

Hao Lin

List of Publications by Year in descending order

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197
papers

15,478
citations

10389

72
h-index

19190

118
g-index

199
all docs

199
docs citations

199
times ranked

4417
citing authors

#	ARTICLE	IF	CITATIONS
1	iRSpot-PseDNC: identify recombination spots with pseudo dinucleotide composition. <i>Nucleic Acids Research</i> , 2013, 41, e68-e68.	14.5	562
2	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.	14.5	467
3	PseKNC: A flexible web server for generating pseudo K-tuple nucleotide composition. <i>Analytical Biochemistry</i> , 2014, 456, 53-60.	2.4	409
4	iACP: a sequence-based tool for identifying anticancer peptides. <i>Oncotarget</i> , 2016, 7, 16895-16909.	1.8	354
5	iRNA-Methyl: Identifying N6-methyladenosine sites using pseudo nucleotide composition. <i>Analytical Biochemistry</i> , 2015, 490, 26-33.	2.4	350
6	iNuc-PseKNC: a sequence-based predictor for predicting nucleosome positioning in genomes with pseudo k-tuple nucleotide composition. <i>Bioinformatics</i> , 2014, 30, 1522-1529.	4.1	349
7	Pseudo nucleotide composition or PseKNC: an effective formulation for analyzing genomic sequences. <i>Molecular BioSystems</i> , 2015, 11, 2620-2634.	2.9	289
8	The modified Mahalanobis Discriminant for predicting outer membrane proteins by using Chou's pseudo amino acid composition. <i>Journal of Theoretical Biology</i> , 2008, 252, 350-356.	1.7	287
9	iHSP-PseRAAAC: Identifying the heat shock protein families using pseudo reduced amino acid alphabet composition. <i>Analytical Biochemistry</i> , 2013, 442, 118-125.	2.4	287
10	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.	5.1	259
11	iDNA4mC: identifying DNA N4-methylcytosine sites based on nucleotide chemical properties. <i>Bioinformatics</i> , 2017, 33, 3518-3523.	4.1	256
12	iTIS-PseTNC: A sequence-based predictor for identifying translation initiation site in human genes using pseudo trinucleotide composition. <i>Analytical Biochemistry</i> , 2014, 462, 76-83.	2.4	245
13	iDNA6mA-PseKNC: Identifying DNA N6-methyladenosine sites by incorporating nucleotide physicochemical properties into PseKNC. <i>Genomics</i> , 2019, 111, 96-102.	2.9	234
14	iLoc-lncRNA: predict the subcellular location of lncRNAs by incorporating octamer composition into general PseKNC. <i>Bioinformatics</i> , 2018, 34, 4196-4204.	4.1	227
15	PseKNC-General: a cross-platform package for generating various modes of pseudo nucleotide compositions. <i>Bioinformatics</i> , 2015, 31, 119-120.	4.1	210
16	Predicting Subcellular Localization of Mycobacterial Proteins by Using Chous Pseudo Amino Acid Composition. <i>Protein and Peptide Letters</i> , 2008, 15, 739-744.	0.9	209
17	iRNA-AI: identifying the adenosine to inosine editing sites in RNA sequences. <i>Oncotarget</i> , 2017, 8, 4208-4217.	1.8	209
18	Predicting protein structural classes for low-similarity sequences by evaluating different features. <i>Knowledge-Based Systems</i> , 2019, 163, 787-793.	7.1	194

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19	Prediction of Cell Wall Lytic Enzymes Using Chous Amphiphilic Pseudo Amino Acid Composition. Protein and Peptide Letters, 2009, 16, 351-355.	0.9	187
20	i6mA-Pred: identifying DNA N6-methyladenine sites in the rice genome. Bioinformatics, 2019, 35, 2796-2800.	4.1	186
21	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
22	iNuc-PhysChem: A Sequence-Based Predictor for Identifying Nucleosomes via Physicochemical Properties. PLoS ONE, 2012, 7, e47843.	2.5	181
23	iRNA-3typeA: Identifying Three Types of Modification at RNA's Adenosine Sites. Molecular Therapy - Nucleic Acids, 2018, 11, 468-474.	5.1	173
24	HBPred: a tool to identify growth hormone-binding proteins. International Journal of Biological Sciences, 2018, 14, 957-964.	6.4	173
25	iTerm-PseKNC: a sequence-based tool for predicting bacterial transcriptional terminators. Bioinformatics, 2019, 35, 1469-1477.	4.1	173
26	Identify origin of replication in <i>Saccharomyces cerevisiae</i> using two-step feature selection technique. Bioinformatics, 2019, 35, 2075-2083.	4.1	172
27	iRNA-PseU: Identifying RNA pseudouridine sites. Molecular Therapy - Nucleic Acids, 2016, 5, e332.	5.1	172
28	iOri-Human: identify human origin of replication by incorporating dinucleotide physicochemical properties into pseudo nucleotide composition. Oncotarget, 2016, 7, 69783-69793.	1.8	166
29	iRNA(m6A)-PseDNC: Identifying N6-methyladenosine sites using pseudo dinucleotide composition. Analytical Biochemistry, 2018, 561-562, 59-65.	2.4	162
30	Using pseudo amino acid composition to predict protein structural class: Approached by incorporating 400 dipeptide components. Journal of Computational Chemistry, 2007, 28, 1463-1466.	3.3	157
31	Identification of immunoglobulins using Chou's pseudo amino acid composition with feature selection technique. Molecular BioSystems, 2016, 12, 1269-1275.	2.9	155
32	RNAlocate: a resource for RNA subcellular localizations. Nucleic Acids Research, 2017, 45, D135-D138.	14.5	149
33	Identification of bacteriophage virion proteins by the ANOVA feature selection and analysis. Molecular BioSystems, 2014, 10, 2229-2235.	2.9	147
34	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
35	Naïve Bayes Classifier with Feature Selection to Identify Phage Virion Proteins. Computational and Mathematical Methods in Medicine, 2013, 2013, 1-6.	1.3	145
36	iRSpot-Pse6NC: Identifying recombination spots in <i>Saccharomyces cerevisiae</i> by incorporating hexamer composition into general PseKNC. International Journal of Biological Sciences, 2018, 14, 883-891.	6.4	145

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37	iSS-PseDNC: Identifying Splicing Sites Using Pseudo Dinucleotide Composition. <i>BioMed Research International</i> , 2014, 2014, 1-12.	1.9	144
38	Identification of hormone binding proteins based on machine learning methods. <i>Mathematical Biosciences and Engineering</i> , 2019, 16, 2466-2480.	1.9	144
39	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.	1.6	137
40	A Brief Survey of Machine Learning Methods in Protein Sub-Golgi Localization. <i>Current Bioinformatics</i> , 2019, 14, 234-240.	1.5	135
41	Prediction of Subcellular Localization of Apoptosis Protein Using Chou's Pseudo Amino Acid Composition. <i>Acta Biotheoretica</i> , 2009, 57, 321-330.	1.5	134
42	Predicting conotoxin superfamily and family by using pseudo amino acid composition and modified Mahalanobis discriminant. <i>Biochemical and Biophysical Research Communications</i> , 2007, 354, 548-551.	2.1	133
43	Identifying Sigma70 Promoters with Novel Pseudo Nucleotide Composition. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1316-1321.	3.0	132
44	iProEP: A Computational Predictor for Predicting Promoter. <i>Molecular Therapy - Nucleic Acids</i> , 2019, 17, 337-346.	5.1	125
45	MethyRNA: a web server for identification of N ⁶ -methyladenosine sites. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017, 35, 683-687.	3.5	124
46	Risk Prediction of Diabetes: Big data mining with fusion of multifarious physical examination indicators. <i>Information Fusion</i> , 2021, 75, 140-149.	19.1	123
47	Identification of Secretory Proteins in <i>Mycobacterium tuberculosis</i> Using Pseudo Amino Acid Composition. <i>BioMed Research International</i> , 2016, 2016, 1-7.	1.9	118
48	Evaluation of different computational methods on 5-methylcytosine sites identification. <i>Briefings in Bioinformatics</i> , 2020, 21, 982-995.	6.5	115
49	MimoDB 2.0: a mimotope database and beyond. <i>Nucleic Acids Research</i> , 2012, 40, D271-D277.	14.5	109
50	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
51	Using deformation energy to analyze nucleosome positioning in genomes. <i>Genomics</i> , 2016, 107, 69-75.	2.9	104
52	Identification of Antioxidants from Sequence Information Using Naïve Bayes. <i>Computational and Mathematical Methods in Medicine</i> , 2013, 2013, 1-5.	1.3	102
53	Design powerful predictor for mRNA subcellular location prediction in <i>Homo sapiens</i> . <i>Briefings in Bioinformatics</i> , 2021, 22, 526-535.	6.5	100
54	Identification of Bacterial Cell Wall Lyases via Pseudo Amino Acid Composition. <i>BioMed Research International</i> , 2016, 2016, 1-8.	1.9	99

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55	Identify Golgi Protein Types with Modified Mahalanobis Discriminant Algorithm and Pseudo Amino Acid Composition. <i>Protein and Peptide Letters</i> , 2011, 18, 58-63.	0.9	96
56	Identification and analysis of the N6-methyladenosine in the <i>Saccharomyces cerevisiae</i> transcriptome. <i>Scientific Reports</i> , 2015, 5, 13859.	3.3	96
57	DM3Loc: multi-label mRNA subcellular localization prediction and analysis based on multi-head self-attention mechanism. <i>Nucleic Acids Research</i> , 2021, 49, e46-e46.	14.5	95
58	Sequence-based predictive modeling to identify cancerlectins. <i>Oncotarget</i> , 2017, 8, 28169-28175.	1.8	95
59	iDNA-MS: An Integrated Computational Tool for Detecting DNA Modification Sites in Multiple Genomes. <i>IScience</i> , 2020, 23, 100991.	4.1	93
60	AcalPred: A Sequence-Based Tool for Discriminating between Acidic and Alkaline Enzymes. <i>PLoS ONE</i> , 2013, 8, e75726.	2.5	92
61	Pro54DB: a database for experimentally verified sigma-54 promoters. <i>Bioinformatics</i> , 2017, 33, 467-469.	4.1	91
62	Identification of mycobacterial membrane proteins and their types using over-represented tripeptide compositions. <i>Journal of Proteomics</i> , 2012, 77, 321-328.	2.4	90
63	Prediction of Golgi-resident protein types by using feature selection technique. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2013, 124, 9-13.	3.5	90
64	Prediction of thermophilic proteins using feature selection technique. <i>Journal of Microbiological Methods</i> , 2011, 84, 67-70.	1.6	89
65	Prediction of cell-penetrating peptides with feature selection techniques. <i>Biochemical and Biophysical Research Communications</i> , 2016, 477, 150-154.	2.1	87
66	Deep-Kcr: accurate detection of lysine crotonylation sites using deep learning method. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	86
67	iRNA-m7G: Identifying N7-methylguanosine Sites by Fusing Multiple Features. <i>Molecular Therapy - Nucleic Acids</i> , 2019, 18, 269-274.	5.1	85
68	SAROTUP: Scanner and Reporter of Target-Unrelated Peptides. <i>Journal of Biomedicine and Biotechnology</i> , 2010, 2010, 1-7.	3.0	84
69	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.	6.5	78
70	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.	3.5	76
71	iRNAD: a computational tool for identifying D modification sites in RNA sequence. <i>Bioinformatics</i> , 2019, 35, 4922-4929.	4.1	75
72	Early Diagnosis of Hepatocellular Carcinoma Using Machine Learning Method. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 254.	4.1	74

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73	Using Over-Represented Tetrapeptides to Predict Protein Submitochondria Locations. <i>Acta Biotheoretica</i> , 2013, 61, 259-268.	1.5	73
74	A computational platform to identify origins of replication sites in eukaryotes. <i>Briefings in Bioinformatics</i> , 2021, 22, 1940-1950.	6.5	73
75	BDB: biopanning data bank. <i>Nucleic Acids Research</i> , 2016, 44, D1127-D1132.	14.5	71
76	Computational identification of N6-methyladenosine sites in multiple tissues of mammals. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1084-1091.	4.1	70
77	DeepYY1: a deep learning approach to identify YY1-mediated chromatin loops. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	63
78	The recognition and prediction of σ^{70} promoters in <i>Escherichia coli</i> K-12. <i>Journal of Theoretical Biology</i> , 2006, 242, 135-141.	1.7	62
79	The celery genome sequence reveals sequential paleo- ϵ -polyploidizations, karyotype evolution and resistance gene reduction in apiales. <i>Plant Biotechnology Journal</i> , 2021, 19, 731-744.	8.3	62
80	iDNA6mA-Rice: A Computational Tool for Detecting N6-Methyladenine Sites in Rice. <i>Frontiers in Genetics</i> , 2019, 10, 793.	2.3	61
81	XG-PseU: an eXtreme Gradient Boosting based method for identifying pseudouridine sites. <i>Molecular Genetics and Genomics</i> , 2020, 295, 13-21.	2.1	61
82	IonchanPred 2.0: A Tool to Predict Ion Channels and Their Types. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1838.	4.1	59
83	iCarPS: a computational tool for identifying protein carbonylation sites by novel encoded features. <i>Bioinformatics</i> , 2021, 37, 171-177.	4.1	59
84	The prediction of protein structural class using averaged chemical shifts. <i>Journal of Biomolecular Structure and Dynamics</i> , 2012, 29, 1147-1153.	3.5	58
85	Identifying N 6-methyladenosine sites in the <i>Arabidopsis thaliana</i> transcriptome. <i>Molecular Genetics and Genomics</i> , 2016, 291, 2225-2229.	2.1	58
86	Prediction of the types of ion channel-targeted conotoxins based on radial basis function network. <i>Toxicology in Vitro</i> , 2013, 27, 852-856.	2.4	57
87	Eukaryotic and prokaryotic promoter prediction using hybrid approach. <i>Theory in Biosciences</i> , 2011, 130, 91-100.	1.4	55
88	Identifying 2'-O-methylation sites by integrating nucleotide chemical properties and nucleotide compositions. <i>Genomics</i> , 2016, 107, 255-258.	2.9	55
89	RNALocate v2.0: an updated resource for RNA subcellular localization with increased coverage and annotation. <i>Nucleic Acids Research</i> , 2022, 50, D333-D339.	14.5	54
90	Prediction of replication origins by calculating DNA structural properties. <i>FEBS Letters</i> , 2012, 586, 934-938.	2.8	53

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91	Recent Advances in Conotoxin Classification by Using Machine Learning Methods. <i>Molecules</i> , 2017, 22, 1057.	3.8	53
92	Identify and analysis crotonylation sites in histone by using support vector machines. <i>Artificial Intelligence in Medicine</i> , 2017, 83, 75-81.	6.5	52
93	Predicting cancerlectins by the optimal g-gap dipeptides. <i>Scientific Reports</i> , 2015, 5, 16964.	3.3	50
94	RAMPred: identifying the N1-methyladenosine sites in eukaryotic transcriptomes. <i>Scientific Reports</i> , 2016, 6, 31080.	3.3	50
95	AOD: the antioxidant protein database. <i>Scientific Reports</i> , 2017, 7, 7449.	3.3	49
96	PSBinder: A Web Service for Predicting Polystyrene Surface-Binding Peptides. <i>BioMed Research International</i> , 2017, 2017, 1-5.	1.9	49
97	Identifying RNA 5-methylcytosine sites via pseudo nucleotide compositions. <i>Molecular BioSystems</i> , 2016, 12, 3307-3311.	2.9	48
98	Prediction of phosphothreonine sites in human proteins by fusing different features. <i>Scientific Reports</i> , 2016, 6, 34817.	3.3	48
99	DeepIPs: comprehensive assessment and computational identification of phosphorylation sites of SARS-CoV-2 infection using a deep learning-based approach. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	48
100	MimoDB: a New Repository for Mimotope Data Derived from Phage Display Technology. <i>Molecules</i> , 2010, 15, 8279-8288.	3.8	47
101	Predicting bacterial essential genes using only sequence composition information. <i>Genetics and Molecular Research</i> , 2014, 13, 4564-4572.	0.2	47
102	PHYPred: a tool for identifying bacteriophage enzymes and hydrolases. <i>Virologica Sinica</i> , 2016, 31, 350-352.	3.0	47
103	PREDICTING SUBCHLOROPLAST LOCATIONS OF PROTEINS BASED ON THE GENERAL FORM OF CHOU'S PSEUDO AMINO ACID COMPOSITION: APPROACHED FROM OPTIMAL TRIPEPTIDE COMPOSITION. <i>International Journal of Biomathematics</i> , 2013, 06, 1350003.	2.9	46
104	Computational Identification of Small Interfering RNA Targets in SARS-CoV-2. <i>Virologica Sinica</i> , 2020, 35, 359-361.	3.0	45
105	Identifying Antioxidant Proteins by Using Optimal Dipeptide Compositions. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2016, 8, 186-191.	3.6	42
106	Deep-4mCW2V: A sequence-based predictor to identify N4-methylcytosine sites in <i>Escherichia coli</i> . <i>Methods</i> , 2022, 203, 558-563.	3.8	42
107	Prediction of subcellular location of mycobacterial protein using feature selection techniques. <i>Molecular Diversity</i> , 2010, 14, 667-671.	3.9	41
108	Identification of cyclin protein using gradient boost decision tree algorithm. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 4123-4131.	4.1	40

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109	Identification of voltage-gated potassium channel subfamilies from sequence information using support vector machine. <i>Computers in Biology and Medicine</i> , 2012, 42, 504-507.	7.0	39
110	Comparative analysis of long noncoding RNAs in angiosperms and characterization of long noncoding RNAs in response to heat stress in Chinese cabbage. <i>Horticulture Research</i> , 2021, 8, 48.	6.3	38
111	PPD: A Manually Curated Database for Experimentally Verified Prokaryotic Promoters. <i>Journal of Molecular Biology</i> , 2021, 433, 166860.	4.2	37
112	Advances in mapping the epigenetic modifications of 5mC, N6mA, and N4mC. <i>Biotechnology and Bioengineering</i> , 2021, 118, 4204-4216.	3.3	37
113	PhD7FASTER: PREDICTING CLONES PROPAGATING FASTER FROM THE Ph.D.-7 PHAGE DISPLAY PEPTIDE LIBRARY. <i>Journal of Bioinformatics and Computational Biology</i> , 2014, 12, 1450005.	0.8	36
114	Identification of apolipoprotein using feature selection technique. <i>Scientific Reports</i> , 2016, 6, 30441.	3.3	36
115	iRNA-m2G: Identifying N2-methylguanosine Sites Based on Sequence-Derived Information. <i>Molecular Therapy - Nucleic Acids</i> , 2019, 18, 253-258.	5.1	35
116	Prediction of midbody, centrosome and kinetochore proteins based on gene ontology information. <i>Biochemical and Biophysical Research Communications</i> , 2010, 401, 382-384.	2.1	33
117	Prediction of CpG island methylation status by integrating DNA physicochemical properties. <i>Genomics</i> , 2014, 104, 229-233.	2.9	33
118	DNA4mC-LIP: a linear integration method to identify N4-methylcytosine site in multiple species. <i>Bioinformatics</i> , 2020, 36, 3327-3335.	4.1	33
119	Prediction of protein structural classes based on feature selection technique. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2014, 6, 235-240.	3.6	32
120	PAI: Predicting adenosine to inosine editing sites by using pseudo nucleotide compositions. <i>Scientific Reports</i> , 2016, 6, 35123.	3.3	32
121	Prediction of ketoacyl synthase family using reduced amino acid alphabets. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2012, 39, 579-584.	3.0	31
122	Predicting the Types of J-Proteins Using Clustered Amino Acids. <i>BioMed Research International</i> , 2014, 2014, 1-8.	1.9	30
123	Identifying the Subfamilies of Voltage-Gated Potassium Channels Using Feature Selection Technique. <i>International Journal of Molecular Sciences</i> , 2014, 15, 12940-12951.	4.1	30
124	Locate-R: Subcellular localization of long non-coding RNAs using nucleotide compositions. <i>Genomics</i> , 2020, 112, 2583-2589.	2.9	29
125	Integrated biomarker profiling of the metabolome associated with impaired fasting glucose and type 2 diabetes mellitus in large-scale Chinese patients. <i>Clinical and Translational Medicine</i> , 2021, 11, e432.	4.0	29
126	Identification of Bacteriophage Virion Proteins Using Multinomial Naïve Bayes with g-Gap Feature Tree. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1779.	4.1	28

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127	Prediction of bacteriophage proteins located in the host cell using hybrid features. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2018, 180, 64-69.	3.5	28
128	Early Diagnosis of Pancreatic Ductal Adenocarcinoma by Combining Relative Expression Orderings With Machine-Learning Method. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 582864.	3.7	28
129	A sequence-based deep learning approach to predict CTCF-mediated chromatin loop. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	28
130	iDHS-Deep: an integrated tool for predicting DNase I hypersensitive sites by deep neural network. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	28
131	DeepKla: An attention mechanism-based deep neural network for protein lysine lactylation site prediction. , 2022, 1, .		26
132	Predicting Preference of Transcription Factors for Methylated DNA Using Sequence Information. <i>Molecular Therapy - Nucleic Acids</i> , 2020, 22, 1043-1050.	5.1	25
133	Identifying RNA N6-Methyladenosine Sites in Escherichia coli Genome. <i>Frontiers in Microbiology</i> , 2018, 9, 955.	3.5	24
134	A Brief Survey of Machine Learning Application in Cancerlectin Identification. <i>Current Gene Therapy</i> , 2018, 18, 257-267.	2.0	24
135	Classifying Included and Excluded Exons in Exon Skipping Event Using Histone Modifications. <i>Frontiers in Genetics</i> , 2018, 9, 433.	2.3	23
136	Rlscoper: a tool for RNA-RNA interaction extraction from the literature. <i>Bioinformatics</i> , 2019, 35, 3199-3202.	4.1	23
137	Deep-4mCGP: A Deep Learning Approach to Predict 4mC Sites in <i>Geobacter pickeringii</i> by Using Correlation-Based Feature Selection Technique. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1251.	4.1	23
138	PSnoD: identifying potential snoRNA-disease associations based on bounded nuclear norm regularization. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	21
139	Sequence analysis of origins of replication in the <i>Saccharomyces cerevisiae</i> genomes. <i>Frontiers in Microbiology</i> , 2014, 5, 574.	3.5	20
140	Recent Advances in Identification of RNA Modifications. <i>Non-coding RNA</i> , 2017, 3, 1.	2.6	20
141	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
142	Predicting the Organelle Location of Noncoding RNAs Using Pseudo Nucleotide Compositions. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2017, 9, 540-544.	3.6	19
143	Towards a better prediction of subcellular location of long non-coding RNA. <i>Frontiers of Computer Science</i> , 2022, 16, 1.	2.4	19
144	The effect of regions flanking target site on siRNA potency. <i>Genomics</i> , 2013, 102, 215-222.	2.9	18

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145	A plot of G + C content against sequence length of 640 bacterial chromosomes shows the points are widely scattered in the upper triangular area. <i>Chromosome Research</i> , 2009, 17, 359-364.	2.2	17
146	Revealing Gene Function and Transcription Relationship by Reconstructing Gene-Level Chromatin Interaction. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 195-205.	4.1	16
147	Entropy Production Rate Changes in Lysogeny/Lysis Switch Regulation of Bacteriophage Lambda. <i>Communications in Theoretical Physics</i> , 2011, 55, 371-375.	2.5	15
148	iRice-MS: An integrated XGBoost model for detecting multitype post-translational modification sites in rice. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	15
149	BDselect: A Package for <i>k</i> -mer Selection Based on the Binomial Distribution. <i>Current Bioinformatics</i> , 2022, 17, 238-244.	1.5	15
150	Chromosome translocation and its consequence in the genome of <i>Burkholderia cenocepacia</i> AU-1054. <i>Biochemical and Biophysical Research Communications</i> , 2010, 403, 375-379.	2.1	14
151	Detection of transcription factors binding to methylated DNA by deep recurrent neural network. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	14
152	VisFeature: a stand-alone program for visualizing and analyzing statistical features of biological sequences. <i>Bioinformatics</i> , 2020, 36, 1277-1278.	4.1	13
153	Risk prediction of diabetes and pre-diabetes based on physical examination data. <i>Mathematical Biosciences and Engineering</i> , 2022, 19, 3597-3608.	1.9	13
154	Prediction of Protein Secondary Structure Using Feature Selection and Analysis Approach. <i>Acta Biotheoretica</i> , 2014, 62, 1-14.	1.5	12
155	Predicting bacteriophage proteins located in host cell with feature selection technique. <i>Computers in Biology and Medicine</i> , 2016, 71, 156-161.	7.0	12
156	Identification of Antioxidant Proteins With Deep Learning From Sequence Information. <i>Frontiers in Pharmacology</i> , 2018, 9, 1036.	3.5	12
157	Screening of Prospective Plant Compounds as H1R and CL1R Inhibitors and Its Antiallergic Efficacy through Molecular Docking Approach. <i>Computational and Mathematical Methods in Medicine</i> , 2021, 2021, 1-9.	1.3	12
158	A deep learning model to identify gene expression level using cobinding transcription factor signals. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	12
159	The Brassicaceae genome resource (TBGR): A comprehensive genome platform for Brassicaceae plants. <i>Plant Physiology</i> , 2022, 190, 226-237.	4.8	12
160	MDC-Analyzer-facilitated combinatorial strategy for improving the activity and stability of halohydrin dehalogenase from <i>Agrobacterium radiobacter</i> AD1. <i>Journal of Biotechnology</i> , 2015, 206, 1-7.	3.8	11
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