

Wei Chen

List of Publications by Year in descending order

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151
papers

14,070
citations

17440

63
h-index

20961

115
g-index

151
all docs

151
docs citations

151
times ranked

5127
citing authors

#	ARTICLE	IF	CITATIONS
1	Repeated polyploidization of <i>Gossypium</i> genomes and the evolution of spinnable cotton fibres. <i>Nature</i> , 2012, 492, 423-427.	27.8	1,204
2	iRSpot-PseDNC: identify recombination spots with pseudo dinucleotide composition. <i>Nucleic Acids Research</i> , 2013, 41, e68-e68.	14.5	562
3	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
4	PseKNC: A flexible web server for generating pseudo K-tuple nucleotide composition. <i>Analytical Biochemistry</i> , 2014, 456, 53-60.	2.4	409
5	iACP: a sequence-based tool for identifying anticancer peptides. <i>Oncotarget</i> , 2016, 7, 16895-16909.	1.8	354
6	iRNA-Methyl: Identifying N6-methyladenosine sites using pseudo nucleotide composition. <i>Analytical Biochemistry</i> , 2015, 490, 26-33.	2.4	350
7	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
8	Pseudo nucleotide composition or PseKNC: an effective formulation for analyzing genomic sequences. <i>Molecular BioSystems</i> , 2015, 11, 2620-2634.	2.9	289
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	iRNA-AI: identifying the adenosine to inosine editing sites in RNA sequences. <i>Oncotarget</i> , 2017, 8, 4208-4217.	1.8	209
17	Predicting protein structural classes for low-similarity sequences by evaluating different features. <i>Knowledge-Based Systems</i> , 2019, 163, 787-793.	7.1	194
18	i6mA-Pred: identifying DNA N6-methyladenine sites in the rice genome. <i>Bioinformatics</i> , 2019, 35, 2796-2800.	4.1	186

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19	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
20	iNuc-PhysChem: A Sequence-Based Predictor for Identifying Nucleosomes via Physicochemical Properties. PLoS ONE, 2012, 7, e47843.	2.5	181
21	iRNA-3typeA: Identifying Three Types of Modification at RNA's Adenosine Sites. Molecular Therapy - Nucleic Acids, 2018, 11, 468-474.	5.1	173
22	iTerm-PseKNC: a sequence-based tool for predicting bacterial transcriptional terminators. Bioinformatics, 2019, 35, 1469-1477.	4.1	173
23	Identify origin of replication in <i>Saccharomyces cerevisiae</i> using two-step feature selection technique. Bioinformatics, 2019, 35, 2075-2083.	4.1	172
24	iRNA-PseU: Identifying RNA pseudouridine sites. Molecular Therapy - Nucleic Acids, 2016, 5, e332.	5.1	172
25	iOri-Human: identify human origin of replication by incorporating dinucleotide physicochemical properties into pseudo nucleotide composition. Oncotarget, 2016, 7, 69783-69793.	1.8	166
26	iRNA(m6A)-PseDNC: Identifying N6-methyladenosine sites using pseudo dinucleotide composition. Analytical Biochemistry, 2018, 561-562, 59-65.	2.4	162
27	Identification of immunoglobulins using Chou's pseudo amino acid composition with feature selection technique. Molecular BioSystems, 2016, 12, 1269-1275.	2.9	155
28	Identification of bacteriophage virion proteins by the ANOVA feature selection and analysis. Molecular BioSystems, 2014, 10, 2229-2235.	2.9	147
29	Naïve Bayes Classifier with Feature Selection to Identify Phage Virion Proteins. Computational and Mathematical Methods in Medicine, 2013, 2013, 1-6.	1.3	145
30	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
31	iSS-PseDNC: Identifying Splicing Sites Using Pseudo Dinucleotide Composition. BioMed Research International, 2014, 2014, 1-12.	1.9	144
32	Identification of hormone binding proteins based on machine learning methods. Mathematical Biosciences and Engineering, 2019, 16, 2466-2480.	1.9	144
33	iRNA-2OM: A Sequence-Based Predictor for Identifying 2'-O-Methylation Sites in <i>Homo sapiens</i> . Journal of Computational Biology, 2018, 25, 1266-1277.	1.6	137
34	Identifying Sigma70 Promoters with Novel Pseudo Nucleotide Composition. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1316-1321.	3.0	132
35	iProEP: A Computational Predictor for Predicting Promoter. Molecular Therapy - Nucleic Acids, 2019, 17, 337-346.	5.1	125
36	MethyRNA: a web server for identification of N ⁶ -methyladenosine sites. Journal of Biomolecular Structure and Dynamics, 2017, 35, 683-687.	3.5	124

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37	Detecting N6-methyladenosine sites from RNA transcriptomes using ensemble Support Vector Machines. Scientific Reports, 2017, 7, 40242.	3.3	123
38	iMRM: a platform for simultaneously identifying multiple kinds of RNA modifications. Bioinformatics, 2020, 36, 3336-3342.	4.1	122
39	Identification of Secretory Proteins in <i>Mycobacterium tuberculosis</i> Using Pseudo Amino Acid Composition. BioMed Research International, 2016, 2016, 1-7.	1.9	118
40	Evaluation of different computational methods on 5-methylcytosine sites identification. Briefings in Bioinformatics, 2020, 21, 982-995.	6.5	115
41	Hierarchically Aligning 10 Legume Genomes Establishes a Family-Level Genomics Platform. Plant Physiology, 2017, 174, 284-300.	4.8	112
42	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
43	Using deformation energy to analyze nucleosome positioning in genomes. Genomics, 2016, 107, 69-75.	2.9	104
44	Identification of Antioxidants from Sequence Information Using Naïve Bayes. Computational and Mathematical Methods in Medicine, 2013, 2013, 1-5.	1.3	102
45	Design powerful predictor for mRNA subcellular location prediction in <i>Homo sapiens</i> . Briefings in Bioinformatics, 2021, 22, 526-535.	6.5	100
46	Identification of Bacterial Cell Wall Lyases via Pseudo Amino Acid Composition. BioMed Research International, 2016, 2016, 1-8.	1.9	99
47	Identification and analysis of the N6-methyladenosine in the <i>Saccharomyces cerevisiae</i> transcriptome. Scientific Reports, 2015, 5, 13859.	3.3	96
48	Sequence-based predictive modeling to identify cancerlectins. Oncotarget, 2017, 8, 28169-28175.	1.8	95
49	AcalPred: A Sequence-Based Tool for Discriminating between Acidic and Alkaline Enzymes. PLoS ONE, 2013, 8, e75726.	2.5	92
50	RNAInter v4.0: RNA interactome repository with redefined confidence scoring system and improved accessibility. Nucleic Acids Research, 2022, 50, D326-D332.	14.5	92
51	Pro54DB: a database for experimentally verified sigma-54 promoters. Bioinformatics, 2017, 33, 467-469.	4.1	91
52	Identification of mycobacterial membrane proteins and their types using over-represented tripeptide compositions. Journal of Proteomics, 2012, 77, 321-328.	2.4	90
53	Prediction of Golgi-resident protein types by using feature selection technique. Chemometrics and Intelligent Laboratory Systems, 2013, 124, 9-13.	3.5	90
54	Prediction of thermophilic proteins using feature selection technique. Journal of Microbiological Methods, 2011, 84, 67-70.	1.6	89

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55	An Overlooked Paleotetraploidization in Cucurbitaceae. <i>Molecular Biology and Evolution</i> , 2018, 35, 16-26.	8.9	89
56	Using Chou's pseudo amino acid composition to predict protein quaternary structure: a sequence-segmented PseAAC approach. <i>Amino Acids</i> , 2008, 35, 591-598.	2.7	87
57	Prediction of cell-penetrating peptides with feature selection techniques. <i>Biochemical and Biophysical Research Communications</i> , 2016, 477, 150-154.	2.1	87
58	iRNA-m7G: Identifying N7-methylguanosine Sites by Fusing Multiple Features. <i>Molecular Therapy - Nucleic Acids</i> , 2019, 18, 269-274.	5.1	85
59	Predicting peroxidase subcellular location by hybridizing different descriptors of Chou's pseudo amino acid patterns. <i>Analytical Biochemistry</i> , 2014, 458, 14-19.	2.4	83
60	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
61	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
62	Recent Advances in Machine Learning Methods for Predicting Heat Shock Proteins. <i>Current Drug Metabolism</i> , 2019, 20, 224-228.	1.2	75
63	iRNAD: a computational tool for identifying D modification sites in RNA sequence. <i>Bioinformatics</i> , 2019, 35, 4922-4929.	4.1	75
64	Using Over-Represented Tetrapeptides to Predict Protein Submitochondria Locations. <i>Acta Biotheoretica</i> , 2013, 61, 259-268.	1.5	73
65	Genetic mapping of the nulliplex-branch gene (gb_nb1) in cotton using next-generation sequencing. <i>Theoretical and Applied Genetics</i> , 2015, 128, 539-547.	3.6	63
66	The celery genome sequence reveals sequential paleopolyploidizations, karyotype evolution and resistance gene reduction in apiales. <i>Plant Biotechnology Journal</i> , 2021, 19, 731-744.	8.3	62
67	The organization of nucleosomes around splice sites. <i>Nucleic Acids Research</i> , 2010, 38, 2788-2798.	14.5	61
68	iDNA6mA-Rice: A Computational Tool for Detecting N6-Methyladenine Sites in Rice. <i>Frontiers in Genetics</i> , 2019, 10, 793.	2.3	61
69	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
70	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
71	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
72	Identifying N 6-methyladenosine sites in the Arabidopsis thaliana transcriptome. <i>Molecular Genetics and Genomics</i> , 2016, 291, 2225-2229.	2.1	58

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73	The role of RNA m ⁵ C modification in cancer metastasis. International Journal of Biological Sciences, 2021, 17, 3369-3380.	6.4	58
74	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
75	Deciphering the high-quality genome sequence of coriander that causes controversial feelings. Plant Biotechnology Journal, 2020, 18, 1444-1456.	8.3	56
76	Identifying 2'-O-methylation sites by integrating nucleotide chemical properties and nucleotide compositions. Genomics, 2016, 107, 255-258.	2.9	55
77	Prediction of replication origins by calculating DNA structural properties. FEBS Letters, 2012, 586, 934-938.	2.8	53
78	Recent Advances in Conotoxin Classification by Using Machine Learning Methods. Molecules, 2017, 22, 1057.	3.8	53
79	Predicting cancerlectins by the optimal g-gap dipeptides. Scientific Reports, 2015, 5, 16964.	3.3	50
80	RAMPred: identifying the N1-methyladenosine sites in eukaryotic transcriptomes. Scientific Reports, 2016, 6, 31080.	3.3	50
81	AOD: the antioxidant protein database. Scientific Reports, 2017, 7, 7449.	3.3	49
82	Identifying RNA 5-methylcytosine sites via pseudo nucleotide compositions. Molecular BioSystems, 2016, 12, 3307-3311.	2.9	48
83	Prediction of phosphothreonine sites in human proteins by fusing different features. Scientific Reports, 2016, 6, 34817.	3.3	48
84	PHYPred: a tool for identifying bacteriophage enzymes and hydrolases. Virologica Sinica, 2016, 31, 350-352.	3.0	47
85	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
86	Computational Identification of Small Interfering RNA Targets in SARS-CoV-2. Virologica Sinica, 2020, 35, 359-361.	3.0	45
87	iATP: A Sequence Based Method for Identifying Anti-tubercular Peptides. Medicinal Chemistry, 2020, 16, 620-625.	1.5	43
88	Identifying Antioxidant Proteins by Using Optimal Dipeptide Compositions. Interdisciplinary Sciences, Computational Life Sciences, 2016, 8, 186-191.	3.6	42
89	mRNALocator: Enhance the prediction accuracy of eukaryotic mRNA subcellular localization by using model fusion strategy. Molecular Therapy, 2021, 29, 2617-2623.	8.2	40
90	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

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91	PPD: A Manually Curated Database for Experimentally Verified Prokaryotic Promoters. Journal of Molecular Biology, 2021, 433, 166860.	4.2	37
92	Identification of apolipoprotein using feature selection technique. Scientific Reports, 2016, 6, 30441.	3.3	36
93	iRNA-m2G: Identifying N2-methylguanosine Sites Based on Sequence-Derived Information. Molecular Therapy - Nucleic Acids, 2019, 18, 253-258.	5.1	35
94	Iterative feature representation algorithm to improve the predictive performance of N7-methylguanosine sites. Briefings in Bioinformatics, 2021, 22, .	6.5	35
95	A Survey for Predicting Enzyme Family Classes Using Machine Learning Methods. Current Drug Targets, 2019, 20, 540-550.	2.1	35
96	Prediction of midbody, centrosome and kinetochore proteins based on gene ontology information. Biochemical and Biophysical Research Communications, 2010, 401, 382-384.	2.1	33
97	Prediction of CpG island methylation status by integrating DNA physicochemical properties. Genomics, 2014, 104, 229-233.	2.9	33
98	DNA4mC-LIP: a linear integration method to identify N4-methylcytosine site in multiple species. Bioinformatics, 2020, 36, 3327-3335.	4.1	33
99	Prediction of protein structural classes based on feature selection technique. Interdisciplinary Sciences, Computational Life Sciences, 2014, 6, 235-240.	3.6	32
100	PAI: Predicting adenosine to inosine editing sites by using pseudo nucleotide compositions. Scientific Reports, 2016, 6, 35123.	3.3	32
101	Prediction of ketoacyl synthase family using reduced amino acid alphabets. Journal of Industrial Microbiology and Biotechnology, 2012, 39, 579-584.	3.0	31
102	A similarity distance of diversity measure for discriminating mesophilic and thermophilic proteins. Amino Acids, 2013, 44, 573-580.	2.7	31
103	Predicting the Types of J-Proteins Using Clustered Amino Acids. BioMed Research International, 2014, 2014, 1-8.	1.9	30
104	Identifying the Subfamilies of Voltage-Gated Potassium Channels Using Feature Selection Technique. International Journal of Molecular Sciences, 2014, 15, 12940-12951.	4.1	30
105	Prediction of bacteriophage proteins located in the host cell using hybrid features. Chemometrics and Intelligent Laboratory Systems, 2018, 180, 64-69.	3.5	28
106	iRNA5hmC: The First Predictor to Identify RNA 5-Hydroxymethylcytosine Modifications Using Machine Learning. Frontiers in Bioengineering and Biotechnology, 2020, 8, 227.	4.1	26
107	Identifying RNA N6-Methyladenosine Sites in Escherichia coli Genome. Frontiers in Microbiology, 2018, 9, 955.	3.5	24
108	Nulliplex-branch, a TERMINAL FLOWER 1 ortholog, controls plant growth habit in cotton. Theoretical and Applied Genetics, 2019, 132, 97-112.	3.6	24

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109	A Brief Survey of Machine Learning Application in Cancerlectin Identification. <i>Current Gene Therapy</i> , 2018, 18, 257-267.	2.0	24
110	Classifying Included and Excluded Exons in Exon Skipping Event Using Histone Modifications. <i>Frontiers in Genetics</i> , 2018, 9, 433.	2.3	23
111	iPhoPred: A Predictor for Identifying Phosphorylation Sites in Human Protein. <i>IEEE Access</i> , 2019, 7, 177517-177528.	4.2	23
112	Genome-wide identification and analyses of the AHL gene family in cotton (<i>Gossypium</i>). <i>BMC Genomics</i> , 2020, 21, 69.	2.8	23
113	Classification of antimicrobial peptide using diversity measure with quadratic discriminant analysis. <i>Journal of Microbiological Methods</i> , 2009, 78, 94-96.	1.6	22
114	Sequence analysis of origins of replication in the <i>Saccharomyces cerevisiae</i> genomes. <i>Frontiers in Microbiology</i> , 2014, 5, 574.	3.5	20
115	Recent Advances in Identification of RNA Modifications. <i>Non-coding RNA</i> , 2017, 3, 1.	2.6	20
116	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
117	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
118	A genome-wide analysis of SWEET gene family in cotton and their expressions under different stresses. <i>Journal of Cotton Research</i> , 2018, 1, .	2.5	19
119	FS-GBDT: identification multicancer-risk module via a feature selection algorithm by integrating Fisher score and GBDT. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	19
120	Cotton DMP gene family: characterization, evolution, and expression profiles during development and stress. <i>International Journal of Biological Macromolecules</i> , 2021, 183, 1257-1269.	7.5	16
121	RNAWRE: a resource of writers, readers and erasers of RNA modifications. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	3.0	15
122	Identifying Antioxidant Proteins by Combining Multiple Methods. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 858.	4.1	13
123	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
124	Recent Advances of Computational Methods for Identifying Bacteriophage Virion Proteins. <i>Protein and Peptide Letters</i> , 2020, 27, 259-264.	0.9	12
125	The pattern of DNA cleavage intensity around indels. <i>Scientific Reports</i> , 2015, 5, 8333.	3.3	11
126	iRNA-m5U: A sequence based predictor for identifying 5-methyluridine modification sites in <i>Saccharomyces cerevisiae</i> . <i>Methods</i> , 2022, 203, 28-31.	3.8	11

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127	Predicting Human Enzyme Family Classes by Using Pseudo Amino Acid Composition. Current Proteomics, 2016, 13, 99-104.	0.3	11
128	Exon skipping event prediction based on histone modifications. Interdisciplinary Sciences, Computational Life Sciences, 2014, 6, 241-249.	3.6	10
129	The development of specific <scp>SNP</scp> markers for chromosome 14 in cotton using nextâ€generation sequencing. Plant Breeding, 2014, 133, 256-261.	1.9	10
130	KNIndex: a comprehensive database of physicochemical properties for k-tuple nucleotides. Briefings in Bioinformatics, 2020, 22, .	6.5	10
131	Benchmark data for identifying N 6 -methyladenosine sites in the Saccharomyces cerevisiae genome. Data in Brief, 2015, 5, 376-378.	1.0	9
132	ncPro-ML: An integrated computational tool for identifying non-coding RNA promoters in multiple species. Computational and Structural Biotechnology Journal, 2020, 18, 2445-2452.	4.1	9
133	DNA Physical Parameters Modulate Nucleosome Positioning in the Saccharomyces cerevisiae Genome. Current Bioinformatics, 2014, 9, 188-193.	1.5	6
134	Briefing in Application of Machine Learning Methods in Ion Channel Prediction. Scientific World Journal, The, 2015, 2015, 1-7.	2.1	5
135	Combinatorial Pattern of Histone Modifications in Exon Skipping Event. Frontiers in Genetics, 2019, 10, 122.	2.3	5
136	Identification of Potential Inhibitors Against SARS-CoV-2 Using Computational Drug Repurposing Study. Current Bioinformatics, 2021, 16, 1320-1327.	1.5	4
137	A tetraploidization event shaped the Aquilaria sinensis genome and contributed to the ability of sesquiterpenes synthesis. BMC Genomics, 2021, 22, 647.	2.8	3
138	Recent Development of Computational Predicting Bioluminescent Proteins. Current Pharmaceutical Design, 2020, 25, 4264-4273.	1.9	3
139	Analysis and Comparison of RNA Pseudouridine Site Prediction Tools. Current Bioinformatics, 2020, 15, 279-286.	1.5	3
140	A Brief Survey for MicroRNA Precursor Identification Using Machine Learning Methods. Current Genomics, 2020, 21, 11-25.	1.6	3
141	Recognition of DNase I hypersensitive sites in multiple cell lines. International Journal of Bioinformatics Research and Applications, 2009, 5, 378.	0.2	2
142	Open-Bud Duplicate Loci Are Identified as MML10s, Orthologs of MIXTA-Like Genes on Homologous Chromosomes of Allotetraploid Cotton. Frontiers in Plant Science, 2020, 11, 81.	3.6	2
143	Genome-Wide Study of NOT2_3_5 Protein Subfamily in Cotton and Their Necessity in Resistance to Verticillium wilt. International Journal of Molecular Sciences, 2021, 22, 5634.	4.1	2
144	Recent Advancement in Predicting Subcellular Localization of Mycobacterial Protein with Machine Learning Methods. Medicinal Chemistry, 2020, 16, 605-619.	1.5	2

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145	The Underlying Mechanisms of Wujiayizhi Granule in Treating Alzheimer's Disease. Current Bioinformatics, 2022, 17, 735-743.	1.5	2
146	Fine mapping and characterization of the Crinkled Dwarf gene in cotton. Industrial Crops and Products, 2022, 184, 115034.	5.2	2
147	Application of Machine Learning Method in Genomics and Proteomics. Scientific World Journal, The, 2015, 2015, 1-2.	2.1	1
148	The Evolution and Expression Profiles of EC1 Gene Family during Development in Cotton. Genes, 2021, 12, 2001.	2.4	1
149	A Novel Method for Lysine Acetylation Sites Prediction. , 2011, , .		0
150	Nucleosome Positioning and RNA Splicing*. Progress in Biochemistry and Biophysics, 2009, 36, 1035-1040.	0.3	0
151	HODD: A Manually Curated Database of Human Ophthalmic Diseases with Symptom Characteristics and Genetic Variants Towards Facilitating Quick and Definite Diagnosis. Interdisciplinary Sciences, Computational Life Sciences, 2021, , 1.	3.6	0