

Wei Chen

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4770648/publications.pdf>

Version: 2024-02-01

151
papers

14,070
citations

17405

63
h-index

20900

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.	13.7	1,204
2	iRSpot-PseDNC: identify recombination spots with pseudo dinucleotide composition. <i>Nucleic Acids Research</i> , 2013, 41, e68-e68.	6.5	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.	6.5	467
4	PseKNC: A flexible web server for generating pseudo K-tuple nucleotide composition. <i>Analytical Biochemistry</i> , 2014, 456, 53-60.	1.1	409
5	iACP: a sequence-based tool for identifying anticancer peptides. <i>Oncotarget</i> , 2016, 7, 16895-16909.	0.8	354
6	iRNA-Methyl: Identifying N6-methyladenosine sites using pseudo nucleotide composition. <i>Analytical Biochemistry</i> , 2015, 490, 26-33.	1.1	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.	1.8	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.	1.1	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.	2.3	259
11	iDNA4mC: identifying DNA N4-methylcytosine sites based on nucleotide chemical properties. <i>Bioinformatics</i> , 2017, 33, 3518-3523.	1.8	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.	1.1	245
13	iDNA6mA-PseKNC: Identifying DNA N6-methyladenosine sites by incorporating nucleotide physicochemical properties into PseKNC. <i>Genomics</i> , 2019, 111, 96-102.	1.3	234
14	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
15	PseKNC-General: a cross-platform package for generating various modes of pseudo nucleotide compositions. <i>Bioinformatics</i> , 2015, 31, 119-120.	1.8	210
16	iRNA-AI: identifying the adenosine to inosine editing sites in RNA sequences. <i>Oncotarget</i> , 2017, 8, 4208-4217.	0.8	209
17	Predicting protein structural classes for low-similarity sequences by evaluating different features. <i>Knowledge-Based Systems</i> , 2019, 163, 787-793.	4.0	194
18	i6mA-Pred: identifying DNA N6-methyladenine sites in the rice genome. <i>Bioinformatics</i> , 2019, 35, 2796-2800.	1.8	186

#	ARTICLE	IF	CITATIONS
19	iCTX-Type: A Sequence-Based Predictor for Identifying the Types of Conotoxins in Targeting Ion Channels. <i>BioMed Research International</i> , 2014, 2014, 1-10.	0.9	185
20	iNuc-PhysChem: A Sequence-Based Predictor for Identifying Nucleosomes via Physicochemical Properties. <i>PLoS ONE</i> , 2012, 7, e47843.	1.1	181
21	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
22	iTerm-PseKNC: a sequence-based tool for predicting bacterial transcriptional terminators. <i>Bioinformatics</i> , 2019, 35, 1469-1477.	1.8	173
23	Identify origin of replication in <i>Saccharomyces cerevisiae</i> using two-step feature selection technique. <i>Bioinformatics</i> , 2019, 35, 2075-2083.	1.8	172
24	iRNA-PseU: Identifying RNA pseudouridine sites. <i>Molecular Therapy - Nucleic Acids</i> , 2016, 5, e332.	2.3	172
25	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
26	iRNA(m6A)-PseDNC: Identifying N6-methyladenosine sites using pseudo dinucleotide composition. <i>Analytical Biochemistry</i> , 2018, 561-562, 59-65.	1.1	162
27	Identification of immunoglobulins using Chou's pseudo amino acid composition with feature selection technique. <i>Molecular BioSystems</i> , 2016, 12, 1269-1275.	2.9	155
28	Identification of bacteriophage virion proteins by the ANOVA feature selection and analysis. <i>Molecular BioSystems</i> , 2014, 10, 2229-2235.	2.9	147
29	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
30	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
31	iSS-PseDNC: Identifying Splicing Sites Using Pseudo Dinucleotide Composition. <i>BioMed Research International</i> , 2014, 2014, 1-12.	0.9	144
32	Identification of hormone binding proteins based on machine learning methods. <i>Mathematical Biosciences and Engineering</i> , 2019, 16, 2466-2480.	1.0	144
33	iRNA-2OM: A Sequence-Based Predictor for Identifying 2-O-Methylation Sites in <i>Homo sapiens</i> . <i>Journal of Computational Biology</i> , 2018, 25, 1266-1277.	0.8	137
34	Identifying Sigma70 Promoters with Novel Pseudo Nucleotide Composition. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1316-1321.	1.9	132
35	iProEP: A Computational Predictor for Predicting Promoter. <i>Molecular Therapy - Nucleic Acids</i> , 2019, 17, 337-346.	2.3	125
36	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

#	ARTICLE	IF	CITATIONS
37	Detecting N6-methyladenosine sites from RNA transcriptomes using ensemble Support Vector Machines. <i>Scientific Reports</i> , 2017, 7, 40242.	1.6	123
38	iMRM: a platform for simultaneously identifying multiple kinds of RNA modifications. <i>Bioinformatics</i> , 2020, 36, 3336-3342.	1.8	122
39	Identification of Secretory Proteins in <i>Mycobacterium tuberculosis</i> Using Pseudo Amino Acid Composition. <i>BioMed Research International</i> , 2016, 2016, 1-7.	0.9	118
40	Evaluation of different computational methods on 5-methylcytosine sites identification. <i>Briefings in Bioinformatics</i> , 2020, 21, 982-995.	3.2	115
41	Hierarchically Aligning 10 Legume Genomes Establishes a Family-Level Genomics Platform. <i>Plant Physiology</i> , 2017, 174, 284-300.	2.3	112
42	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
43	Using deformation energy to analyze nucleosome positioning in genomes. <i>Genomics</i> , 2016, 107, 69-75.	1.3	104
44	Identification of Antioxidants from Sequence Information Using Naïve Bayes. <i>Computational and Mathematical Methods in Medicine</i> , 2013, 2013, 1-5.	0.7	102
45	Design powerful predictor for mRNA subcellular location prediction in <i>Homo sapiens</i> . <i>Briefings in Bioinformatics</i> , 2021, 22, 526-535.	3.2	100
46	Identification of Bacterial Cell Wall Lyases via Pseudo Amino Acid Composition. <i>BioMed Research International</i> , 2016, 2016, 1-8.	0.9	99
47	Identification and analysis of the N6-methyladenosine in the <i>Saccharomyces cerevisiae</i> transcriptome. <i>Scientific Reports</i> , 2015, 5, 13859.	1.6	96
48	Sequence-based predictive modeling to identify cancerlectins. <i>Oncotarget</i> , 2017, 8, 28169-28175.	0.8	95
49	AcalPred: A Sequence-Based Tool for Discriminating between Acidic and Alkaline Enzymes. <i>PLoS ONE</i> , 2013, 8, e75726.	1.1	92
50	RNAInter v4.0: RNA interactome repository with redefined confidence scoring system and improved accessibility. <i>Nucleic Acids Research</i> , 2022, 50, D326-D332.	6.5	92
51	Pro54DB: a database for experimentally verified sigma-54 promoters. <i>Bioinformatics</i> , 2017, 33, 467-469.	1.8	91
52	Identification of mycobacterial membrane proteins and their types using over-represented tripeptide compositions. <i>Journal of Proteomics</i> , 2012, 77, 321-328.	1.2	90
53	Prediction of Golgi-resident protein types by using feature selection technique. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2013, 124, 9-13.	1.8	90
54	Prediction of thermophilic proteins using feature selection technique. <i>Journal of Microbiological Methods</i> , 2011, 84, 67-70.	0.7	89

#	ARTICLE	IF	CITATIONS
55	An Overlooked Paleotetraploidization in Cucurbitaceae. <i>Molecular Biology and Evolution</i> , 2018, 35, 16-26.	3.5	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.	1.2	87
57	Prediction of cell-penetrating peptides with feature selection techniques. <i>Biochemical and Biophysical Research Communications</i> , 2016, 477, 150-154.	1.0	87
58	iRNA-m7G: Identifying N7-methylguanosine Sites by Fusing Multiple Features. <i>Molecular Therapy - Nucleic Acids</i> , 2019, 18, 269-274.	2.3	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.	1.1	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.	3.2	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.	1.8	76
62	Recent Advances in Machine Learning Methods for Predicting Heat Shock Proteins. <i>Current Drug Metabolism</i> , 2019, 20, 224-228.	0.7	75
63	iRNAD: a computational tool for identifying D modification sites in RNA sequence. <i>Bioinformatics</i> , 2019, 35, 4922-4929.	1.8	75
64	Using Over-Represented Tetrapeptides to Predict Protein Submitochondria Locations. <i>Acta Biotheoretica</i> , 2013, 61, 259-268.	0.7	73
65	Genetic mapping of the nulliplex-branch gene (<i>gb_nb1</i>) in cotton using next-generation sequencing. <i>Theoretical and Applied Genetics</i> , 2015, 128, 539-547.	1.8	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.	4.1	62
67	The organization of nucleosomes around splice sites. <i>Nucleic Acids Research</i> , 2010, 38, 2788-2798.	6.5	61
68	iDNA6mA-Rice: A Computational Tool for Detecting N6-Methyladenine Sites in Rice. <i>Frontiers in Genetics</i> , 2019, 10, 793.	1.1	61
69	XG-PseU: an eXtreme Gradient Boosting based method for identifying pseudouridine sites. <i>Molecular Genetics and Genomics</i> , 2020, 295, 13-21.	1.0	61
70	IonchanPred 2.0: A Tool to Predict Ion Channels and Their Types. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1838.	1.8	59
71	The prediction of protein structural class using averaged chemical shifts. <i>Journal of Biomolecular Structure and Dynamics</i> , 2012, 29, 1147-1153.	2.0	58
72	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

#	ARTICLE	IF	CITATIONS
73	The role of RNA m ⁵ C modification in cancer metastasis. <i>International Journal of Biological Sciences</i> , 2021, 17, 3369-3380.	2.6	58
74	Prediction of the types of ion channel-targeted conotoxins based on radial basis function network. <i>Toxicology in Vitro</i> , 2013, 27, 852-856.	1.1	57
75	Deciphering the high-quality genome sequence of coriander that causes controversial feelings. <i>Plant Biotechnology Journal</i> , 2020, 18, 1444-1456.	4.1	56
76	Identifying 2'-O-methylation sites by integrating nucleotide chemical properties and nucleotide compositions. <i>Genomics</i> , 2016, 107, 255-258.	1.3	55
77	Prediction of replication origins by calculating DNA structural properties. <i>FEBS Letters</i> , 2012, 586, 934-938.	1.3	53
78	Recent Advances in Conotoxin Classification by Using Machine Learning Methods. <i>Molecules</i> , 2017, 22, 1057.	1.7	53
79	Predicting cancerlectins by the optimal g-gap dipeptides. <i>Scientific Reports</i> , 2015, 5, 16964.	1.6	50
80	RAMPred: identifying the N1-methyladenosine sites in eukaryotic transcriptomes. <i>Scientific Reports</i> , 2016, 6, 31080.	1.6	50
81	AOD: the antioxidant protein database. <i>Scientific Reports</i> , 2017, 7, 7449.	1.6	49
82	Identifying RNA 5-methylcytosine sites via pseudo nucleotide compositions. <i>Molecular BioSystems</i> , 2016, 12, 3307-3311.	2.9	48
83	Prediction of phosphothreonine sites in human proteins by fusing different features. <i>Scientific Reports</i> , 2016, 6, 34817.	1.6	48
84	PHYPred: a tool for identifying bacteriophage enzymes and hydrolases. <i>Virologica Sinica</i> , 2016, 31, 350-352.	1.2	47
85	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.	1.5	46
86	Computational Identification of Small Interfering RNA Targets in SARS-CoV-2. <i>Virologica Sinica</i> , 2020, 35, 359-361.	1.2	45
87	iATP: A Sequence Based Method for Identifying Anti-tubercular Peptides. <i>Medicinal Chemistry</i> , 2020, 16, 620-625.	0.7	43
88	Identifying Antioxidant Proteins by Using Optimal Dipeptide Compositions. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2016, 8, 186-191.	2.2	42
89	mRNALocater: Enhance the prediction accuracy of eukaryotic mRNA subcellular localization by using model fusion strategy. <i>Molecular Therapy</i> , 2021, 29, 2617-2623.	3.7	40
90	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.	3.9	39

#	ARTICLE	IF	CITATIONS
91	PPD: A Manually Curated Database for Experimentally Verified Prokaryotic Promoters. <i>Journal of Molecular Biology</i> , 2021, 433, 166860.	2.0	37
92	Identification of apolipoprotein using feature selection technique. <i>Scientific Reports</i> , 2016, 6, 30441.	1.6	36
93	iRNA-m2G: Identifying N2-methylguanosine Sites Based on Sequence-Derived Information. <i>Molecular Therapy - Nucleic Acids</i> , 2019, 18, 253-258.	2.3	35
94	Iterative feature representation algorithm to improve the predictive performance of N7-methylguanosine sites. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	35
95	A Survey for Predicting Enzyme Family Classes Using Machine Learning Methods. <i>Current Drug Targets</i> , 2019, 20, 540-550.	1.0	35
96	Prediction of midbody, centrosome and kinetochore proteins based on gene ontology information. <i>Biochemical and Biophysical Research Communications</i> , 2010, 401, 382-384.	1.0	33
97	Prediction of CpG island methylation status by integrating DNA physicochemical properties. <i>Genomics</i> , 2014, 104, 229-233.	1.3	33
98	DNA4mC-LIP: a linear integration method to identify N4-methylcytosine site in multiple species. <i>Bioinformatics</i> , 2020, 36, 3327-3335.	1.8	33
99	Prediction of protein structural classes based on feature selection technique. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2014, 6, 235-240.	2.2	32
100	PAI: Predicting adenosine to inosine editing sites by using pseudo nucleotide compositions. <i>Scientific Reports</i> , 2016, 6, 35123.	1.6	32
101	Prediction of ketoacyl synthase family using reduced amino acid alphabets. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2012, 39, 579-584.	1.4	31
102	A similarity distance of diversity measure for discriminating mesophilic and thermophilic proteins. <i>Amino Acids</i> , 2013, 44, 573-580.	1.2	31
103	Predicting the Types of J-Proteins Using Clustered Amino Acids. <i>BioMed Research International</i> , 2014, 2014, 1-8.	0.9	30
104	Identifying the Subfamilies of Voltage-Gated Potassium Channels Using Feature Selection Technique. <i>International Journal of Molecular Sciences</i> , 2014, 15, 12940-12951.	1.8	30
105	Prediction of bacteriophage proteins located in the host cell using hybrid features. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2018, 180, 64-69.	1.8	28
106	iRNA5hmC: The First Predictor to Identify RNA 5-Hydroxymethylcytosine Modifications Using Machine Learning. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 227.	2.0	26
107	Identifying RNA N6-Methyladenosine Sites in Escherichia coli Genome. <i>Frontiers in Microbiology</i> , 2018, 9, 955.	1.5	24
108	Nulliplex-branch, a TERMINAL FLOWER 1 ortholog, controls plant growth habit in cotton. <i>Theoretical and Applied Genetics</i> , 2019, 132, 97-112.	1.8	24

#	ARTICLE	IF	CITATIONS
109	A Brief Survey of Machine Learning Application in Cancerlectin Identification. <i>Current Gene Therapy</i> , 2018, 18, 257-267.	0.9	24
110	Classifying Included and Excluded Exons in Exon Skipping Event Using Histone Modifications. <i>Frontiers in Genetics</i> , 2018, 9, 433.	1.1	23
111	iPhoPred: A Predictor for Identifying Phosphorylation Sites in Human Protein. <i>IEEE Access</i> , 2019, 7, 177517-177528.	2.6	23
112	Genome-wide identification and analyses of the AHL gene family in cotton (<i>Gossypium</i>). <i>BMC Genomics</i> , 2020, 21, 69.	1.2	23
113	Classification of antimicrobial peptide using diversity measure with quadratic discriminant analysis. <i>Journal of Microbiological Methods</i> , 2009, 78, 94-96.	0.7	22
114	Sequence analysis of origins of replication in the <i>Saccharomyces cerevisiae</i> genomes. <i>Frontiers in Microbiology</i> , 2014, 5, 574.	1.5	20
115	Recent Advances in Identification of RNA Modifications. <i>Non-coding RNA</i> , 2017, 3, 1.	1.3	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.	2.2	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, .	1.0	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, .	3.2	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.	3.6	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, .	1.4	15
122	Identifying Antioxidant Proteins by Combining Multiple Methods. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 858.	2.0	13
123	Predicting bacteriophage proteins located in host cell with feature selection technique. <i>Computers in Biology and Medicine</i> , 2016, 71, 156-161.	3.9	12
124	Recent Advances of Computational Methods for Identifying Bacteriophage Virion Proteins. <i>Protein and Peptide Letters</i> , 2020, 27, 259-264.	0.4	12
125	The pattern of DNA cleavage intensity around indels. <i>Scientific Reports</i> , 2015, 5, 8333.	1.6	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.	1.9	11

#	ARTICLE	IF	CITATIONS
127	Predicting Human Enzyme Family Classes by Using Pseudo Amino Acid Composition. <i>Current Proteomics</i> , 2016, 13, 99-104.	0.1	11
128	Exon skipping event prediction based on histone modifications. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2014, 6, 241-249.	2.2	10
129	The development of specific <sc>SNP</sc> markers for chromosome 14 in cotton using next-generation sequencing. <i>Plant Breeding</i> , 2014, 133, 256-261.	1.0	10
130	KNIndex: a comprehensive database of physicochemical properties for k-tuple nucleotides. <i>Briefings in Bioinformatics</i> , 2020, 22, .	3.2	10
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	ncPro-ML: An integrated computational tool for identifying non-coding RNA promoters in multiple species. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 2445-2452.	1.9	9
133	DNA Physical Parameters Modulate Nucleosome Positioning in the <i>Saccharomyces cerevisiae</i> Genome. <i>Current Bioinformatics</i> , 2014, 9, 188-193.	0.7	6
134	Briefing in Application of Machine Learning Methods in Ion Channel Prediction. <i>Scientific World Journal, The</i> , 2015, 2015, 1-7.	0.8	5
135	Combinatorial Pattern of Histone Modifications in Exon Skipping Event. <i>Frontiers in Genetics</i> , 2019, 10, 122.	1.1	5
136	Identification of Potential Inhibitors Against SARS-CoV-2 Using Computational Drug Repurposing Study. <i>Current Bioinformatics</i> , 2021, 16, 1320-1327.	0.7	4
137	A tetraploidization event shaped the <i>Aquilaria sinensis</i> genome and contributed to the ability of sesquiterpenes synthesis. <i>BMC Genomics</i> , 2021, 22, 647.	1.2	3
138	Recent Development of Computational Predicting Bioluminescent Proteins. <i>Current Pharmaceutical Design</i> , 2020, 25, 4264-4273.	0.9	3
139	Analysis and Comparison of RNA Pseudouridine Site Prediction Tools. <i>Current Bioinformatics</i> , 2020, 15, 279-286.	0.7	3
140	A Brief Survey for MicroRNA Precursor Identification Using Machine Learning Methods. <i>Current Genomics</i> , 2020, 21, 11-25.	0.7	3
141	Recognition of DNase I hypersensitive sites in multiple cell lines. <i>International Journal of Bioinformatics Research and Applications</i> , 2009, 5, 378.	0.1	2
142	Open-Bud Duplicate Loci Are Identified as MML10s, Orthologs of MIXTA-Like Genes on Homologous Chromosomes of Allotetraploid Cotton. <i>Frontiers in Plant Science</i> , 2020, 11, 81.	1.7	2
143	Genome-Wide Study of NOT2_3_5 Protein Subfamily in Cotton and Their Necessity in Resistance to Verticillium wilt. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5634.	1.8	2
144	Recent Advancement in Predicting Subcellular Localization of Mycobacterial Protein with Machine Learning Methods. <i>Medicinal Chemistry</i> , 2020, 16, 605-619.	0.7	2

#	ARTICLE	IF	CITATIONS
145	The Underlying Mechanisms of Wujjayizhi Granule in Treating Alzheimer's Disease. Current Bioinformatics, 2022, 17, 735-743.	0.7	2
146	Fine mapping and characterization of the Crinkled Dwarf gene in cotton. Industrial Crops and Products, 2022, 184, 115034.	2.5	2
147	Application of Machine Learning Method in Genomics and Proteomics. Scientific World Journal, The, 2015, 2015, 1-2.	0.8	1
148	The Evolution and Expression Profiles of EC1 Gene Family during Development in Cotton. Genes, 2021, 12, 2001.	1.0	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.	2.2	0