational and Structural Biotechnology Journal, 2020, 18, 834-842.	1.9	37
408	Deep4mC: systematic assessment and computational prediction for DNA N4-methylcytosine sites by deep learning. Briefings in Bioinformatics, 2021, 22, .	3.2	49
409	The prediction of human DNase I hypersensitive sites based on DNA sequence information. Chemometrics and Intelligent Laboratory Systems, 2021, 209, 104223.	1.8	4
410	RNA Secondary Structure Prediction with Pseudoknots Using Chemical Reaction Optimization Algorithm. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1195-1207.	1.9	8
411	Prediction of Piwi-Interacting RNAs and Their Functions via Convolutional Neural Network. IEEE Access, 2021, 9, 54233-54240.	2.6	2
412	iEnhancer-DHF: Identification of Enhancers and Their Strengths Using Optimize Deep Neural Network With Multiple Features Extraction Methods. IEEE Access, 2021, 9, 40783-40796.	2.6	22
413	The Remarkable Impacts of Gordon Life Science Institute. Natural Science, 2021, 13, 43-75.	0.2	2
414	Classification Technology and Application of Multifunctional Enzymes. Computer Science and Application, 2021, 11, 476-488.	0.0	0

#	ARTICLE	IF	CITATIONS
415	iDRP-PseAAC: Identification of DNA Replication Proteins Using General PseAAC and Position Dependent Features. <i>International Journal of Peptide Research and Therapeutics</i> , 2021, 27, 1315-1329.	0.9	1
416	Prediction and Analysis of Protein Ubiquitin Sites in the Model Plant <i>A. thaliana</i> . <i>Scientific Programming</i> , 2021, 2021, 1-7.	0.5	0
417	Using Chou's 5-Step Rule to Predict DNA-Protein Binding with Multi-scale Complementary Feature. <i>Journal of Proteome Research</i> , 2021, 20, 1639-1656.	1.8	3
418	Sequence-based Identification of Allergen Proteins Developed by Integration of PseAAC and Statistical Moments via 5-Step Rule. <i>Current Bioinformatics</i> , 2020, 15, 1046-1055.	0.7	41
419	Comparison and Analysis of Computational Methods for Identifying N6-Methyladenosine Sites in <i>Saccharomyces cerevisiae</i> . <i>Current Pharmaceutical Design</i> , 2021, 27, 1219-1229.	0.9	1
420	A convolution neural network-based computational model to identify the occurrence sites of various RNA modifications by fusing varied features. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2021, 211, 104233.	1.8	10
421	Splicing sites prediction of human genome using machine learning techniques. <i>Multimedia Tools and Applications</i> , 2021, 80, 30439-30460.	2.6	9
422	RFhy-m2G: Identification of RNA N2-methylguanosine modification sites based on random forest and hybrid features. <i>Methods</i> , 2022, 203, 32-39.	1.9	32
423	Epigenetic Marks and Variation of Sequence-Based Information Along Genomic Regions Are Predictive of Recombination Hot/Cold Spots in <i>Saccharomyces cerevisiae</i> . <i>Frontiers in Genetics</i> , 2021, 12, 705038.	1.1	0
424	Evaluating machine learning methodologies for identification of cancer driver genes. <i>Scientific Reports</i> , 2021, 11, 12281.	1.6	53
425	piEnPred: a bi-layered discriminative model for enhancers and their subtypes via novel cascade multi-level subset feature selection algorithm. <i>Frontiers of Computer Science</i> , 2021, 15, 1.	1.6	22
427	Accurate Prediction and Key Feature Recognition of Immunoglobulin. <i>Applied Sciences (Switzerland)</i> , 2021, 11, 6894.	1.3	5
428	Identifying Enhancers and Their Strength Based on PCWM Feature by A Two-Layer Predictor. , 2021, , .		1
429	Application of artificial intelligence for detection of chemico-biological interactions associated with oxidative stress and DNA damage. <i>Chemico-Biological Interactions</i> , 2021, 345, 109533.	1.7	19
430	Prediction of protein ubiquitination sites via multi-view features based on eXtreme gradient boosting classifier. <i>Journal of Molecular Graphics and Modelling</i> , 2021, 107, 107962.	1.3	9
431	The evolutionary relationship of S15/NS1RNA binding domains with a similar protein domain pattern - A computational approach. <i>Informatics in Medicine Unlocked</i> , 2021, 24, 100611.	1.9	1
432	The Significant and Profound Impacts of Gordon Life Science Institute. <i>Voice of the Publisher</i> , 2021, 07, 6-31.	0.0	0
433	A method for characterizing Cas9 variants via a one-million target sequence library of self-targeting sgRNAs. <i>Nucleic Acids Research</i> , 2021, 49, e31-e31.	6.5	12

#	ARTICLE	IF	CITATIONS
434	An intelligent computational model for prediction of promoters and their strength via natural language processing. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2020, 202, 104034.	1.8	11
435	Prediction of piRNAs and their function based on discriminative intelligent model using hybrid features into Chou's PseKNC. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2020, 203, 104056.	1.8	20
436	iRNA-PseU: Identifying RNA pseudouridine sites. <i>Molecular Therapy - Nucleic Acids</i> , 2016, 5, e332.	2.3	172
438	Protein Sub-Nuclear Localization Prediction Using SVM and Pfam Domain Information. <i>PLoS ONE</i> , 2014, 9, e98345.	1.1	25
439	iDNA-Prot dis: Identifying DNA-Binding Proteins by Incorporating Amino Acid Distance-Pairs and Reduced Alphabet Profile into the General Pseudo Amino Acid Composition. <i>PLoS ONE</i> , 2014, 9, e106691.	1.1	242
440	Assessing the Effects of Data Selection and Representation on the Development of Reliable E. coli Sigma 70 Promoter Region Predictors. <i>PLoS ONE</i> , 2015, 10, e0119721.	1.1	9
441	Identification of Real MicroRNA Precursors with a Pseudo Structure Status Composition Approach. <i>PLoS ONE</i> , 2015, 10, e0121501.	1.1	193
442	Identify Beta-Hairpin Motifs with Quadratic Discriminant Algorithm Based on the Chemical Shifts. <i>PLoS ONE</i> , 2015, 10, e0139280.	1.1	10
443	Identification of Multi-Functional Enzyme with Multi-Label Classifier. <i>PLoS ONE</i> , 2016, 11, e0153503.	1.1	24
444	Improved Species-Specific Lysine Acetylation Site Prediction Based on a Large Variety of Features Set. <i>PLoS ONE</i> , 2016, 11, e0155370.	1.1	26
445	2L-PCA: a two-level principal component analyzer for quantitative drug design and its applications. <i>Oncotarget</i> , 2017, 8, 70564-70578.	0.8	17
446	iPhos-PseEn: Identifying phosphorylation sites in proteins by fusing different pseudo components into an ensemble classifier. <i>Oncotarget</i> , 2016, 7, 51270-51283.	0.8	142
447	Improving the Prediction of Protein Structural Class for Low-Similarity Sequences by Incorporating Evolutionary and Structural Information. <i>Journal of Advanced Computational Intelligence and Intelligent Informatics</i> , 2016, 20, 402-411.	0.5	2
448	A Novel Amino Acid Properties Selection Method for Protein Fold Classification. <i>Protein and Peptide Letters</i> , 2020, 27, 287-294.	0.4	3
449	Metabolism of Oxalate in Humans: A Potential Role Kynurenine Aminotransferase/Glutamine Transaminase/Cysteine Conjugate Betalyase Plays in Hyperoxaluria. <i>Current Medicinal Chemistry</i> , 2019, 26, 4944-4963.	1.2	7
450	Mechanistic Insights of Chemicals and Drugs as Risk Factors for Systemic Lupus Erythematosus. <i>Current Medicinal Chemistry</i> , 2020, 27, 5175-5188.	1.2	7
451	Advances in Predicting Subcellular Localization of Multi-label Proteins and its Implication for Developing Multi-target Drugs. <i>Current Medicinal Chemistry</i> , 2019, 26, 4918-4943.	1.2	86
452	¹⁹ F-NMR in Target-based Drug Discovery. <i>Current Medicinal Chemistry</i> , 2019, 26, 4964-4983.	1.2	22

#	ARTICLE	IF	CITATIONS
453	An Insightful 10-year Recollection Since the Emergence of the 5-steps Rule. <i>Current Pharmaceutical Design</i> , 2020, 25, 4223-4234.	0.9	10
454	Antioxidant Proteins [™] Identification Based on Support Vector Machine. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2020, 23, 319-325.	0.6	4
455	Research/Review: Insights into the Mutation-Induced Dysfunction of Arachidonic Acid Metabolism from Modeling of Human CYP2J2. <i>Current Drug Metabolism</i> , 2014, 15, 502-513.	0.7	13
456	Survey of Machine Learning Techniques for Prediction of the Isoform Specificity of Cytochrome P450 Substrates. <i>Current Drug Metabolism</i> , 2019, 20, 229-235.	0.7	26
457	iMethylK-PseAAC: Improving Accuracy of Lysine Methylation Sites Identification by Incorporating Statistical Moments and Position Relative Features into General PseAAC via Chou [™] 's 5-steps Rule. <i>Current Genomics</i> , 2019, 20, 275-292.	0.7	42
458	iSulfoTyr-PseAAC: Identify Tyrosine Sulfation Sites by Incorporating Statistical Moments via Chou [™] 's 5-steps Rule and Pseudo Components. <i>Current Genomics</i> , 2019, 20, 306-320.	0.7	45
459	Recent Advances in Computational Methods for Identifying Anticancer Peptides. <i>Current Drug Targets</i> , 2019, 20, 481-487.	1.0	6
460	Established and In-trial GPCR Families in Clinical Trials: A Review for Target Selection. <i>Current Drug Targets</i> , 2019, 20, 522-539.	1.0	17
461	The Impact of Statin Therapy on the Survival of Patients with Gastrointestinal Cancer. <i>Current Drug Targets</i> , 2019, 20, 738-747.	1.0	6
462	Recent Advances on QSAR-Based Profiling of Agonist and Antagonist A3 Adenosine Receptor Ligands. <i>Current Topics in Medicinal Chemistry</i> , 2013, 13, 1048-1068.	1.0	4
463	Recent Progresses in Identifying Nuclear Receptors and Their Families. <i>Current Topics in Medicinal Chemistry</i> , 2013, 13, 1192-1200.	1.0	28
464	Interplay between Catalysts and Substrates for Activity of Class Ib Aminoacyl-tRNA Synthetases and Implications for Pharmacology. <i>Current Topics in Medicinal Chemistry</i> , 2015, 16, 616-633.	1.0	2
465	Identifying Cancer Targets Based on Machine Learning Methods via Chou [™] 's 5-steps Rule and General Pseudo Components. <i>Current Topics in Medicinal Chemistry</i> , 2019, 19, 2301-2317.	1.0	24
466	A Possible Modulation Mechanism of Intramolecular and Intermolecular Interactions for NCAM Polysialylation and Cell Migration. <i>Current Topics in Medicinal Chemistry</i> , 2019, 19, 2271-2282.	1.0	10
467	Impacts of Pseudo Amino Acid Components and 5-steps Rule to Proteomics and Proteome Analysis. <i>Current Topics in Medicinal Chemistry</i> , 2019, 19, 2283-2300.	1.0	30
468	Biological Production of (S)-acetoin: A State-of-the-Art Review. <i>Current Topics in Medicinal Chemistry</i> , 2019, 19, 2348-2356.	1.0	4
469	A Study for Therapeutic Treatment against Parkinson [™] 's Disease via Chou [™] 's 5-steps Rule. <i>Current Topics in Medicinal Chemistry</i> , 2019, 19, 2318-2333.	1.0	23
470	An Epidemic Avian Influenza Prediction Model Based on Google Trends. <i>Letters in Organic Chemistry</i> , 2019, 16, 303-310.	0.2	34

#	ARTICLE	IF	CITATIONS
471	iAFP-gap-SMOTE: An Efficient Feature Extraction Scheme Gapped Dipeptide Composition is Coupled with an Oversampling Technique for Identification of Antifreeze Proteins. <i>Letters in Organic Chemistry</i> , 2019, 16, 294-302.	0.2	23
472	N-MyristoylG-PseAAC: Sequence-based Prediction of N-Myristoyl Glycine Sites in Proteins by Integration of PseAAC and Statistical Moments. <i>Letters in Organic Chemistry</i> , 2019, 16, 226-234.	0.2	18
473	Association of EGF rs4444903 and XPD rs13181 Polymorphisms with Cutaneous Melanoma in Caucasians. <i>Medicinal Chemistry</i> , 2015, 11, 551-559.	0.7	8
474	Impacts of Bioinformatics to Medicinal Chemistry. <i>Medicinal Chemistry</i> , 2015, 11, 218-234.	0.7	496
475	Structural Variability in the RLR-MAVS Pathway and Sensitive Detection of Viral RNAs. <i>Medicinal Chemistry</i> , 2019, 15, 443-458.	0.7	16
476	Molecular Docking and Dynamics Simulation Analysis of Thymoquinone and Thymol Compounds from <i>Nigella sativa</i> L. that Inhibit Cag A and Vac A Oncoprotein of <i>Helicobacter pylori</i> : Probable Treatment of <i>H. pylori</i> Infections. <i>Medicinal Chemistry</i> , 2020, 17, 146-157.	0.7	3
477	A Review on the Recent Developments of Sequence-based Protein Feature Extraction Methods. <i>Current Bioinformatics</i> , 2019, 14, 190-199.	0.7	117
478	A Short Survey on Genetic Sequences, Chou's Pseudo Amino Acid Composition and its Combination with Fuzzy Set Theory. <i>Open Bioinformatics Journal</i> , 2013, 7, 41-48.	1.0	57
479	Using Chou's Pseudo Amino Acid Composition and Machine Learning Method to Predict the Antiviral Peptides. <i>Open Bioinformatics Journal</i> , 2015, 9, 13-19.	1.0	23
480	Anticancer peptide: Physicochemical property, functional aspect and trend in clinical application (Review). <i>International Journal of Oncology</i> , 2020, 57, 678-696.	1.4	176
481	pLoc_Deep-mGneg: Predict Subcellular Localization of Gram Negative Bacterial Proteins by Deep Learning. <i>Advances in Bioscience and Biotechnology (Print)</i> , 2020, 11, 141-152.	0.3	7
482	PFP-RFSM: Protein fold prediction by using random forests and sequence motifs. <i>Journal of Biomedical Science and Engineering</i> , 2013, 06, 1161-1170.	0.2	10
483	pLoc_Deep-mGpos: Predict Subcellular Localization of Gram Positive Bacteria Proteins by Deep Learning. <i>Journal of Biomedical Science and Engineering</i> , 2020, 13, 55-65.	0.2	4
484	Pse-in-One 2.0: An Improved Package of Web Servers for Generating Various Modes of Pseudo Components of DNA, RNA, and Protein Sequences. <i>Natural Science</i> , 2017, 09, 67-91.	0.2	115
485	pLoc-mGpos: Incorporate Key Gene Ontology Information into General PseAAC for Predicting Subcellular Localization of Gram-Positive Bacterial Proteins. <i>Natural Science</i> , 2017, 09, 330-349.	0.2	51
486	pLoc_Deep-mPlant: Predict Subcellular Localization of Plant Proteins by Deep Learning. <i>Natural Science</i> , 2020, 12, 237-247.	0.2	14
487	pLoc_Deep-mVirus: A CNN Model for Predicting Subcellular Localization of Virus Proteins by Deep Learning. <i>Natural Science</i> , 2020, 12, 388-399.	0.2	16
488	pLoc_Deep-mEuk: Predict Subcellular Localization of Eukaryotic Proteins by Deep Learning. <i>Natural Science</i> , 2020, 12, 400-428.	0.2	7

#	ARTICLE	IF	CITATIONS
489	pLoc_Deep-mHum: Predict Subcellular Localization of Human Proteins by Deep Learning. <i>Natural Science</i> , 2020, 12, 526-551.	0.2	12
490	SNARE-CNN: a 2D convolutional neural network architecture to identify SNARE proteins from high-throughput sequencing data. <i>PeerJ Computer Science</i> , 2019, 5, e177.	2.7	39
491	iSNO-AAPair: incorporating amino acid pairwise coupling into PseAAC for predicting cysteine<i>S</i>-nitrosylation sites in proteins. <i>PeerJ</i> , 2013, 1, e171.	0.9	259
492	An unprecedented revolution in medicinal science. , 0, , .		4
494	Prediction of LncRNA by Using Multiple Feature Information Fusion and Feature Selection Technique. <i>Lecture Notes in Computer Science</i> , 2018, , 318-329.	1.0	1
495	Quantitative Structure-activity Relationship of Acetylcholinesterase Inhibitors based on mRMR Combined with Support Vector Regression. <i>Letters in Organic Chemistry</i> , 2019, 16, 311-316.	0.2	0
496	Identification of Phage Virion Proteins by Using the g-gap Tripeptide Composition. <i>Letters in Organic Chemistry</i> , 2019, 16, 332-339.	0.2	2
497	iAI-DSAE: A Computational Method for Adenosine to Inosine Editing Site Prediction. <i>Letters in Organic Chemistry</i> , 2019, 16, 347-355.	0.2	1
498	Prediction of Acetylation and Succinylation in Proteins Based on Multilabel Learning RankSVM. <i>Letters in Organic Chemistry</i> , 2019, 16, 275-282.	0.2	3
499	The Cradle of Gordon Life Science Institute and Its Development and Driving Force. <i>International Journal of Biology and Genetics</i> , 0, , 1-28.	0.0	1
500	The Cradle of Gordon Life Science Institute and its Development and Driving Force. <i>Biomedical Journal of Scientific & Technical Research</i> , 2019, 23, .	0.0	10
501	Improved recognition of splice sites in <i>A. thaliana</i> by incorporating secondary structure information into sequence-derived features: a computational study. <i>3 Biotech</i> , 2021, 11, 484.	1.1	1
502	pLoc_Deep-mAnimal: A Novel Deep CNN-BLSTM Network to Predict Subcellular Localization of Animal Proteins. <i>Natural Science</i> , 2020, 12, 281-291.	0.2	7
503	Use Chou's 5-Steps Rule to Predict Remote Homology Proteins by Merging Grey Incidence Analysis and Domain Similarity Analysis. <i>Natural Science</i> , 2020, 12, 181-198.	0.2	23
504	The Pandemic Pestilences and Internet Institutes. <i>Natural Science</i> , 2020, 12, 495-515.	0.2	3
505	An Insightful Recollection for Predicting Protein Subcellular Locations in Multi-Label Systems. <i>Natural Science</i> , 2020, 12, 441-469.	0.2	2
506	Identify Lysine Neddylatation Sites Using Bi-profile Bayes Feature Extraction via the Chou's 5-steps Rule and General Pseudo Components. <i>Current Genomics</i> , 2020, 20, 592-601.	0.7	18
507	Gordon Life Science Institute and Its Impacts on Computational Biology and Drug Development. <i>Natural Science</i> , 2020, 12, 125-161.	0.2	3

#	ARTICLE	IF	CITATIONS
508	ASRmiRNA: Abiotic Stress-Responsive miRNA Prediction in Plants by Using Machine Learning Algorithms with Pseudo K-Tuple Nucleotide Compositional Features. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1612.	1.8	10
509	Deep-piRNA: Bi-Layered Prediction Model for PIWI-Interacting RNA Using Discriminative Features. <i>Computers, Materials and Continua</i> , 2022, 72, 2243-2258.	1.5	5
510	A Novel Method for Predicting DNA N4-Methylcytosine Sites Based on Deep Forest Algorithm. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
511	Integrating LASSO Feature Selection and Soft Voting Classifier to Identify Origins of Replication Sites. <i>Current Genomics</i> , 2022, 23, 83-93.	0.7	1
512	Prediction model for lcrRNA aubcellular localization using machine learning. , 2021, , .		0
513	Deep learning identifies and quantifies recombination hotspot determinants. <i>Bioinformatics</i> , 2022, 38, 2683-2691.	1.8	4
522	PSP-PJMI: An innovative feature representation algorithm for identifying DNA N4-methylcytosine sites. <i>Information Sciences</i> , 2022, , .	4.0	4
523	An Effective Deep Learning-Based Architecture for Prediction of N7-Methylguanosine Sites in Health Systems. <i>Electronics (Switzerland)</i> , 2022, 11, 1917.	1.8	1
524	DNA/RNA sequence feature representation algorithms for predicting methylation-modified sites. <i>Scientia Sinica Vitae</i> , 2023, 53, 841-875.	0.1	2
525	The Development and Progress in Machine Learning for Protein Subcellular Localization Prediction. <i>Open Bioinformatics Journal</i> , 2022, 15, .	1.0	0
526	A Survey on ensemble learning under the era of deep learning. <i>Artificial Intelligence Review</i> , 2023, 56, 5545-5589.	9.7	33
527	Identification of intelligence-related proteins through a robust two-layer predictor. <i>Communicative and Integrative Biology</i> , 2022, 15, 253-264.	0.6	0
528	DNA-MP: a generalized DNA modifications predictor for multiple species based on powerful sequence encoding method. <i>Briefings in Bioinformatics</i> , 2023, 24, .	3.2	5
529	Computational prediction of disease related lncRNAs using machine learning. <i>Scientific Reports</i> , 2023, 13, .	1.6	3
530	Identify essential genes based on clustering based synthetic minority oversampling technique. <i>Computers in Biology and Medicine</i> , 2023, 153, 106523.	3.9	4
531	iEnhancer-SKNN: a stacking ensemble learning-based method for enhancer identification and classification using sequence information. <i>Briefings in Functional Genomics</i> , 2023, 22, 302-311.	1.3	1
532	A novel method for predicting DNA N ⁴ -methylcytosine sites based on deep forest algorithm. <i>Journal of Bioinformatics and Computational Biology</i> , 0, , .	0.3	0
534	iEnhancer-ELM: improve enhancer identification by extracting position-related multiscale contextual information based on enhancer language models. <i>Bioinformatics Advances</i> , 2023, 3, .	0.9	3

#	ARTICLE	IF	CITATIONS
539	SulfoTyr-PseAAC: A Machine Learning Framework to Identify SulfoTyrosine Sites. , 2022, , .		1
545	Classification of Coding and Non-coding Genes in Paeonia Lactiflora Pall Based on Machine Learning. Lecture Notes in Computer Science, 2023, , 578-586.	1.0	0
560	Nucleotide Sequence Classification of Paeonia Lactiflora Based on Feature Representation Learning. Communications in Computer and Information Science, 2024, , 57-64.	0.4	0