

Wei Chen

List of Publications by Citations

Source: <https://exaly.com/author-pdf/4770648/wei-chen-publications-by-citations.pdf>

Version: 2024-04-23

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

146
papers

10,960
citations

59
h-index

103
g-index

151
ext. papers

12,863
ext. citations

5.8
avg, IF

7
L-index

#	Paper	IF	Citations
146	Repeated polyploidization of <i>Gossypium</i> genomes and the evolution of spinnable cotton fibres. <i>Nature</i> , 2012 , 492, 423-7	50.4	839
145	iRSpot-PseDNC: identify recombination spots with pseudo dinucleotide composition. <i>Nucleic Acids Research</i> , 2013 , 41, e68	20.1	492
144	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, 12961-72	20.1	412
143	PseKNC: a flexible web server for generating pseudo K-tuple nucleotide composition. <i>Analytical Biochemistry</i> , 2014 , 456, 53-60	3.1	341
142	iNuc-PseKNC: a sequence-based predictor for predicting nucleosome positioning in genomes with pseudo k-tuple nucleotide composition. <i>Bioinformatics</i> , 2014 , 30, 1522-9	7.2	303
141	iACP: a sequence-based tool for identifying anticancer peptides. <i>Oncotarget</i> , 2016 , 7, 16895-909	3.3	283
140	iRNA-Methyl: Identifying N(6)-methyladenosine sites using pseudo nucleotide composition. <i>Analytical Biochemistry</i> , 2015 , 490, 26-33	3.1	276
139	Pseudo nucleotide composition or PseKNC: an effective formulation for analyzing genomic sequences. <i>Molecular BioSystems</i> , 2015 , 11, 2620-34		256
138	iHSP-PseRAAAC: Identifying the heat shock protein families using pseudo reduced amino acid alphabet composition. <i>Analytical Biochemistry</i> , 2013 , 442, 118-25	3.1	254
137	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	10.7	228
136	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	3.1	218
135	iDNA4mC: identifying DNA N4-methylcytosine sites based on nucleotide chemical properties. <i>Bioinformatics</i> , 2017 , 33, 3518-3523	7.2	198
134	iRNA-AI: identifying the adenosine to inosine editing sites in RNA sequences. <i>Oncotarget</i> , 2017 , 8, 4208-4217	3.5	191
133	iDNA6mA-PseKNC: Identifying DNA N-methyladenosine sites by incorporating nucleotide physicochemical properties into PseKNC. <i>Genomics</i> , 2019 , 111, 96-102	4.3	190
132	PseKNC-General: a cross-platform package for generating various modes of pseudo nucleotide compositions. <i>Bioinformatics</i> , 2015 , 31, 119-20	7.2	172
131	iCTX-type: a sequence-based predictor for identifying the types of conotoxins in targeting ion channels. <i>BioMed Research International</i> , 2014 , 2014, 286419	3	171
130	iNuc-PhysChem: a sequence-based predictor for identifying nucleosomes via physicochemical properties. <i>PLoS ONE</i> , 2012 , 7, e47843	3.7	160

129	iOri-Human: identify human origin of replication by incorporating dinucleotide physicochemical properties into pseudo nucleotide composition. <i>Oncotarget</i> , 2016 , 7, 69783-69793	3.3	156
128	Predicting protein structural classes for low-similarity sequences by evaluating different features. <i>Knowledge-Based Systems</i> , 2019 , 163, 787-793	7.3	156
127	iRNA-PseU: Identifying RNA pseudouridine sites. <i>Molecular Therapy - Nucleic Acids</i> , 2016 , 5, e332	10.7	145
126	i6mA-Pred: identifying DNA N6-methyladenine sites in the rice genome. <i>Bioinformatics</i> , 2019 , 35, 2796-2800	7.0	144
125	Identification of immunoglobulins using Chou's pseudo amino acid composition with feature selection technique. <i>Molecular BioSystems</i> , 2016 , 12, 1269-75		141
124	iTerm-PseKNC: a sequence-based tool for predicting bacterial transcriptional terminators. <i>Bioinformatics</i> , 2019 , 35, 1469-1477	7.2	141
123	Identify origin of replication in <i>Saccharomyces cerevisiae</i> using two-step feature selection technique. <i>Bioinformatics</i> , 2019 , 35, 2075-2083	7.2	137
122	iRNA-3typeA: Identifying Three Types of Modification at RNA's Adenosine Sites. <i>Molecular Therapy - Nucleic Acids</i> , 2018 , 11, 468-474	10.7	135
121	iRSpot-Pse6NC: Identifying recombination spots in by incorporating hexamer composition into general PseKNC. <i>International Journal of Biological Sciences</i> , 2018 , 14, 883-891	11.2	130
120	iSS-PseDNC: identifying splicing sites using pseudo dinucleotide composition. <i>BioMed Research International</i> , 2014 , 2014, 623149	3	130
119	iLoc-lncRNA: predict the subcellular location of lncRNAs by incorporating octamer composition into general PseKNC. <i>Bioinformatics</i> , 2018 , 34, 4196-4204	7.2	118
118	Naïve Bayes classifier with feature selection to identify phage virion proteins. <i>Computational and Mathematical Methods in Medicine</i> , 2013 , 2013, 530696	2.8	118
117	iRNA(m6A)-PseDNC: Identifying N-methyladenosine sites using pseudo dinucleotide composition. <i>Analytical Biochemistry</i> , 2018 , 561-562, 59-65	3.1	117
116	Identification of hormone binding proteins based on machine learning methods. <i>Mathematical Biosciences and Engineering</i> , 2019 , 16, 2466-2480	2.1	115
115	Identification of Secretory Proteins in <i>Mycobacterium tuberculosis</i> Using Pseudo Amino Acid Composition. <i>BioMed Research International</i> , 2016 , 2016, 5413903	3	110
114	Identification of bacteriophage virion proteins by the ANOVA feature selection and analysis. <i>Molecular BioSystems</i> , 2014 , 10, 2229-35		107
113	iRNA-2OM: A Sequence-Based Predictor for Identifying 2FO-Methylation Sites in <i>Homo sapiens</i> . <i>Journal of Computational Biology</i> , 2018 , 25, 1266-1277	1.7	103
112	Using deformation energy to analyze nucleosome positioning in genomes. <i>Genomics</i> , 2016 , 107, 69-75	4.3	99

111	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, 558-63		97
110	Identifying Sigma70 Promoters with Novel Pseudo Nucleotide Composition. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019 , 16, 1316-1321	3	94
109	Identification of antioxidants from sequence information using naïve Bayes. <i>Computational and Mathematical Methods in Medicine</i> , 2013 , 2013, 567529	2.8	89
108	Identification of Bacterial Cell Wall Lyases via Pseudo Amino Acid Composition. <i>BioMed Research International</i> , 2016 , 2016, 1654623	3	89
107	MethyRNA: a web server for identification of N-methyladenosine sites. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017 , 35, 683-687	3.6	86
106	Sequence-based predictive modeling to identify cancerlectins. <i>Oncotarget</i> , 2017 , 8, 28169-28175	3.3	86
105	Detecting N-methyladenosine sites from RNA transcriptomes using ensemble Support Vector Machines. <i>Scientific Reports</i> , 2017 , 7, 40242	4.9	85
104	Using Chou's pseudo amino acid composition to predict protein quaternary structure: a sequence-segmented PseAAC approach. <i>Amino Acids</i> , 2008 , 35, 591-8	3.5	80
103	Identification of mycobacterial membrane proteins and their types using over-represented tripeptide compositions. <i>Journal of Proteomics</i> , 2012 , 77, 321-8	3.9	79
102	iMRM: a platform for simultaneously identifying multiple kinds of RNA modifications. <i>Bioinformatics</i> , 2020 , 36, 3336-3342	7.2	78
101	AcalPred: a sequence-based tool for discriminating between acidic and alkaline enzymes. <i>PLoS ONE</i> , 2013 , 8, e75726	3.7	78
100	Prediction of Golgi-resident protein types by using feature selection technique. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2013 , 124, 9-13	3.8	77
99	iProEP: A Computational Predictor for Predicting Promoter. <i>Molecular Therapy - Nucleic Acids</i> , 2019 , 17, 337-346	10.7	74
98	Predicting peroxidase subcellular location by hybridizing different descriptors of Chou's pseudo amino acid patterns. <i>Analytical Biochemistry</i> , 2014 , 458, 14-9	3.1	74
97	Evaluation of different computational methods on 5-methylcytosine sites identification. <i>Briefings in Bioinformatics</i> , 2020 , 21, 982-995	13.4	72
96	Prediction of thermophilic proteins using feature selection technique. <i>Journal of Microbiological Methods</i> , 2011 , 84, 67-70	2.8	71
95	Identification and analysis of the N(6)-methyladenosine in the <i>Saccharomyces cerevisiae</i> transcriptome. <i>Scientific Reports</i> , 2015 , 5, 13859	4.9	68
94	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	3.8	67

93	Hierarchically Aligning 10 Legume Genomes Establishes a Family-Level Genomics Platform. <i>Plant Physiology</i> , 2017 , 174, 284-300	6.6	66
92	Recent Advances in Machine Learning Methods for Predicting Heat Shock Proteins. <i>Current Drug Metabolism</i> , 2019 , 20, 224-228	3.5	65
91	Using over-represented tetrapeptides to predict protein submitochondria locations. <i>Acta Biotheoretica</i> , 2013 , 61, 259-68	1.1	65
90	Prediction of cell-penetrating peptides with feature selection techniques. <i>Biochemical and Biophysical Research Communications</i> , 2016 , 477, 150-154	3.4	63
89	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	13.4	60
88	Design powerful predictor for mRNA subcellular location prediction in <i>Homo sapiens</i> . <i>Briefings in Bioinformatics</i> , 2021 , 22, 526-535	13.4	59
87	iRNAD: a computational tool for identifying D modification sites in RNA sequence. <i>Bioinformatics</i> , 2019 , 35, 4922-4929	7.2	53
86	The prediction of protein structural class using averaged chemical shifts. <i>Journal of Biomolecular Structure and Dynamics</i> , 2012 , 29, 643-9	3.6	53
85	iRNA-m7G: Identifying N-methylguanosine Sites by Fusing Multiple Features. <i>Molecular Therapy - Nucleic Acids</i> , 2019 , 18, 269-274	10.7	50
84	The organization of nucleosomes around splice sites. <i>Nucleic Acids Research</i> , 2010 , 38, 2788-98	20.1	49
83	Prediction of the types of ion channel-targeted conotoxins based on radial basis function network. <i>Toxicology in Vitro</i> , 2013 , 27, 852-6	3.6	48
82	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, 539-47	6	47
81	Pro54DB: a database for experimentally verified sigma-54 promoters. <i>Bioinformatics</i> , 2017 , 33, 467-469	7.2	47
80	Prediction of phosphothreonine sites in human proteins by fusing different features. <i>Scientific Reports</i> , 2016 , 6, 34817	4.9	46
79	Prediction of replication origins by calculating DNA structural properties. <i>FEBS Letters</i> , 2012 , 586, 934-8	3.8	46
78	An Overlooked Paleotetraploidization in Cucurbitaceae. <i>Molecular Biology and Evolution</i> , 2018 , 35, 16-26	3.3	45
77	IonChanPred 2.0: A Tool to Predict Ion Channels and Their Types. <i>International Journal of Molecular Sciences</i> , 2017 , 18,	6.3	45
76	Predicting cancerlectins by the optimal g-gap dipeptides. <i>Scientific Reports</i> , 2015 , 5, 16964	4.9	44

75	AOD: the antioxidant protein database. <i>Scientific Reports</i> , 2017 , 7, 7449	4.9	43
74	PHYPred: a tool for identifying bacteriophage enzymes and hydrolases. <i>Virologica Sinica</i> , 2016 , 31, 350-26.4		43
73	XG-PseU: an eXtreme Gradient Boosting based method for identifying pseudouridine sites. <i>Molecular Genetics and Genomics</i> , 2020 , 295, 13-21	3.1	42
72	iDNA6mA-Rice: A Computational Tool for Detecting N6-Methyladenine Sites in Rice. <i>Frontiers in Genetics</i> , 2019 , 10, 793	4.5	41
71	Recent Advances in Conotoxin Classification by Using Machine Learning Methods. <i>Molecules</i> , 2017 , 22,	4.8	40
70	Identifying RNA 5-methylcytosine sites via pseudo nucleotide compositions. <i>Molecular BioSystems</i> , 2016 , 12, 3307-3311		39
69	Identifying 2FO-methylation sites by integrating nucleotide chemical properties and nucleotide compositions. <i>Genomics</i> , 2016 , 107, 255-8	4.3	39
68	Identification of voltage-gated potassium channel subfamilies from sequence information using support vector machine. <i>Computers in Biology and Medicine</i> , 2012 , 42, 504-7	7	37
67	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	1.8	37
66	Identifying N -methyladenosine sites in the Arabidopsis thaliana transcriptome. <i>Molecular Genetics and Genomics</i> , 2016 , 291, 2225-2229	3.1	37
65	Computational Identification of Small Interfering RNA Targets in SARS-CoV-2. <i>Virologica Sinica</i> , 2020 , 35, 359-361	6.4	35
64	Identification of apolipoprotein using feature selection technique. <i>Scientific Reports</i> , 2016 , 6, 30441	4.9	34
63	RAMPred: identifying the N(1)-methyladenosine sites in eukaryotic transcriptomes. <i>Scientific Reports</i> , 2016 , 6, 31080	4.9	31
62	Identifying Antioxidant Proteins by Using Optimal Dipeptide Compositions. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2016 , 8, 186-191	3.5	30
61	Prediction of CpG island methylation status by integrating DNA physicochemical properties. <i>Genomics</i> , 2014 , 104, 229-33	4.3	30
60	Prediction of ketoacyl synthase family using reduced amino acid alphabets. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2012 , 39, 579-84	4.2	30
59	Prediction of midbody, centrosome and kinetochore proteins based on gene ontology information. <i>Biochemical and Biophysical Research Communications</i> , 2010 , 401, 382-4	3.4	30
58	Prediction of protein structural classes based on feature selection technique. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2014 , 6, 235-40	3.5	28

57	Identifying the subfamilies of voltage-gated potassium channels using feature selection technique. <i>International Journal of Molecular Sciences</i> , 2014 , 15, 12940-51	6.3	28
56	Predicting the types of J-proteins using clustered amino acids. <i>BioMed Research International</i> , 2014 , 2014, 935719	3	26
55	iATP: A Sequence Based Method for Identifying Anti-tubercular Peptides. <i>Medicinal Chemistry</i> , 2020 , 16, 620-625	1.8	26
54	PAI: Predicting adenosine to inosine editing sites by using pseudo nucleotide compositions. <i>Scientific Reports</i> , 2016 , 6, 35123	4.9	26
53	Prediction of bacteriophage proteins located in the host cell using hybrid features. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2018 , 180, 64-69	3.8	24
52	Deciphering the high-quality genome sequence of coriander that causes controversial feelings. <i>Plant Biotechnology Journal</i> , 2020 , 18, 1444-1456	11.6	24
51	A similarity distance of diversity measure for discriminating mesophilic and thermophilic proteins. <i>Amino Acids</i> , 2013 , 44, 573-80	3.5	23
50	DNA4mC-LIP: a linear integration method to identify N4-methylcytosine site in multiple species. <i>Bioinformatics</i> , 2020 , 36, 3327-3335	7.2	21
49	A Survey for Predicting Enzyme Family Classes Using Machine Learning Methods. <i>Current Drug Targets</i> , 2019 , 20, 540-550	3	21
48	A Brief Survey of Machine Learning Application in Cancerlectin Identification. <i>Current Gene Therapy</i> , 2018 , 18, 257-267	4.3	21
47	iPhoPred: A Predictor for Identifying Phosphorylation Sites in Human Protein. <i>IEEE Access</i> , 2019 , 7, 177517-177528	3.5	21
46	iRNA-m2G: Identifying N-methylguanosine Sites Based on Sequence-Derived Information. <i>Molecular Therapy - Nucleic Acids</i> , 2019 , 18, 253-258	10.7	19
45	Identifying RNA N-Methyladenosine Sites in Genome. <i>Frontiers in Microbiology</i> , 2018 , 9, 955	5.7	18
44	Classification of antimicrobial peptide using diversity measure with quadratic discriminant analysis. <i>Journal of Microbiological Methods</i> , 2009 , 78, 94-6	2.8	18
43	Classifying Included and Excluded Exons in Exon Skipping Event Using Histone Modifications. <i>Frontiers in Genetics</i> , 2018 , 9, 433	4.5	18
42	Iterative feature representation algorithm to improve the predictive performance of N7-methylguanosine sites. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	16
41	Sequence analysis of origins of replication in the <i>Saccharomyces cerevisiae</i> genomes. <i>Frontiers in Microbiology</i> , 2014 , 5, 574	5.7	15
40	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, 2893-900		15

39	Nulliplex-branch, a TERMINAL FLOWER 1 ortholog, controls plant growth habit in cotton. <i>Theoretical and Applied Genetics</i> , 2019 , 132, 97-112	6	15
38	iRNA5hmC: The First Predictor to Identify RNA 5-Hydroxymethylcytosine Modifications Using Machine Learning. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020 , 8, 227	5.8	14
37	Predicting the Organelle Location of Noncoding RNAs Using Pseudo Nucleotide Compositions. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2017 , 9, 540-544	3.5	14
36	PPD: A Manually Curated Database for Experimentally Verified Prokaryotic Promoters. <i>Journal of Molecular Biology</i> , 2021 , 433, 166860	6.5	14
35	Genome-wide identification and analyses of the AHL gene family in cotton (<i>Gossypium</i>). <i>BMC Genomics</i> , 2020 , 21, 69	4.5	13
34	The celery genome sequence reveals sequential paleo-polyploidizations, karyotype evolution and resistance gene reduction in apiales. <i>Plant Biotechnology Journal</i> , 2021 , 19, 731-744	11.6	13
33	Predicting bacteriophage proteins located in host cell with feature selection technique. <i>Computers in Biology and Medicine</i> , 2016 , 71, 156-61	7	12
32	A genome-wide analysis of SWEET gene family in cotton and their expressions under different stresses. <i>Journal of Cotton Research</i> , 2018 , 1,	2.3	12
31	Recent Advances in Identification of RNA Modifications. <i>Non-coding RNA</i> , 2016 , 3,	7.1	12
30	mRNALocater: Enhance the prediction accuracy of eukaryotic mRNA subcellular localization by using model fusion strategy. <i>Molecular Therapy</i> , 2021 , 29, 2617-2623	11.7	12
29	The development of specific SNP markers for chromosome 14 in cotton using next-generation sequencing. <i>Plant Breeding</i> , 2014 , 133, 256-261	2.4	10
28	Recent Advances of Computational Methods for Identifying Bacteriophage Virion Proteins. <i>Protein and Peptide Letters</i> , 2020 , 27, 259-264	1.9	10
27	Benchmark data for identifying N(6)-methyladenosine sites in the <i>Saccharomyces cerevisiae</i> genome. <i>Data in Brief</i> , 2015 , 5, 376-8	1.2	9
26	Predicting Human Enzyme Family Classes by Using Pseudo Amino Acid Composition. <i>Current Proteomics</i> , 2016 , 13, 99-104	0.7	9
25	Identifying Antioxidant Proteins by Combining Multiple Methods. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020 , 8, 858	5.8	9
24	KNIndex: a comprehensive database of physicochemical properties for k-tuple nucleotides. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	8
23	Exon skipping event prediction based on histone modifications. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2014 , 6, 241-9	3.5	8
22	The pattern of DNA cleavage intensity around indels. <i>Scientific Reports</i> , 2015 , 5, 8333	4.9	8

21	FS-GBDT: identification multicancer-risk module via a feature selection algorithm by integrating Fisher score and GBDT. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	8
20	RNAWRE: a resource of writers, readers and erasers of RNA modifications. <i>Database: the Journal of Biological Databases and Curation</i> , 2020 , 2020,	5	7
19	DNA Physical Parameters Modulate Nucleosome Positioning in the <i>Saccharomyces cerevisiae</i> Genome. <i>Current Bioinformatics</i> , 2014 , 9, 188-193	4.7	6
18	RNAInter v4.0: RNA interactome repository with redefined confidence scoring system and improved accessibility. <i>Nucleic Acids Research</i> , 2021 ,	20.1	5
17	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	6.8	3
16	Briefing in application of machine learning methods in ion channel prediction. <i>Scientific World Journal, The</i> , 2015 , 2015, 945927	2.2	3
15	Analysis and Comparison of RNA Pseudouridine Site Prediction Tools. <i>Current Bioinformatics</i> , 2020 , 15, 279-286	4.7	3
14	The role of RNA mC modification in cancer metastasis. <i>International Journal of Biological Sciences</i> , 2021 , 17, 3369-3380	11.2	3
13	Combinatorial Pattern of Histone Modifications in Exon Skipping Event. <i>Frontiers in Genetics</i> , 2019 , 10, 122	4.5	2
12	Recognition of DNase I hypersensitive sites in multiple cell lines. <i>International Journal of Bioinformatics Research and Applications</i> , 2009 , 5, 378-84	0.9	2
11	Recent Development of Computational Predicting Bioluminescent Proteins. <i>Current Pharmaceutical Design</i> , 2019 , 25, 4264-4273	3.3	2
10	Identification of Potential Inhibitors against SARS-Cov-2 using Computational Drug Repurposing Study. <i>Current Bioinformatics</i> , 2021 , 16,	4.7	2
9	Cotton DMP gene family: characterization, evolution, and expression profiles during development and stress. <i>International Journal of Biological Macromolecules</i> , 2021 , 183, 1257-1269	7.9	2
8	Open-Bud Duplicate Loci Are Identified as , Orthologs of MIXTA-Like Genes on Homologous Chromosomes of Allotetraploid Cotton. <i>Frontiers in Plant Science</i> , 2020 , 11, 81	6.2	1
7	A Brief Survey for MicroRNA Precursor Identification Using Machine Learning Methods. <i>Current Genomics</i> , 2020 , 21, 11-25	2.6	1
6	Genome-Wide Study of NOT2_3_5 Protein Subfamily in Cotton and Their Necessity in Resistance to. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	1
5	Recent Advancement in Predicting Subcellular Localization of Mycobacterial Protein with Machine Learning Methods. <i>Medicinal Chemistry</i> , 2020 , 16, 605-619	1.8	0
4	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	4.5	0

- 3 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 3.5
- 2 Nucleosome Positioning and RNA Splicing*. *Progress in Biochemistry and Biophysics*, **2009**, 36, 1035-1040
- 1 Fine mapping and characterization of the Crinkled Dwarf gene in cotton. *Industrial Crops and Products*, **2022**, 184, 115034 5.9