Wei Chen

List of Publications by Year in Descending Order

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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	Fine mapping and characterization of the Crinkled Dwarf gene in cotton. *Industrial Crops and Products*, **2022**, 184, 115034	5.9	
145	KNIndex: a comprehensive database of physicochemical properties for k-tuple nucleotides. *Briefings in Bioinformatics*, **2021**, 22,	13.4	8
144	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	
143	RNAInter v4.0: RNA interactome repository with redefined confidence scoring system and improved accessibility. *Nucleic Acids Research*, **2021**,	20.1	5
142	Iterative feature representation algorithm to improve the predictive performance of N7-methylguanosine sites. *Briefings in Bioinformatics*, **2021**, 22,	13.4	16
141	PPD: A Manually Curated Database for Experimentally Verified Prokaryotic Promoters. *Journal of Molecular Biology*, **2021**, 433, 166860	6.5	14
140	Genome-Wide Study of NOT2_3_5 Protein Subfamily in Cotton and Their Necessity in Resistance to. *International Journal of Molecular Sciences*, **2021**, 22,	6.3	1
139	Identification of Potential Inhibitors against SARS-Cov-2 using Computational Drug Repurposing Study. *Current Bioinformatics*, **2021**, 16,	4.7	2
138	Design powerful predictor for mRNA subcellular location prediction in Homo sapiens. *Briefings in Bioinformatics*, **2021**, 22, 526-535	13.4	59
137	The celery genome sequence reveals sequential paleo-polyploidizations, karyotype evolution and resistance gene reduction in apiales. *Plant Biotechnology Journal*, **2021**, 19, 731-744	11.6	13
136	FS-GBDT: identification multicancer-risk module via a feature selection algorithm by integrating Fisher score and GBDT. *Briefings in Bioinformatics*, **2021**, 22,	13.4	8
135	Cotton DMP gene family: characterization, evolution, and expression profiles during development and stress. *International Journal of Biological Macromolecules*, **2021**, 183, 1257-1269	7.9	2
134	mRNALocater: Enhance the prediction accuracy of eukaryotic mRNA subcellular localization by using model fusion strategy. *Molecular Therapy*, **2021**, 29, 2617-2623	11.7	12
133	A tetraploidization event shaped the Aquilaria sinensis genome and contributed to the ability of sesquiterpenes synthesis. *BMC Genomics*, **2021**, 22, 647	4.5	0
132	The role of RNA mC modification in cancer metastasis. *International Journal of Biological Sciences*, **2021**, 17, 3369-3380	11.2	3
131	ncPro-ML: An integrated computational tool for identifying non-coding RNA promoters in multiple species. *Computational and Structural Biotechnology Journal*, **2020**, 18, 2445-2452	6.8	3
130	iMRM: a platform for simultaneously identifying multiple kinds of RNA modifications. *Bioinformatics*, **2020**, 36, 3336-3342	7.2	78

129	Open-Bud Duplicate Loci Are Identified as , Orthologs of MIXTA-Like Genes on Homologous Chromosomes of Allotetraploid Cotton. *Frontiers in Plant Science*, **2020**, 11, 81	6.2	1
128	RNAWRE: a resource of writers, readers and erasers of RNA modifications. *Database: the Journal of Biological Databases and Curation*, **2020**, 2020,	5	7
127	DNA4mC-LIP: a linear integration method to identify N4-methylcytosine site in multiple species. *Bioinformatics*, **2020**, 36, 3327-3335	7.2	21
126	Genome-wide identification and analyses of the AHL gene family in cotton (Gossypium). *BMC Genomics*, **2020**, 21, 69	4.5	13
125	iRNA5hmC: The First Predictor to Identify RNA 5-Hydroxymethylcytosine Modifications Using Machine Learning. *Frontiers in Bioengineering and Biotechnology*, **2020**, 8, 227	5.8	14
124	A Brief Survey for MicroRNA Precursor Identification Using Machine Learning Methods. *Current Genomics*, **2020**, 21, 11-25	2.6	1
123	Recent Advances of Computational Methods for Identifying Bacteriophage Virion Proteins. *Protein and Peptide Letters*, **2020**, 27, 259-264	1.9	10
122	iATP: A Sequence Based Method for Identifying Anti-tubercular Peptides. *Medicinal Chemistry*, **2020** , 16, 620-625	1.8	26
121	Analysis and Comparison of RNA Pseudouridine Site Prediction Tools. *Current Bioinformatics*, **2020**, 15, 279-286	4.7	3
120	Recent Advancement in Predicting Subcellular Localization of Mycobacterial Protein with Machine Learning Methods. *Medicinal Chemistry*, **2020**, 16, 605-619	1.8	0
119	Evaluation of different computational methods on 5-methylcytosine sites identification. *Briefings in Bioinformatics*, **2020**, 21, 982-995	13.4	72
118	Deciphering the high-quality genome sequence of coriander that causes controversial feelings. *Plant Biotechnology Journal*, **2020**, 18, 1444-1456	11.6	24
117	Identifying Antioxidant Proteins by Combining Multiple Methods. *Frontiers in Bioengineering and Biotechnology*, **2020**, 8, 858	5.8	9
116	A comparison and assessment of computational method for identifying recombination hotspots in Saccharomyces cerevisiae. *Briefings in Bioinformatics*, **2020**, 21, 1568-1580	13.4	60
115	XG-PseU: an eXtreme Gradient Boosting based method for identifying pseudouridine sites. *Molecular Genetics and Genomics*, **2020**, 295, 13-21	3.1	42
114	Computational Identification of Small Interfering RNA Targets in SARS-CoV-2. *Virologica Sinica*, **2020**, 35, 359-361	6.4	35
113	i6mA-Pred: identifying DNA N6-methyladenine sites in the rice genome. *Bioinformatics*, **2019**, 35, 2796-2800	7.2	144
112	iRNA-m2G: Identifying N-methylguanosine Sites Based on Sequence-Derived Information. *Molecular Therapy - Nucleic Acids*, **2019**, 18, 253-258	10.7	19

111	iRNAD: a computational tool for identifying D modification sites in RNA sequence. *Bioinformatics*, **2019**, 35, 4922-4929	7.2	53
110	Combinatorial Pattern of Histone Modifications in Exon Skipping Event. *Frontiers in Genetics*, **2019**, 10, 122	4.5	2
109	iProEP: A Computational Predictor for Predicting Promoter. *Molecular Therapy - Nucleic Acids*, **2019**, 17, 337-346	10.7	74
108	iDNA6mA-Rice: A Computational Tool for Detecting N6-Methyladenine Sites in Rice. *Frontiers in Genetics*, **2019**, 10, 793	4.5	41
107	Recent Advances in Machine Learning Methods for Predicting Heat Shock Proteins. *Current Drug Metabolism*, **2019**, 20, 224-228	3.5	65
106	iRNA-m7G: Identifying N-methylguanosine Sites by Fusing Multiple Features. *Molecular Therapy - Nucleic Acids*, **2019**, 18, 269-274	10.7	50
105	Recent Development of Computational Predicting Bioluminescent Proteins. *Current Pharmaceutical Design*, **2019**, 25, 4264-4273	3.3	2
104	A Survey for Predicting Enzyme Family Classes Using Machine Learning Methods. *Current Drug Targets*, **2019**, 20, 540-550	3	21
103	Identification of hormone binding proteins based on machine learning methods. *Mathematical Biosciences and Engineering*, **2019**, 16, 2466-2480	2.1	115
102	iPhoPred: A Predictor for Identifying Phosphorylation Sites in Human Protein. *IEEE Access*, **2019**, 7, 177517-177528	3.5	22
101	Identify origin of replication in Saccharomyces cerevisiae using two-step feature selection technique. *Bioinformatics*, **2019**, 35, 2075-2083	7.2	137
100	Predicting protein structural classes for low-similarity sequences by evaluating different features. *Knowledge-Based Systems*, **2019**, 163, 787-793	7.3	156
99	iTerm-PseKNC: a sequence-based tool for predicting bacterial transcriptional terminators. *Bioinformatics*, **2019**, 35, 1469-1477	7.2	141
98	Nulliplex-branch, a TERMINAL FLOWER 1 ortholog, controls plant growth habit in cotton. *Theoretical and Applied Genetics*, **2019**, 132, 97-112	6	15
97	iDNA6mA-PseKNC: Identifying DNA N-methyladenosine sites by incorporating nucleotide physicochemical properties into PseKNC. *Genomics*, **2019**, 111, 96-102	4.3	190
96	Identifying Sigma70 Promoters with Novel Pseudo Nucleotide Composition. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2019**, 16, 1316-1321	3	94
95	An Overlooked Paleotetraploidization in Cucurbitaceae. *Molecular Biology and Evolution*, **2018**, 35, 16-26	8.3	45
94	iRSpot-Pse6NC: Identifying recombination spots in by incorporating hexamer composition into general PseKNC. *International Journal of Biological Sciences*, **2018**, 14, 883-891	11.2	130

93	iLoc-lncRNA: predict the subcellular location of lncRNAs by incorporating octamer composition into general PseKNC. *Bioinformatics*, **2018**, 34, 4196-4204	7.2	118
92	Identifying RNA N-Methyladenosine Sites in Genome. *Frontiers in Microbiology*, **2018**, 9, 955	5.7	18
91	Prediction of bacteriophage proteins located in the host cell using hybrid features. *Chemometrics and Intelligent Laboratory Systems*, **2018**, 180, 64-69	3.8	24
90	iRNA-2OM: A Sequence-Based Predictor for Identifying 2ŦO-Methylation Sites in Homo sapiens. *Journal of Computational Biology*, **2018**, 25, 1266-1277	1.7	103
89	A genome-wide analysis of SWEET gene family in cotton and their expressions under different stresses. *Journal of Cotton Research*, **2018**, 1,	2.3	12
88	A Brief Survey of Machine Learning Application in Cancerlectin Identification. *Current Gene Therapy*, **2018**, 18, 257-267	4.3	21
87	Classifying Included and Excluded Exons in Exon Skipping Event Using Histone Modifications. *Frontiers in Genetics*, **2018**, 9, 433	4.5	18
86	iRNA(m6A)-PseDNC: Identifying N-methyladenosine sites using pseudo dinucleotide composition. *Analytical Biochemistry*, **2018**, 561-562, 59-65	3.1	117
85	iRNA-3typeA: Identifying Three Types of Modification at RNAŦs Adenosine Sites. *Molecular Therapy - Nucleic Acids*, **2018**, 11, 468-474	10.7	135
84	MethyRNA: a web server for identification of N-methyladenosine sites. *Journal of Biomolecular Structure and Dynamics*, **2017**, 35, 683-687	3.6	86
83	Detecting N-methyladenosine sites from RNA transcriptomes using ensemble Support Vector Machines. *Scientific Reports*, **2017**, 7, 40242	4.9	85
82	iRNA-PseColl: Identifying the Occurrence Sites of Different RNA Modifications by Incorporating Collective Effects of Nucleotides into PseKNC. *Molecular Therapy - Nucleic Acids*, **2017**, 7, 155-163	10.7	228
81	Hierarchically Aligning 10 Legume Genomes Establishes a Family-Level Genomics Platform. *Plant Physiology*, **2017**, 174, 284-300	6.6	66
80	iRNA-AI: identifying the adenosine to inosine editing sites in RNA sequences. *Oncotarget*, **2017**, 8, 4208-4217	5.3	191
79	iDNA4mC: identifying DNA N4-methylcytosine sites based on nucleotide chemical properties. *Bioinformatics*, **2017**, 33, 3518-3523	7.2	198
78	AOD: the antioxidant protein database. *Scientific Reports*, **2017**, 7, 7449	4.9	43
77	Predicting the Organelle Location of Noncoding RNAs Using Pseudo Nucleotide Compositions. *Interdisciplinary Sciences, Computational Life Sciences*, **2017**, 9, 540-544	3.5	14
76	Recent Advances in Conotoxin Classification by Using Machine Learning Methods. *Molecules*, **2017**, 22,	4.8	40

75	IonchanPred 2.0: A Tool to Predict Ion Channels and Their Types. *International Journal of Molecular Sciences*, **2017**, 18,	6.3	45
74	Sequence-based predictive modeling to identify cancerlectins. *Oncotarget*, **2017**, 8, 28169-28175	3.3	86
73	Pro54DB: a database for experimentally verified sigma-54 promoters. *Bioinformatics*, **2017**, 33, 467-469	7.2	47
72	Identifying Antioxidant Proteins by Using Optimal Dipeptide Compositions. *Interdisciplinary Sciences, Computational Life Sciences*, **2016**, 8, 186-191	3.5	30
71	Identifying RNA 5-methylcytosine sites via pseudo nucleotide compositions. *Molecular BioSystems*, **2016**, 12, 3307-3311		39
70	RAMPred: identifying the N(1)-methyladenosine sites in eukaryotic transcriptomes. *Scientific Reports*, **2016**, 6, 31080	4.9	31
69	Prediction of phosphothreonine sites in human proteins by fusing different features. *Scientific Reports*, **2016**, 6, 34817	4.9	46
68	Prediction of cell-penetrating peptides with feature selection techniques. *Biochemical and Biophysical Research Communications*, **2016**, 477, 150-154	3.4	63
67	Identification of immunoglobulins using ChouTs pseudo amino acid composition with feature selection technique. *Molecular BioSystems*, **2016**, 12, 1269-75		141
66	Predicting bacteriophage proteins located in host cell with feature selection technique. *Computers in Biology and Medicine*, **2016**, 71, 156-61	7	12
65	Using deformation energy to analyze nucleosome positioning in genomes. *Genomics*, **2016**, 107, 69-75	4.3	99
64	Recent Advances in Identification of RNA Modifications. *Non-coding RNA*, **2016**, 3,	7.1	12
63	Predicting Human Enzyme Family Classes by Using Pseudo Amino Acid Composition. *Current Proteomics*, **2016**, 13, 99-104	0.7	9
62	iRNA-PseU: Identifying RNA pseudouridine sites. *Molecular Therapy - Nucleic Acids*, **2016**, 5, e332	10.7	145
61	iOri-Human: identify human origin of replication by incorporating dinucleotide physicochemical properties into pseudo nucleotide composition. *Oncotarget*, **2016**, 7, 69783-69793	3.3	156
60	iACP: a sequence-based tool for identifying anticancer peptides. *Oncotarget*, **2016**, 7, 16895-909	3.3	283
59	Identification of Bacterial Cell Wall Lyases via Pseudo Amino Acid Composition. *BioMed Research International*, **2016**, 2016, 1654623	3	89
58	Identification of Secretory Proteins in Mycobacterium tuberculosis Using Pseudo Amino Acid Composition. *BioMed Research International*, **2016**, 2016, 5413903	3	110

57	Combining pseudo dinucleotide composition with the Z curve method to improve the accuracy of predicting DNA elements: a case study in recombination spots. *Molecular BioSystems*, **2016**, 12, 2893-900		15
56	PAI: Predicting adenosine to inosine editing sites by using pseudo nucleotide compositions. *Scientific Reports*, **2016**, 6, 35123	4.9	26
55	Identification of apolipoprotein using feature selection technique. *Scientific Reports*, **2016**, 6, 30441	4.9	34
54	Identifying 2ŦO-methylationation sites by integrating nucleotide chemical properties and nucleotide compositions. *Genomics*, **2016**, 107, 255-8	4.3	39
53	PHYPred: a tool for identifying bacteriophage enzymes and hydrolases. *Virologica Sinica*, **2016**, 31, 350-2	6.4	43
52	Identifying N -methyladenosine sites in the Arabidopsis thaliana transcriptome. *Molecular Genetics and Genomics*, **2016**, 291, 2225-2229	3.1	37
51	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, 558-63		97
50	PseKNC-General: a cross-platform package for generating various modes of pseudo nucleotide compositions. *Bioinformatics*, **2015**, 31, 119-20	7.2	172
49	Pseudo nucleotide composition or PseKNC: an effective formulation for analyzing genomic sequences. *Molecular BioSystems*, **2015**, 11, 2620-34		256
48	Benchmark data for identifying N(6)-methyladenosine sites in the Saccharomyces cerevisiae genome. *Data in Brief*, **2015**, 5, 376-8	1.2	9
47	iRNA-Methyl: Identifying N(6)-methyladenosine sites using pseudo nucleotide composition. *Analytical Biochemistry*, **2015**, 490, 26-33	3.1	276
46	Identification and analysis of the N(6)-methyladenosine in the Saccharomyces cerevisiae transcriptome. *Scientific Reports*, **2015**, 5, 13859	4.9	68
45	The pattern of DNA cleavage intensity around indels. *Scientific Reports*, **2015**, 5, 8333	4.9	8
44	Predicting cancerlectins by the optimal g-gap dipeptides. *Scientific Reports*, **2015**, 5, 16964	4.9	44
43	Briefing in application of machine learning methods in ion channel prediction. *Scientific World Journal, The*, **2015**, 2015, 945927	2.2	3
42	iORI-PseKNC: A predictor for identifying origin of replication with pseudo k-tuple nucleotide composition. *Chemometrics and Intelligent Laboratory Systems*, **2015**, 141, 100-106	3.8	67
41	Genetic mapping of the nulliplex-branch gene (gb_nb1) in cotton using next-generation sequencing. *Theoretical and Applied Genetics*, **2015**, 128, 539-47	6	47
40	Exon skipping event prediction based on histone modifications. *Interdisciplinary Sciences, Computational Life Sciences*, **2014**, 6, 241-9	3.5	8

39	Prediction of protein structural classes based on feature selection technique. *Interdisciplinary Sciences, Computational Life Sciences*, **2014**, 6, 235-40	3.5	28
38	Identification of bacteriophage virion proteins by the ANOVA feature selection and analysis. *Molecular BioSystems*, **2014**, 10, 2229-35		107
37	Prediction of CpG island methylation status by integrating DNA physicochemical properties. *Genomics*, **2014**, 104, 229-33	4.3	30
36	PseKNC: a flexible web server for generating pseudo K-tuple nucleotide composition. *Analytical Biochemistry*, **2014**, 456, 53-60	3.1	341
35	The development of specific SNP markers for chromosome 14 in cotton using next-generation sequencing. *Plant Breeding*, **2014**, 133, 256-261	2.4	10
34	iSS-PseDNC: identifying splicing sites using pseudo dinucleotide composition. *BioMed Research International*, **2014**, 2014, 623149	3	130
33	iPro54-PseKNC: a sequence-based predictor for identifying sigma-54 promoters in prokaryote with pseudo k-tuple nucleotide composition. *Nucleic Acids Research*, **2014**, 42, 12961-72	20.1	412
32	Predicting the types of J-proteins using clustered amino acids. *BioMed Research International*, **2014**, 2014, 935719	3	26
31	Identifying the subfamilies of voltage-gated potassium channels using feature selection technique. *International Journal of Molecular Sciences*, **2014**, 15, 12940-51	6.3	28
30	Sequence analysis of origins of replication in the Saccharomyces cerevisiae genomes. *Frontiers in Microbiology*, **2014**, 5, 574	5.7	15
29	iCTX-type: a sequence-based predictor for identifying the types of conotoxins in targeting ion channels. *BioMed Research International*, **2014**, 2014, 286419	3	171
28	iTIS-PseTNC: a sequence-based predictor for identifying translation initiation site in human genes using pseudo trinucleotide composition. *Analytical Biochemistry*, **2014**, 462, 76-83	3.1	218
27	iNuc-PseKNC: a sequence-based predictor for predicting nucleosome positioning in genomes with pseudo k-tuple nucleotide composition. *Bioinformatics*, **2014**, 30, 1522-9	7.2	303
26	Predicting peroxidase subcellular location by hybridizing different descriptors of ChouTpseudo amino acid patterns. *Analytical Biochemistry*, **2014**, 458, 14-9	3.1	74
25	DNA Physical Parameters Modulate Nucleosome Positioning in the Saccharomyces cerevisiae Genome. *Current Bioinformatics*, **2014**, 9, 188-193	4.7	6
24	A similarity distance of diversity measure for discriminating mesophilic and thermophilic proteins. *Amino Acids*, **2013**, 44, 573-80	3.5	23
23	Using over-represented tetrapeptides to predict protein submitochondria locations. *Acta Biotheoretica*, **2013**, 61, 259-68	1.1	65
22	iHSP-PseRAAAC: Identifying the heat shock protein families using pseudo reduced amino acid alphabet composition. *Analytical Biochemistry*, **2013**, 442, 118-25	3.1	254

21	Prediction of the types of ion channel-targeted conotoxins based on radial basis function network. *Toxicology in Vitro*, **2013**, 27, 852-6	3.6	48
20	Prediction of Golgi-resident protein types by using feature selection technique. *Chemometrics and Intelligent Laboratory Systems*, **2013**, 124, 9-13	3.8	77
19	iRSpot-PseDNC: identify recombination spots with pseudo dinucleotide composition. *Nucleic Acids Research*, **2013**, 41, e68	20.1	492
18	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	1.8	37
17	AcalPred: a sequence-based tool for discriminating between acidic and alkaline enzymes. *PLoS ONE*, **2013**, 8, e75726	3.7	78
16	Naïve Bayes classifier with feature selection to identify phage virion proteins. *Computational and Mathematical Methods in Medicine*, **2013**, 2013, 530696	2.8	118
15	Identification of antioxidants from sequence information using naïve Bayes. *Computational and Mathematical Methods in Medicine*, **2013**, 2013, 567529	2.8	89
14	Identification of mycobacterial membrane proteins and their types using over-represented tripeptide compositions. *Journal of Proteomics*, **2012**, 77, 321-8	3.9	79
13	The prediction of protein structural class using averaged chemical shifts. *Journal of Biomolecular Structure and Dynamics*, **2012**, 29, 643-9	3.6	53
12	Identification of voltage-gated potassium channel subfamilies from sequence information using support vector machine. *Computers in Biology and Medicine*, **2012**, 42, 504-7	7	37
11	Repeated polyploidization of Gossypium genomes and the evolution of spinnable cotton fibres. *Nature*, **2012**, 492, 423-7	50.4	839
10	iNuc-PhysChem: a sequence-based predictor for identifying nucleosomes via physicochemical properties. *PLoS ONE*, **2012**, 7, e47843	3.7	160
9	Prediction of ketoacyl synthase family using reduced amino acid alphabets. *Journal of Industrial Microbiology and Biotechnology*, **2012**, 39, 579-84	4.2	30
8	Prediction of replication origins by calculating DNA structural properties. *FEBS Letters*, **2012**, 586, 934-8	3.8	46
7	Prediction of thermophilic proteins using feature selection technique. *Journal of Microbiological Methods*, **2011**, 84, 67-70	2.8	71
6	The organization of nucleosomes around splice sites. *Nucleic Acids Research*, **2010**, 38, 2788-98	20.1	49
5	Prediction of midbody, centrosome and kinetochore proteins based on gene ontology information. *Biochemical and Biophysical Research Communications*, **2010**, 401, 382-4	3.4	30
4	Classification of antimicrobial peptide using diversity measure with quadratic discriminant analysis. *Journal of Microbiological Methods*, **2009**, 78, 94-6	2.8	18

3	Recognition of DNase I hypersensitive sites in multiple cell lines. *International Journal of Bioinformatics Research and Applications*, **2009**, 5, 378-84	0.9	2
2	Nucleosome Positioning and RNA Splicing*. *Progress in Biochemistry and Biophysics*, **2009**, 36, 1035-1040		
1	Using Chou's pseudo amino acid composition to predict protein quaternary structure: a sequence-segmented PseAAC approach. *Amino Acids*, **2008**, 35, 591-8	3.5	80