Hao Lin

List of Publications by Year
in descending order

197	15,478	10389 72	19190 118
papers	citations	h-index	g-index

199	199	199	4417
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Deep-4mCW2V: A sequence-based predictor to identify N4-methylcytosine sites in Escherichia coli. Methods, 2022, 203, 558-563.	3.8	42
2	RNALocate v2.0: an updated resource for RNA subcellular localization with increased coverage and annotation. Nucleic Acids Research, 2022, 50, D333-D339.	14.5	54
3	iRice-MS: An integrated XGBoost model for detecting multitype post-translational modification sites in rice. Briefings in Bioinformatics, 2022, 23, .	6.5	15
4	BDselect: A Package for k-mer Selection Based on the Binomial Distribution. Current Bioinformatics, 2022, 17, 238-244.	1.5	15
5	A deep learning model to identify gene expression level using cobinding transcription factor signals. Briefings in Bioinformatics, 2022, 23, .	6.5	12
6	Detection of transcription factors binding to methylated DNA by deep recurrent neural network. Briefings in Bioinformatics, 2022, 23, .	6.5	14
7	Deep-4mCGP: A Deep Learning Approach to Predict 4mC Sites in Geobacter pickeringii by Using Correlation-Based Feature Selection Technique. International Journal of Molecular Sciences, 2022, 23, 1251.	4.1	23
8	Towards a better prediction of subcellular location of long non-coding RNA. Frontiers of Computer Science, 2022, 16, 1.	2.4	19
9	Risk prediction of diabetes and pre-diabetes based on physical examination data. Mathematical Biosciences and Engineering, 2022, 19, 3597-3608.	1.9	13
10	DeepKla: An attention mechanismâ€based deep neural network for protein lysine lactylation site prediction. , 2022, 1, .		26
11	The Brassicaceae genome resource (TBGR): A comprehensive genome platform for Brassicaceae plants. Plant Physiology, 2022, 190, 226-237.	4.8	12
12	PSnoD: identifying potential snoRNA-disease associations based on bounded nuclear norm regularization. Briefings in Bioinformatics, 2022, 23, .	6.5	21
13	DeepYY1: a deep learning approach to identify YY1-mediated chromatin loops. Briefings in Bioinformatics, 2021, 22, .	6.5	63
14	Deep-Kcr: accurate detection of lysine crotonylation sites using deep learning method. Briefings in Bioinformatics, 2021, 22, .	6.5	86
15	Design powerful predictor for mRNA subcellular location prediction inHomo sapiens. Briefings in Bioinformatics, 2021, 22, 526-535.	6.5	100
16	A computational platform to identify origins of replication sites in eukaryotes. Briefings in Bioinformatics, 2021, 22, 1940-1950.	6.5	73
17	iCarPS: a computational tool for identifying protein carbonylation sites by novel encoded features. Bioinformatics, 2021, 37, 171-177.	4.1	59
18	The celery genome sequence reveals sequential paleoâ€polyploidizations, karyotype evolution and resistance gene reduction in apiales. Plant Biotechnology Journal, 2021, 19, 731-744.	8.3	62

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19	A computational framework for identifying the transcription factors involved in enhancer-promoter loop formation. Molecular Therapy - Nucleic Acids, 2021, 23, 347-354.	5.1	9
20	Screening of Prospective Plant Compounds as H1R and CL1R Inhibitors and Its Antiallergic Efficacy through Molecular Docking Approach. Computational and Mathematical Methods in Medicine, 2021, 2021, 1-9.	1.3	12
21	DM3Loc: multi-label mRNA subcellular localization prediction and analysis based on multi-head self-attention mechanism. Nucleic Acids Research, 2021, 49, e46-e46.	14.5	95
22	Comprehensive identification and characterization of simple sequence repeats based on the whole-genome sequences of 14 forest and fruit trees. Forestry Research, 2021, 1, 1-10.	1.1	7
23	DeepIPs: comprehensive assessment and computational identification of phosphorylation sites of SARS-CoV-2 infection using a deep learning-based approach. Briefings in Bioinformatics, 2021, 22, .	6.5	48
24	EMCBOW-GPCR: A method for identifying G-protein coupled receptors based on word embedding and wordbooks. Computational and Structural Biotechnology Journal, 2021, 19, 4961-4969.	4.1	6
25	A sequence-based deep learning approach to predict CTCF-mediated chromatin loop. Briefings in Bioinformatics, 2021, 22, .	6.5	28
26	Comparative analysis of long noncoding RNAs in angiosperms and characterization of long noncoding RNAs in response to heat stress in Chinese cabbage. Horticulture Research, 2021, 8, 48.	6.3	38
27	iDHS-Deep: an integrated tool for predicting DNase I hypersensitive sites by deep neural network. Briefings in Bioinformatics, 2021, 22, .	6.5	28
28	PPD: A Manually Curated Database for Experimentally Verified Prokaryotic Promoters. Journal of Molecular Biology, 2021, 433, 166860.	4.2	37
29	Integrated biomarker profiling of the metabolome associated with impaired fasting glucose and type 2 diabetes mellitus in largeâ€scale Chinese patients. Clinical and Translational Medicine, 2021, 11, e432.	4.0	29
30	Identification of Potential Inhibitors Against SARS-CoV-2 Using Computational Drug Repurposing Study. Current Bioinformatics, 2021, 16, 1320-1327.	1.5	4
31	Advances in mapping the epigenetic modifications of 5â€methylcytosine (5mC), N6â€methyladenine (6mA), and N4â€methylcytosine (4mC). Biotechnology and Bioengineering, 2021, 118, 4204-4216.	3.3	37
32	A Survey for Predicting ATP Binding Residues of Proteins Using Machine Learning Methods. Current Medicinal Chemistry, 2021, 28, .	2.4	1
33	Risk Prediction of Diabetes: Big data mining with fusion of multifarious physical examination indicators. Information Fusion, 2021, 75, 140-149.	19.1	123
34	Identification of cyclin protein using gradient boost decision tree algorithm. Computational and Structural Biotechnology Journal, 2021, 19, 4123-4131.	4.1	40
35	Comparative analysis of the <i>TCP</i> gene family in celery, coriander and carrot (family) Tj ETQq1 1 0.784314 rgBT /Over	0.7	9
36	VisFeature: a stand-alone program for visualizing and analyzing statistical features of biological sequences. Bioinformatics, 2020, 36, 1277-1278.	4.1	13

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37	A comparison and assessment of computational method for identifying recombination hotspots inSaccharomyces cerevisiae. Briefings in Bioinformatics, 2020, 21, 1568-1580.	6.5	78
38	XG-PseU: an eXtreme Gradient Boosting based method for identifying pseudouridine sites. Molecular Genetics and Genomics, 2020, 295, 13-21.	2.1	61
39	Predicting Preference of Transcription Factors for Methylated DNA Using Sequence Information. Molecular Therapy - Nucleic Acids, 2020, 22, 1043-1050.	5.1	25
40	Early Diagnosis of Pancreatic Ductal Adenocarcinoma by Combining Relative Expression Orderings With Machine-Learning Method. Frontiers in Cell and Developmental Biology, 2020, 8, 582864.	3.7	28
41	Deform-nu: A DNA Deformation Energy-Based Predictor for Nucleosome Positioning. Frontiers in Cell and Developmental Biology, 2020, 8, 596341.	3.7	2
42	Computational identification of N6-methyladenosine sites in multiple tissues of mammals. Computational and Structural Biotechnology Journal, 2020, 18, 1084-1091.	4.1	70
43	Computational Method in Protein Structure and Function Data. Protein and Peptide Letters, 2020, 27, 257-258.	0.9	1
44	iDNA-MS: An Integrated Computational Tool for Detecting DNA Modification Sites in Multiple Genomes. IScience, 2020, 23, 100991.	4.1	93
45	DNA4mC-LIP: a linear integration method to identify N4-methylcytosine site in multiple species. Bioinformatics, 2020, 36, 3327-3335.	4.1	33
46	Locate-R: Subcellular localization of long non-coding RNAs using nucleotide compositions. Genomics, 2020, 112, 2583-2589.	2.9	29
47	Early Diagnosis of Hepatocellular Carcinoma Using Machine Learning Method. Frontiers in Bioengineering and Biotechnology, 2020, 8, 254.	4.1	74
48	Computational Identification of Small Interfering RNA Targets in SARS-CoV-2. Virologica Sinica, 2020, 35, 359-361.	3.0	45
49	Identification of Key Histone Modifications and Their Regulatory Regions on Gene Expression Level Changes in Chronic Myelogenous Leukemia. Frontiers in Cell and Developmental Biology, 2020, 8, 621578.	3.7	6
50	Prevention and Control of Pathogens Based on Big-Data Mining and Visualization Analysis. Frontiers in Molecular Biosciences, 2020, 7, 626595.	3.5	0
51	Evaluation of different computational methods on 5-methylcytosine sites identification. Briefings in Bioinformatics, 2020, 21, 982-995.	6.5	115
52	Recent Development of Computational Predicting Bioluminescent Proteins. Current Pharmaceutical Design, 2020, 25, 4264-4273.	1.9	3
53	Development and Application of Artificial Intelligence Methods in Biological and Medical Data. Current Bioinformatics, 2020, 15, 515-516.	1.5	6
54	Computational Analysis in Medicinal Chemistry. The Case of Pharmacogenomics and Pharmacoproteomics. Medicinal Chemistry, 2020, 16, 593-593.	1.5	1

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55	Recent Advancement in Predicting Subcellular Localization of Mycobacterial Protein with Machine Learning Methods. Medicinal Chemistry, 2020, 16, 605-619.	1.5	2
56	A Fast Projection-Based Algorithm for Clustering Big Data. Interdisciplinary Sciences, Computational Life Sciences, 2019, 11, 360-366.	3.6	6
57	DNA physical properties outperform sequence compositional information in classifying nucleosome-enriched and -depleted regions. Genomics, 2019, 111, 1167-1175.	2.9	11
58	iProEP: A Computational Predictor for Predicting Promoter. Molecular Therapy - Nucleic Acids, 2019, 17, 337-346.	5.1	125
59	iDNA6mA-Rice: A Computational Tool for Detecting N6-Methyladenine Sites in Rice. Frontiers in Genetics, 2019, 10, 793.	2.3	61
60	Maternal energy insufficiency affects testicular development of the offspring in a swine model. Scientific Reports, 2019, 9, 14533.	3.3	2
61	iRNA-m7G: Identifying N7-methylguanosine Sites by Fusing Multiple Features. Molecular Therapy - Nucleic Acids, 2019, 18, 269-274.	5.1	85
62	i6mA-Pred: identifying DNA N6-methyladenine sites in the rice genome. Bioinformatics, 2019, 35, 2796-2800.	4.1	186
63	iRNA-m2G: Identifying N2-methylguanosine Sites Based on Sequence-Derived Information. Molecular Therapy - Nucleic Acids, 2019, 18, 253-258.	5.1	35
64	RIscoper: a tool for RNAâ€“RNA interaction extraction from the literature. Bioinformatics, 2019, 35, 3199-3202.	4.1	23
65	Revealing Gene Function and Transcription Relationship by Reconstructing Gene-Level Chromatin Interaction. Computational and Structural Biotechnology Journal, 2019, 17, 195-205.	4.1	16
66	iRNAD: a computational tool for identifying D modification sites in RNA sequence. Bioinformatics, 2019, 35, 4922-4929.	4.1	75
67	Combinatorial Pattern of Histone Modifications in Exon Skipping Event. Frontiers in Genetics, 2019, 10, 122.	2.3	5
68	Development and Application of Computational Methods to Analysis and Identify Biological Organic Molecular. Letters in Organic Chemistry, 2019, 16, 245-246.	0.5	0
69	The Computational Methods in Drug Targets Discovery. Current Drug Targets, 2019, 20, 479-480.	2.1	5
70	Identify origin of replication inSaccharomyces cerevisiaeusing two-step feature selection technique. Bioinformatics, 2019, 35, 2075-2083.	4.1	172
71	Predicting protein structural classes for low-similarity sequences by evaluating different features. Knowledge-Based Systems, 2019, 163, 787-793.	7.1	194
72	iTerm-PseKNC: a sequence-based tool for predicting bacterial transcriptional terminators. Bioinformatics, 2019, 35, 1469-1477.	4.1	173

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73	iDNA6mA-PseKNC: Identifying DNA N6-methyladenosine sites by incorporating nucleotide physicochemical properties into PseKNC. Genomics, 2019, 111, 96-102.	2.9	234
74	Identifying Sigma70 Promoters with Novel Pseudo Nucleotide Composition. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1316-1321.	3.0	132
75	The Development of Machine Learning Methods in Cell-Penetrating Peptides Identification: A Brief Review. Current Drug Metabolism, 2019, 20, 217-223.	1.2	9
76	A Brief Survey of Machine Learning Methods in Protein Sub-Golgi Localization. Current Bioinformatics, 2019, 14, 234-240.	1.5	135
77	Identification of hormone binding proteins based on machine learning methods. Mathematical Biosciences and Engineering, 2019, 16, 2466-2480.	1.9	144
78	Identification of Antioxidant Proteins With Deep Learning From Sequence Information. Frontiers in Pharmacology, 2018, 9, 1036.	3.5	12
79	Classifying Included and Excluded Exons in Exon Skipping Event Using Histone Modifications. Frontiers in Genetics, 2018, 9, 433.	2.3	23
80	iRNA(m6A)-PseDNC: Identifying N6-methyladenosine sites using pseudo dinucleotide composition. Analytical Biochemistry, 2018, 561-562, 59-65.	2.4	162
81	iRNA-3typeA: Identifying Three Types of Modification at RNAâ€™s Adenosine Sites. Molecular Therapy - Nucleic Acids, 2018, 11, 468-474.	5.1	173
82	iRSpot-Pse6NC: Identifying recombination spots in Saccharomyces cerevisiae by incorporating hexamer composition into general PseKNC. International Journal of Biological Sciences, 2018, 14, 883-891.	6.4	145
83	Identification of Bacteriophage Virion Proteins Using Multinomial NaÃ¯ve Bayes with g-Gap Feature Tree. International Journal of Molecular Sciences, 2018, 19, 1779.	4.1	28
84	iLoc-lncRNA: predict the subcellular location of lncRNAs by incorporating octamer composition into general PseKNC. Bioinformatics, 2018, 34, 4196-4204.	4.1	227
85	HBPred: a tool to identify growth hormone-binding proteins. International Journal of Biological Sciences, 2018, 14, 957-964.	6.4	173
86	Special issue on Computational Resources and Methods in Biological Sciences. International Journal of Biological Sciences, 2018, 14, 807-810.	6.4	3
87	Identifying RNA N6-Methyladenosine Sites in Escherichia coli Genome. Frontiers in Microbiology, 2018, 9, 955.	3.5	24
88	Prediction of bacteriophage proteins located in the host cell using hybrid features. Chemometrics and Intelligent Laboratory Systems, 2018, 180, 64-69.	3.5	28
89	iRNA-2OM: A Sequence-Based Predictor for Identifying 2â€²-O-Methylation Sites inHomo sapiens. Journal of Computational Biology, 2018, 25, 1266-1277.	1.6	137
90	A Brief Survey of Machine Learning Application in Cancerlectin Identification. Current Gene Therapy, 2018, 18, 257-267.	2.0	24

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91	Pro54DB: a database for experimentally verified sigma-54 promoters. Bioinformatics, 2017, 33, 467-469.	4.1	91
92	RNALocate: a resource for RNA subcellular localizations. Nucleic Acids Research, 2017, 45, D135-D138.	14.5	149
93	MethyRNA: a web server for identification of N⁶-methyladenosine sites. Journal of Biomolecular Structure and Dynamics, 2017, 35, 683-687.	3.5	124
94	Identify and analysis crotonylation sites in histone by using support vector machines. Artificial Intelligence in Medicine, 2017, 83, 75-81.	6.5	52
95	iRNA-PseColl: Identifying the Occurrence Sites of Different RNA Modifications by Incorporating Collective Effects of Nucleotides into PseKNC. Molecular Therapy - Nucleic Acids, 2017, 7, 155-163.	5.1	259
96	iDNA4mC: identifying DNA N4-methylcytosine sites based on nucleotide chemical properties. Bioinformatics, 2017, 33, 3518-3523.	4.1	256
97	AOD: the antioxidant protein database. Scientific Reports, 2017, 7, 7449.	3.3	49
98	Predicting the Organelle Location of Noncoding RNAs Using Pseudo Nucleotide Compositions. Interdisciplinary Sciences, Computational Life Sciences, 2017, 9, 540-544.	3.6	19
99	Editorial: Development and Application of Feature Selection Techniques in Protein Data Analysis and Prediction. Letters in Organic Chemistry, 2017, 14, .	0.5	0
100	Recent Advances in Conotoxin Classification by Using Machine Learning Methods. Molecules, 2017, 22, 1057.	3.8	53
101	Recent Advances in Identification of RNA Modifications. Non-coding RNA, 2017, 3, 1.	2.6	20
102	IonchanPred 2.0: A Tool to Predict Ion Channels and Their Types. International Journal of Molecular Sciences, 2017, 18, 1838.	4.1	59
103	PSBinder: A Web Service for Predicting Polystyrene Surface-Binding Peptides. BioMed Research International, 2017, 2017, 1-5.	1.9	49
104	iRNA-AI: identifying the adenosine to inosine editing sites in RNA sequences. Oncotarget, 2017, 8, 4208-4217.	1.8	209
105	Sequence-based predictive modeling to identify cancerlectins. Oncotarget, 2017, 8, 28169-28175.	1.8	95
106	iOri-Human: identify human origin of replication by incorporating dinucleotide physicochemical properties into pseudo nucleotide composition. Oncotarget, 2016, 7, 69783-69793.	1.8	166
107	iACP: a sequence-based tool for identifying anticancer peptides. Oncotarget, 2016, 7, 16895-16909.	1.8	354
108	Identification of Bacterial Cell Wall Lyases via Pseudo Amino Acid Composition. BioMed Research International, 2016, 2016, 1-8.	1.9	99

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109	Identification of Secretory Proteins inMycobacterium tuberculosisUsing Pseudo Amino Acid Composition. BioMed Research International, 2016, 2016, 1-7.	1.9	118
110	Combining pseudo dinucleotide composition with the Z curve method to improve the accuracy of predicting DNA elements: a case study in recombination spots. Molecular BioSystems, 2016, 12, 2893-2900.	2.9	19
111	PAI: Predicting adenosine to inosine editing sites by using pseudo nucleotide compositions. Scientific Reports, 2016, 6, 35123.	3.3	32
112	Identification of apolipoprotein using feature selection technique. Scientific Reports, 2016, 6, 30441.	3.3	36
113	Identifying 2â€²-O-methylationation sites by integrating nucleotide chemical properties and nucleotide compositions. Genomics, 2016, 107, 255-258.	2.9	55
114	PHYPred: a tool for identifying bacteriophage enzymes and hydrolases. Virologica Sinica, 2016, 31, 350-352.	3.0	47
115	Identifying N 6-methyladenosine sites in the Arabidopsis thaliana transcriptome. Molecular Genetics and Genomics, 2016, 291, 2225-2229.	2.1	58
116	Identifying RNA 5-methylcytosine sites via pseudo nucleotide compositions. Molecular BioSystems, 2016, 12, 3307-3311.	2.9	48
117	RAMPred: identifying the N1-methyladenosine sites in eukaryotic transcriptomes. Scientific Reports, 2016, 6, 31080.	3.3	50
118	Prediction of phosphothreonine sites in human proteins by fusing different features. Scientific Reports, 2016, 6, 34817.	3.3	48
119	Prediction of cell-penetrating peptides with feature selection techniques. Biochemical and Biophysical Research Communications, 2016, 477, 150-154.	2.1	87
120	Identification of immunoglobulins using Chou's pseudo amino acid composition with feature selection technique. Molecular BioSystems, 2016, 12, 1269-1275.	2.9	155
121	Predicting bacteriophage proteins located in host cell with feature selection technique. Computers in Biology and Medicine, 2016, 71, 156-161.	7.0	12
122	Using deformation energy to analyze nucleosome positioning in genomes. Genomics, 2016, 107, 69-75.	2.9	104
123	BDB: biopanning data bank. Nucleic Acids Research, 2016, 44, D1127-D1132.	14.5	71
124	Identifying Antioxidant Proteins by Using Optimal Dipeptide Compositions. Interdisciplinary Sciences, Computational Life Sciences, 2016, 8, 186-191.	3.6	42
125	iRNA-PseU: Identifying RNA pseudouridine sites. Molecular Therapy - Nucleic Acids, 2016, 5, e332.	5.1	172
126	Predicting Human Enzyme Family Classes by Using Pseudo Amino Acid Composition. Current Proteomics, 2016, 13, 99-104.	0.3	11

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127	Identification and analysis of the N6-methyladenosine in the Saccharomyces cerevisiae transcriptome. Scientific Reports, 2015, 5, 13859.	3.3	96
128	Predicting cancerlectins by the optimal g-gap dipeptides. Scientific Reports, 2015, 5, 16964.	3.3	50
129	Application of Machine Learning Method in Genomics and Proteomics. Scientific World Journal, The, 2015, 2015, 1-2.	2.1	1
130	Briefing in Application of Machine Learning Methods in Ion Channel Prediction. Scientific World Journal, The, 2015, 2015, 1-7.	2.1	5
131	iORI-PseKNC: A predictor for identifying origin of replication with pseudo k-tuple nucleotide composition. Chemometrics and Intelligent Laboratory Systems, 2015, 141, 100-106.	3.5	76
132	Predicting the subcellular localization of mycobacterial proteins by incorporating the optimal tripeptides into the general form of pseudo amino acid composition. Molecular BioSystems, 2015, 11, 558-563.	2.9	106
133	PseKNC-General: a cross-platform package for generating various modes of pseudo nucleotide compositions. Bioinformatics, 2015, 31, 119-120.	4.1	210
134	Pseudo nucleotide composition or PseKNC: an effective formulation for analyzing genomic sequences. Molecular BioSystems, 2015, 11, 2620-2634.	2.9	289
135	MDC-Analyzer-facilitated combinatorial strategy for improving the activity and stability of halohydrin dehalogenase from Agrobacterium radiobacter AD1. Journal of Biotechnology, 2015, 206, 1-7.	3.8	11
136	Benchmark data for identifying N 6 -methyladenosine sites in the Saccharomyces cerevisiae genome. Data in Brief, 2015, 5, 376-378.	1.0	9
137	iRNA-Methyl: Identifying N6-methyladenosine sites using pseudo nucleotide composition. Analytical Biochemistry, 2015, 490, 26-33.	2.4	350
138	Predicting bacterial essential genes using only sequence composition information. Genetics and Molecular Research, 2014, 13, 4564-4572.	0.2	47
139	iSS-PseDNC: Identifying Splicing Sites Using Pseudo Dinucleotide Composition. BioMed Research International, 2014, 2014, 1-12.	1.9	144
140	iPro54-PseKNC: a sequence-based predictor for identifying sigma-54 promoters in prokaryote with pseudo k-tuple nucleotide composition. Nucleic Acids Research, 2014, 42, 12961-12972.	14.5	467
141	PhD7FASTER: PREDICTING CLONES PROPAGATING FASTER FROM THE Ph.D.-7 PHAGE DISPLAY PEPTIDE LIBRARY. Journal of Bioinformatics and Computational Biology, 2014, 12, 1450005.	0.8	36
142	Predicting the Types of J-Proteins Using Clustered Amino Acids. BioMed Research International, 2014, 2014, 1-8.	1.9	30
143	Identifying the Subfamilies of Voltage-Gated Potassium Channels Using Feature Selection Technique. International Journal of Molecular Sciences, 2014, 15, 12940-12951.	4.1	30
144	Sequence analysis of origins of replication in the Saccharomyces cerevisiae genomes. Frontiers in Microbiology, 2014, 5, 574.	3.5	20

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145	iCTX-Type: A Sequence-Based Predictor for Identifying the Types of Conotoxins in Targeting Ion Channels. BioMed Research International, 2014, 2014, 1-10.	1.9	185
146	iTIS-PseTNC: A sequence-based predictor for identifying translation initiation site in human genes using pseudo trinucleotide composition. Analytical Biochemistry, 2014, 462, 76-83.	2.4	245
147	iNuc-PseKNC: a sequence-based predictor for predicting nucleosome positioning in genomes with pseudo k-tuple nucleotide composition. Bioinformatics, 2014, 30, 1522-1529.	4.1	349
148	A two stages sparse SVM training. International Journal of Machine Learning and Cybernetics, 2014, 5, 425-434.	3.6	6
149	Exon skipping event prediction based on histone modifications. Interdisciplinary Sciences, Computational Life Sciences, 2014, 6, 241-249.	3.6	10
150	Prediction of protein structural classes based on feature selection technique. Interdisciplinary Sciences, Computational Life Sciences, 2014, 6, 235-240.	3.6	32
151	Identification of bacteriophage virion proteins by the ANOVA feature selection and analysis. Molecular BioSystems, 2014, 10, 2229-2235.	2.9	147
152	Prediction of CpG island methylation status by integrating DNA physicochemical properties. Genomics, 2014, 104, 229-233.	2.9	33
153	Analysis of connection networks among miRNAs differentially expressed in early gastric cancer for disclosing some biological features of disease development. Gene, 2014, 548, 159-165.	2.2	2
154	Prediction of Protein Secondary Structure Using Feature Selection and Analysis Approach. Acta Biotheoretica, 2014, 62, 1-14.	1.5	12
155	PseKNC: A flexible web server for generating pseudo K-tuple nucleotide composition. Analytical Biochemistry, 2014, 456, 53-60.	2.4	409
156	Training sparse SVM on the core sets of fitting-planes. Neurocomputing, 2014, 130, 20-27.	5.9	10
157	DNA Physical Parameters Modulate Nucleosome Positioning in the Saccharomyces cerevisiae Genome. Current Bioinformatics, 2014, 9, 188-193.	1.5	6
158	The rate of opening and closing of the DNA gate for topoisomerase II. Theory in Biosciences, 2013, 132, 61-64.	1.4	1
159	Using Over-Represented Tetrapeptides to Predict Protein Submitochondria Locations. Acta Biotheoretica, 2013, 61, 259-268.	1.5	73
160	iHSP-PseRAAAC: Identifying the heat shock protein families using pseudo reduced amino acid alphabet composition. Analytical Biochemistry, 2013, 442, 118-125.	2.4	287
161	The effect of regions flanking target site on siRNA potency. Genomics, 2013, 102, 215-222.	2.9	18
162	Prediction of the types of ion channel-targeted conotoxins based on radial basis function network. Toxicology in Vitro, 2013, 27, 852-856.	2.4	57

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163	Prediction of Golgi-resident protein types by using feature selection technique. Chemometrics and Intelligent Laboratory Systems, 2013, 124, 9-13.	3.5	90
164	iRSpot-PseDNC: identify recombination spots with pseudo dinucleotide composition. Nucleic Acids Research, 2013, 41, e68-e68.	14.5	562
165	PREDICTING SUBCHLOROPLAST LOCATIONS OF PROTEINS BASED ON THE GENERAL FORM OF CHOU'S PSEUDO AMINO ACID COMPOSITION: APPROACHED FROM OPTIMAL TRIPEPTIDE COMPOSITION. International Journal of Biomathematics, 2013, 06, 1350003.	2.9	46
166	AcalPred: A Sequence-Based Tool for Discriminating between Acidic and Alkaline Enzymes. PLoS ONE, 2013, 8, e75726.	2.5	92
167	NaÃ¯ve Bayes Classifier with Feature Selection to Identify Phage Virion Proteins. Computational and Mathematical Methods in Medicine, 2013, 2013, 1-6.	1.3	145
168	Identification of Antioxidants from Sequence Information Using NaÃ¯ve Bayes. Computational and Mathematical Methods in Medicine, 2013, 2013, 1-5.	1.3	102
169	Recombination spots prediction using DNA physical properties in the saccharomyces cerevisiae genome. , 2012, , .		3
170	Identification of mycobacterial membrane proteins and their types using over-represented tripeptide compositions. Journal of Proteomics, 2012, 77, 321-328.	2.4	90
171	The prediction of protein structural class using averaged chemical shifts. Journal of Biomolecular Structure and Dynamics, 2012, 29, 1147-1153.	3.5	58
172	MimoDB 2.0: a mimotope database and beyond. Nucleic Acids Research, 2012, 40, D271-D277.	14.5	109
173	Identification of voltage-gated potassium channel subfamilies from sequence information using support vector machine. Computers in Biology and Medicine, 2012, 42, 504-507.	7.0	39
174	Co-evolution of genomic islands and their bacterial hosts revealed through phylogenetic analyses of 17 groups of homologous genomic islands. Genetics and Molecular Research, 2012, 11, 3735-3743.	0.2	9
175	iNuc-PhysChem: A Sequence-Based Predictor for Identifying Nucleosomes via Physicochemical Properties. PLoS ONE, 2012, 7, e47843.	2.5	181
176	Prediction of ketoacyl synthase family using reduced amino acid alphabets. Journal of Industrial Microbiology and Biotechnology, 2012, 39, 579-584.	3.0	31
177	Prediction of replication origins by calculating DNA structural properties. FEBS Letters, 2012, 586, 934-938.	2.8	53
178	Prediction of thermophilic proteins using feature selection technique. Journal of Microbiological Methods, 2011, 84, 67-70.	1.6	89
179	Identify Golgi Protein Types with Modified Mahalanobis Discriminant Algorithm and Pseudo Amino Acid Composition. Protein and Peptide Letters, 2011, 18, 58-63.	0.9	96
180	Predicting ion channels and their types by the dipeptide mode of pseudo amino acid composition. Journal of Theoretical Biology, 2011, 269, 64-69.	1.7	146

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181	Eukaryotic and prokaryotic promoter prediction using hybrid approach. Theory in Biosciences, 2011, 130, 91-100.	1.4	55
182	Entropy Production Rate Changes in Lysogeny/Lysis Switch Regulation of Bacteriophage Lambda. Communications in Theoretical Physics, 2011, 55, 371-375.	2.5	15
183	MimoDB: a New Repository for Mimotope Data Derived from Phage Display Technology. Molecules, 2010, 15, 8279-8288.	3.8	47
184	Prediction of subcellular location of mycobacterial protein using feature selection techniques. Molecular Diversity, 2010, 14, 667-671.	3.9	41
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