List of Publications by Year
in descending order

151	14,070	17440	20961
151	**14,070**	**63**	**115**
papers	citations	h-index	g-index
151	**151**	**151**	**5127**
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	iRNA-m5U: A sequence based predictor for identifying 5-methyluridine modification sites in Saccharomyces cerevisiae. Methods, 2022, 203, 28-31.	3.8	11
2	RNAInter v4.0: RNA interactome repository with redefined confidence scoring system and improved accessibility. Nucleic Acids Research, 2022, 50, D326-D332.	14.5	92
3	The Underlying Mechanisms of Wujiayizhi Granule in Treating Alzheimer's Disease. Current Bioinformatics, 2022, 17, 735-743.	1.5	2
4	Fine mapping and characterization of the Crinkled Dwarf gene in cotton. Industrial Crops and Products, 2022, 184, 115034.	5.2	2
5	Iterative feature representation algorithm to improve the predictive performance of N7-methylguanosine sites. Briefings in Bioinformatics, 2021, 22, .	6.5	35
6	Design powerful predictor for mRNA subcellular location prediction in *Homo sapiens*. Briefings in Bioinformatics, 2021, 22, 526-535.	6.5	100
7	The celery genome sequence reveals sequential paleo€polyploidizations, karyotype evolution and resistance gene reduction in apiales. Plant Biotechnology Journal, 2021, 19, 731-744.	8.3	62
8	FS€"GBDT: identification multicancer-risk module via a feature selection algorithm by integrating Fisher score and GBDT. Briefings in Bioinformatics, 2021, 22, .	6.5	19
9	PPD: A Manually Curated Database for Experimentally Verified Prokaryotic Promoters. Journal of Molecular Biology, 2021, 433, 166860.	4.2	37
10	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
11	Identification of Potential Inhibitors Against SARS-CoV-2 Using Computational Drug Repurposing Study. Current Bioinformatics, 2021, 16, 1320-1327.	1.5	4
12	Cotton DMP gene family: characterization, evolution, and expression profiles during development and stress. International Journal of Biological Macromolecules, 2021, 183, 1257-1269.	7.5	16
13	mRNALocater: Enhance the prediction accuracy of eukaryotic mRNA subcellular localization by using model fusion strategy. Molecular Therapy, 2021, 29, 2617-2623.	8.2	40
14	A tetraploidization event shaped the Aquilaria sinensis genome and contributed to the ability of sesquiterpenes synthesis. BMC Genomics, 2021, 22, 647.	2.8	3
15	The role of RNA m^{5}C modification in cancer metastasis. International Journal of Biological Sciences, 2021, 17, 3369-3380.	6.4	58
16	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
17	The Evolution and Expression Profiles of EC1 Gene Family during Development in Cotton. Genes, 2021, 12, 2001.	2.4	1
18	A comparison and assessment of computational method for identifying recombination hotspots in *Saccharomyces cerevisiae*. Briefings in Bioinformatics, 2020, 21, 1568-1580.	6.5	78

#	Article	IF	Citations
19	XG-PseU: an eXtreme Gradient Boosting based method for identifying pseudouridine sites. Molecular Genetics and Genomics, 2020, 295, 13-21.	2.1	61
20	Deciphering the high‐quality genome sequence of coriander that causes controversial feelings. Plant Biotechnology Journal, 2020, 18, 1444-1456.	8.3	56
21	Identifying Antioxidant Proteins by Combining Multiple Methods. Frontiers in Bioengineering and Biotechnology, 2020, 8, 858.	4.1	13
22	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
23	KNIndex: a comprehensive database of physicochemical properties for k-tuple nucleotides. Briefings in Bioinformatics, 2020, 22, .	6.5	10
24	iMRM: a platform for simultaneously identifying multiple kinds of RNA modifications. Bioinformatics, 2020, 36, 3336-3342.	4.1	122
25	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
26	RNAWRE: a resource of writers, readers and erasers of RNA modifications. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	3.0	15
27	DNA4mC-LIP: a linear integration method to identify N4-methylcytosine site in multiple species. Bioinformatics, 2020, 36, 3327-3335.	4.1	33
28	Genome-wide identification and analyses of the AHL gene family in cotton (Gossypium). BMC Genomics, 2020, 21, 69.	2.8	23
29	iRNA5hmC: The First Predictor to Identify RNA 5-Hydroxymethylcytosine Modifications Using Machine Learning. Frontiers in Bioengineering and Biotechnology, 2020, 8, 227.	4.1	26
30	Computational Identification of Small Interfering RNA Targets in SARS-CoV-2. Virologica Sinica, 2020, 35, 359-361.	3.0	45
31	Evaluation of different computational methods on 5-methylcytosine sites identification. Briefings in Bioinformatics, 2020, 21, 982-995.	6.5	115
32	Recent Advances of Computational Methods for Identifying Bacteriophage Virion Proteins. Protein and Peptide Letters, 2020, 27, 259-264.	0.9	12
33	Recent Development of Computational Predicting Bioluminescent Proteins. Current Pharmaceutical Design, 2020, 25, 4264-4273.	1.9	3
34	iATP: A Sequence Based Method for Identifying Anti-tubercular Peptides. Medicinal Chemistry, 2020, 16, 620-625.	1.5	43
35	Analysis and Comparison of RNA Pseudouridine Site Prediction Tools. Current Bioinformatics, 2020, 15, 279-286.	1.5	3
36	Recent Advancement in Predicting Subcellular Localization of Mycobacterial Protein with Machine Learning Methods. Medicinal Chemistry, 2020, 16, 605-619.	1.5	2

#	Article	IF	Citations
37	A Brief Survey for MicroRNA Precursor Identification Using Machine Learning Methods. Current Genomics, 2020, 21, 11-25.	1.6	3
38	iProEP: A Computational Predictor for Predicting Promoter. Molecular Therapy - Nucleic Acids, 2019, 17, 337-346.	5.1	125
39	iDNA6mA-Rice: A Computational Tool for Detecting N6-Methyladenine Sites in Rice. Frontiers in Genetics, 2019, 10, 793.	2.3	61
40	Recent Advances in Machine Learning Methods for Predicting Heat Shock Proteins. Current Drug Metabolism, 2019, 20, 224-228.	1.2	75
41	iRNA-m7G: Identifying N7-methylguanosine Sites by Fusing Multiple Features. Molecular Therapy - Nucleic Acids, 2019, 18, 269-274.	5.1	85
42	i6mA-Pred: identifying DNA N6-methyladenine sites in the rice genome. Bioinformatics, 2019, 35, 2796-2800.	4.1	186
43	iRNA-m2G: Identifying N2-methylguanosine Sites Based on Sequence-Derived Information. Molecular Therapy - Nucleic Acids, 2019, 18, 253-258.	5.1	35
44	iRNAD: a computational tool for identifying D modification sites in RNA sequence. Bioinformatics, 2019, 35, 4922-4929.	4.1	75
45	Combinatorial Pattern of Histone Modifications in Exon Skipping Event. Frontiers in Genetics, 2019, 10, 122.	2.3	5
46	iPhoPred: A Predictor for Identifying Phosphorylation Sites in Human Protein. IEEE Access, 2019, 7, 177517-177528.	4.2	23
47	Identify origin of replication in *Saccharomyces cerevisiae* using two-step feature selection technique. Bioinformatics, 2019, 35, 2075-2083.	4.1	172
48	Predicting protein structural classes for low-similarity sequences by evaluating different features. Knowledge-Based Systems, 2019, 163, 787-793.	7.1	194
49	iTerm-PseKNC: a sequence-based tool for predicting bacterial transcriptional terminators. Bioinformatics, 2019, 35, 1469-1477.	4.1	173
50	Nulliplex-branch, a TERMINAL FLOWER 1 ortholog, controls plant growth habit in cotton. Theoretical and Applied Genetics, 2019, 132, 97-112.	3.6	24
51	iDNA6mA-PseKNC: Identifying DNA N6-methyladenosine sites by incorporating nucleotide physicochemical properties into PseKNC. Genomics, 2019, 111, 96-102.	2.9	234
52	Identifying Sigma70 Promoters with Novel Pseudo Nucleotide Composition. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1316-1321.	3.0	132
53	A Survey for Predicting Enzyme Family Classes Using Machine Learning Methods. Current Drug Targets, 2019, 20, 540-550.	2.1	35
54	Identification of hormone binding proteins based on machine learning methods. Mathematical Biosciences and Engineering, 2019, 16, 2466-2480.	1.9	144

#	Article	IF	Citations
55	An Overlooked Paleotetraploidization in Cucurbitaceae. Molecular Biology and Evolution, 2018, 35, 16-26.	8.9	89
56	Classifying Included and Excluded Exons in Exon Skipping Event Using Histone Modifications. Frontiers in Genetics, 2018, 9, 433.	2.3	23
57	iRNA(m6A)-PseDNC: Identifying N6-methyladenosine sites using pseudo dinucleotide composition. Analytical Biochemistry, 2018, 561-562, 59-65.	2.4	162
58	iRNA-3typeA: Identifying Three Types of Modification at RNAâ€™s Adenosine Sites. Molecular Therapy - Nucleic Acids, 2018, 11, 468-474.	5.1	173
59	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
60	iLoc-lncRNA: predict the subcellular location of lncRNAs by incorporating octamer composition into general PseKNC. Bioinformatics, 2018, 34, 4196-4204.	4.1	227
61	Identifying RNA N6-Methyladenosine Sites in Escherichia coli Genome. Frontiers in Microbiology, 2018, 9, 955.	3.5	24
62	Prediction of bacteriophage proteins located in the host cell using hybrid features. Chemometrics and Intelligent Laboratory Systems, 2018, 180, 64-69.	3.5	28
63	iRNA-2OM: A Sequence-Based Predictor for Identifying 2â€²-O-Methylation Sites in<i>Homo sapiens</i>. Journal of Computational Biology, 2018, 25, 1266-1277.	1.6	137
64	A genome-wide analysis of SWEET gene family in cotton and their expressions under different stresses. Journal of Cotton Research, 2018, 1, .	2.5	19
65	A Brief Survey of Machine Learning Application in Cancerlectin Identification. Current Gene Therapy, 2018, 18, 257-267.	2.0	24
66	Pro54DB: a database for experimentally verified sigma-54 promoters. Bioinformatics, 2017, 33, 467-469.	4.1	91
67	MethyRNA: a web server for identification of N⁶-methyladenosine sites. Journal of Biomolecular Structure and Dynamics, 2017, 35, 683-687.	3.5	124
68	Detecting N6-methyladenosine sites from RNA transcriptomes using ensemble Support Vector Machines. Scientific Reports, 2017, 7, 40242.	3.3	123
69	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.	5.1	259
70	Hierarchically Aligning 10 Legume Genomes Establishes a Family-Level Genomics Platform. Plant Physiology, 2017, 174, 284-300.	4.8	112
71	iDNA4mC: identifying DNA N4-methylcytosine sites based on nucleotide chemical properties. Bioinformatics, 2017, 33, 3518-3523.	4.1	256
72	AOD: the antioxidant protein database. Scientific Reports, 2017, 7, 7449.	3.3	49

#	Article	IF	Citations
73	Predicting the Organelle Location of Noncoding RNAs Using Pseudo Nucleotide Compositions. Interdisciplinary Sciences, Computational Life Sciences, 2017, 9, 540-544.	3.6	19
74	Recent Advances in Conotoxin Classification by Using Machine Learning Methods. Molecules, 2017, 22, 1057.	3.8	53
75	Recent Advances in Identification of RNA Modifications. Non-coding RNA, 2017, 3, 1.	2.6	20
76	IonchanPred 2.0: A Tool to Predict Ion Channels and Their Types. International Journal of Molecular Sciences, 2017, 18, 1838.	4.1	59
77	iRNA-AI: identifying the adenosine to inosine editing sites in RNA sequences. Oncotarget, 2017, 8, 4208-4217.	1.8	209
78	Sequence-based predictive modeling to identify cancerlectins. Oncotarget, 2017, 8, 28169-28175.	1.8	95
79	iOri-Human: identify human origin of replication by incorporating dinucleotide physicochemical properties into pseudo nucleotide composition. Oncotarget, 2016, 7, 69783-69793.	1.8	166
80	iACP: a sequence-based tool for identifying anticancer peptides. Oncotarget, 2016, 7, 16895-16909.	1.8	354
81	Identification of Bacterial Cell Wall Lyases via Pseudo Amino Acid Composition. BioMed Research International, 2016, 2016, 1-8.	1.9	99
82	Identification of Secretory Proteins in<i>Mycobacterium tuberculosis</i>Using Pseudo Amino Acid Composition. BioMed Research International, 2016, 2016, 1-7.	1.9	118
83	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, 2893-2900.	2.9	19
84	PAI: Predicting adenosine to inosine editing sites by using pseudo nucleotide compositions. Scientific Reports, 2016, 6, 35123.	3.3	32
85	Identification of apolipoprotein using feature selection technique. Scientific Reports, 2016, 6, 30441.	3.3	36
86	Identifying 2â€²-O-methylationation sites by integrating nucleotide chemical properties and nucleotide compositions. Genomics, 2016, 107, 255-258.	2.9	55
87	PHYPred: a tool for identifying bacteriophage enzymes and hydrolases. Virologica Sinica, 2016, 31, 350-352.	3.0	47
88	Identifying N 6-methyladenosine sites in the Arabidopsis thaliana transcriptome. Molecular Genetics and Genomics, 2016, 291, 2225-2229.	2.1	58
89	Identifying RNA 5-methylcytosine sites via pseudo nucleotide compositions. Molecular BioSystems, 2016, 12, 3307-3311.	2.9	48
90	RAMPred: identifying the N1-methyladenosine sites in eukaryotic transcriptomes. Scientific Reports, 2016, 6, 31080.	3.3	50

#	Article	IF	Citations
91	Prediction of phosphothreonine sites in human proteins by fusing different features. Scientific Reports, 2016, 6, 34817.	3.3	48
92	Prediction of cell-penetrating peptides with feature selection techniques. Biochemical and Biophysical Research Communications, 2016, 477, 150-154.	2.1	87
93	Identification of immunoglobulins using Chou's pseudo amino acid composition with feature selection technique. Molecular BioSystems, 2016, 12, 1269-1275.	2.9	155
94	Predicting bacteriophage proteins located in host cell with feature selection technique. Computers in Biology and Medicine, 2016, 71, 156-161.	7.0	12
95	Using deformation energy to analyze nucleosome positioning in genomes. Genomics, 2016, 107, 69-75.	2.9	104
96	Identifying Antioxidant Proteins by Using Optimal Dipeptide Compositions. Interdisciplinary Sciences, Computational Life Sciences, 2016, 8, 186-191.	3.6	42
97	iRNA-PseU: Identifying RNA pseudouridine sites. Molecular Therapy - Nucleic Acids, 2016, 5, e332.	5.1	172
98	Predicting Human Enzyme Family Classes by Using Pseudo Amino Acid Composition. Current Proteomics, 2016, 13, 99-104.	0.3	11
99	Identification and analysis of the N6-methyladenosine in the Saccharomyces cerevisiae transcriptome. Scientific Reports, 2015, 5, 13859.	3.3	96
100	The pattern of DNA cleavage intensity around indels. Scientific Reports, 2015, 5, 8333.	3.3	11
101	Predicting cancerlectins by the optimal g-gap dipeptides. Scientific Reports, 2015, 5, 16964.	3.3	50
102	Application of Machine Learning Method in Genomics and Proteomics. Scientific World Journal, The, 2015, 2015, 1-2.	2.1	1
103	Briefing in Application of Machine Learning Methods in Ion Channel Prediction. Scientific World Journal, The, 2015, 2015, 1-7.	2.1	5
104	iORI-PseKNC: A predictor for identifying origin of replication with pseudo k-tuple nucleotide composition. Chemometrics and Intelligent Laboratory Systems, 2015, 141, 100-106.	3.5	76
105	Genetic mapping of the nulliplex-branch gene (gb_nb1) in cotton using next-generation sequencing. Theoretical and Applied Genetics, 2015, 128, 539-547.	3.6	63
106	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
107	PseKNC-General: a cross-platform package for generating various modes of pseudo nucleotide compositions. Bioinformatics, 2015, 31, 119-120.	4.1	210
108	Pseudo nucleotide composition or PseKNC: an effective formulation for analyzing genomic sequences. Molecular BioSystems, 2015, 11, 2620-2634.	2.9	289

#	Article	IF	Citations
109	Benchmark data for identifying N 6 -methyladenosine sites in the Saccharomyces cerevisiae genome. Data in Brief, 2015, 5, 376-378.	1.0	9
110	iRNA-Methyl: Identifying N6-methyladenosine sites using pseudo nucleotide composition. Analytical Biochemistry, 2015, 490, 26-33.	2.4	350
111	iSS-PseDNC: Identifying Splicing Sites Using Pseudo Dinucleotide Composition. BioMed Research International, 2014, 2014, 1-12.	1.9	144
112	iPro54-PseKNC: a sequence-based predictor for identifying sigma-54 promoters in prokaryote with pseudo k-tuple nucleotide composition. Nucleic Acids Research, 2014, 42, 12961-12972.	14.5	467
113	Predicting the Types of J-Proteins Using Clustered Amino Acids. BioMed Research International, 2014, 2014, 1-8.	1.9	30
114	Identifying the Subfamilies of Voltage-Gated Potassium Channels Using Feature Selection Technique. International Journal of Molecular Sciences, 2014, 15, 12940-12951.	4.1	30
115	Sequence analysis of origins of replication in the Saccharomyces cerevisiae genomes. Frontiers in Microbiology, 2014, 5, 574.	3.5	20
116	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
117	iTIS-PseTNC: A sequence-based predictor for identifying translation initiation site in human genes using pseudo trinucleotide composition. Analytical Biochemistry, 2014, 462, 76-83.	2.4	245
118	iNuc-PseKNC: a sequence-based predictor for predicting nucleosome positioning in genomes with pseudo k-tuple nucleotide composition. Bioinformatics, 2014, 30, 1522-1529.	4.1	349
119	Predicting peroxidase subcellular location by hybridizing different descriptors of Chou' pseudo amino acid patterns. Analytical Biochemistry, 2014, 458, 14-19.	2.4	83
120	Exon skipping event prediction based on histone modifications. Interdisciplinary Sciences, Computational Life Sciences, 2014, 6, 241-249.	3.6	10
121	Prediction of protein structural classes based on feature selection technique. Interdisciplinary Sciences, Computational Life Sciences, 2014, 6, 235-240.	3.6	32
122	Identification of bacteriophage virion proteins by the ANOVA feature selection and analysis. Molecular BioSystems, 2014, 10, 2229-2235.	2.9	147
123	Prediction of CpG island methylation status by integrating DNA physicochemical properties. Genomics, 2014, 104, 229-233.	2.9	33
124	PseKNC: A flexible web server for generating pseudo K-tuple nucleotide composition. Analytical Biochemistry, 2014, 456, 53-60.	2.4	409
125	The development of specific <scp>SNP</scp> markers for chromosome 14 in cotton using next-generation sequencing. Plant Breeding, 2014, 133, 256-261.	1.9	10
126	DNA Physical Parameters Modulate Nucleosome Positioning in the Saccharomyces cerevisiae Genome. Current Bioinformatics, 2014, 9, 188-193.	1.5	6

#	Article	IF	Citations
127	A similarity distance of diversity measure for discriminating mesophilic and thermophilic proteins. Amino Acids, 2013, 44, 573-580.	2.7	31
128	Using Over-Represented Tetrapeptides to Predict Protein Submitochondria Locations. Acta Biotheoretica, 2013, 61, 259-268.	1.5	73
129	iHSP-PseRAAAC: Identifying the heat shock protein families using pseudo reduced amino acid alphabet composition. Analytical Biochemistry, 2013, 442, 118-125.	2.4	287
130	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
131	Prediction of Golgi-resident protein types by using feature selection technique. Chemometrics and Intelligent Laboratory Systems, 2013, 124, 9-13.	3.5	90
132	iRSpot-PseDNC: identify recombination spots with pseudo dinucleotide composition. Nucleic Acids Research, 2013, 41, e68-e68.	14.5	562
133	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
134	AcalPred: A Sequence-Based Tool for Discriminating between Acidic and Alkaline Enzymes. PLoS ONE, 2013, 8, e75726.	2.5	92
135	Naïve Bayes Classifier with Feature Selection to Identify Phage Virion Proteins. Computational and Mathematical Methods in Medicine, 2013, 2013, 1-6.	1.3	145
136	Identification of Antioxidants from Sequence Information Using Naïve Bayes. Computational and Mathematical Methods in Medicine, 2013, 2013, 1-5.	1.3	102
137	Identification of mycobacterial membrane proteins and their types using over-represented tripeptide compositions. Journal of Proteomics, 2012, 77, 321-328.	2.4	90
138	The prediction of protein structural class using averaged chemical shifts. Journal of Biomolecular Structure and Dynamics, 2012, 29, 1147-1153.	3.5	58
139	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
140	Repeated polyploidization of Gossypium genomes and the evolution of spinnable cotton fibres. Nature, 2012, 492, 423-427.	27.8	1,204
141	iNuc-PhysChem: A Sequence-Based Predictor for Identifying Nucleosomes via Physicochemical Properties. PLoS ONE, 2012, 7, e47843.	2.5	181
142	Prediction of ketoacyl synthase family using reduced amino acid alphabets. Journal of Industrial Microbiology and Biotechnology, 2012, 39, 579-584.	3.0	31
143	Prediction of replication origins by calculating DNA structural properties. FEBS Letters, 2012, 586, 934-938.	2.8	53
144	Prediction of thermophilic proteins using feature selection technique. Journal of Microbiological Methods, 2011, 84, 67-70.	1.6	89

#	Article	IF	Citations
145	A Novel Method for Lysine Acetylation Sites Prediction. , 2011, , .		0
146	The organization of nucleosomes around splice sites. Nucleic Acids Research, 2010, 38, 2788-2798.	14.5	61
147	Prediction of midbody, centrosome and kinetochore proteins based on gene ontology information. Biochemical and Biophysical Research Communications, 2010, 401, 382-384.	2.1	33
148	Classification of antimicrobial peptide using diversity measure with quadratic discriminant analysis. Journal of Microbiological Methods, 2009, 78, 94-96.	1.6	22
149	Recognition of DNase I hypersensitive sites in multiple cell lines. International Journal of Bioinformatics Research and Applications, 2009, 5, 378.	0.2	2
150	Nucleosome Positioning and RNA Splicing*. Progress in Biochemistry and Biophysics, 2009, 36, 1035-1040.	0.3	0
151	Using Chouâ€™s pseudo amino acid composition to predict protein quaternary structure: a sequence-segmented PseAAC approach. Amino Acids, 2008, 35, 591-598.	2.7	87