Pengmian Feng

List of Publications by Year
in descending order

49 papers	4,609 citations	159585 30 h-index	197818 49 g-index
49 all docs	49 docs citations	49 times ranked	2057 citing authors

#	Article	IF	Citations
1	iRSpot-PseDNC: identify recombination spots with pseudo dinucleotide composition. Nucleic Acids Research, 2013, 41, e68-e68.	14.5	562
2	iACP: a sequence-based tool for identifying anticancer peptides. Oncotarget, 2016, 7, 16895-16909.	1.8	354
3	iRNA-Methyl: Identifying N6-methyladenosine sites using pseudo nucleotide composition. Analytical Biochemistry, 2015, 490, 26-33.	2.4	350
4	iHSP-PseRAAAC: Identifying the heat shock protein families using pseudo reduced amino acid alphabet composition. Analytical Biochemistry, 2013, 442, 118-125.	2.4	287
5	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
6	iDNA4mC: identifying DNA N4-methylcytosine sites based on nucleotide chemical properties. Bioinformatics, 2017, 33, 3518-3523.	4.1	256
7	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
8	iDNA6mA-PseKNC: Identifying DNA N6-methyladenosine sites by incorporating nucleotide physicochemical properties into PseKNC. Genomics, 2019, 111, 96-102.	2.9	234
9	iRNA-AI: identifying the adenosine to inosine editing sites in RNA sequences. Oncotarget, 2017, 8, 4208-4217.	1.8	209
10	iNuc-PhysChem: A Sequence-Based Predictor for Identifying Nucleosomes via Physicochemical Properties. PLoS ONE, 2012, 7, e47843.	2.5	181
11	iRNA-3typeA: Identifying Three Types of Modification at RNAâ€™s Adenosine Sites. Molecular Therapy - Nucleic Acids, 2018, 11, 468-474.	5.1	173
12	Identification of bacteriophage virion proteins by the ANOVA feature selection and analysis. Molecular BioSystems, 2014, 10, 2229-2235.	2.9	147
13	NaÃ¯ve Bayes Classifier with Feature Selection to Identify Phage Virion Proteins. Computational and Mathematical Methods in Medicine, 2013, 2013, 1-6.	1.3	145
14	Using deformation energy to analyze nucleosome positioning in genomes. Genomics, 2016, 107, 69-75.	2.9	104
15	Identification of Antioxidants from Sequence Information Using NaÃ¯ve Bayes. Computational and Mathematical Methods in Medicine, 2013, 2013, 1-5.	1.3	102
16	iRNA-m7G: Identifying N7-methylguanosine Sites by Fusing Multiple Features. Molecular Therapy - Nucleic Acids, 2019, 18, 269-274.	5.1	85
17	Recent Advances in Machine Learning Methods for Predicting Heat Shock Proteins. Current Drug Metabolism, 2019, 20, 224-228.	1.2	75
18	Identifying N 6-methyladenosine sites in the Arabidopsis thaliana transcriptome. Molecular Genetics and Genomics, 2016, 291, 2225-2229.	2.1	58

#	Article	IF	Citations
19	Identifying 2â€²-O-methylationation sites by integrating nucleotide chemical properties and nucleotide compositions. Genomics, 2016, 107, 255-258.	2.9	55
20	Prediction of replication origins by calculating DNA structural properties. FEBS Letters, 2012, 586, 934-938.	2.8	53
21	RAMPred: identifying the N1-methyladenosine sites in eukaryotic transcriptomes. Scientific Reports, 2016, 6, 31080.	3.3	50
22	AOD: the antioxidant protein database. Scientific Reports, 2017, 7, 7449.	3.3	49
23	Identifying RNA 5-methylcytosine sites via pseudo nucleotide compositions. Molecular BioSystems, 2016, 12, 3307-3311.	2.9	48
24	PHYPred: a tool for identifying bacteriophage enzymes and hydrolases. Virologica Sinica, 2016, 31, 350-352.	3.0	47
25	Computational Identification of Small Interfering RNA Targets in SARS-CoV-2. Virologica Sinica, 2020, 35, 359-361.	3.0	45
26	iATP: A Sequence Based Method for Identifying Anti-tubercular Peptides. Medicinal Chemistry, 2020, 16, 620-625.	1.5	43
27	Identifying Antioxidant Proteins by Using Optimal Dipeptide Compositions. Interdisciplinary Sciences, Computational Life Sciences, 2016, 8, 186-191.	3.6	42
28	Iterative feature representation algorithm to improve the predictive performance of N7-methylguanosine sites. Briefings in Bioinformatics, 2021, 22, .	6.5	35
29	Prediction of CpG island methylation status by integrating DNA physicochemical properties. Genomics, 2014, 104, 229-233.	2.9	33
30	PAI: Predicting adenosine to inosine editing sites by using pseudo nucleotide compositions. Scientific Reports, 2016, 6, 35123.	3.3	32
31	Prediction of ketoacyl synthase family using reduced amino acid alphabets. Journal of Industrial Microbiology and Biotechnology, 2012, 39, 579-584.	3.0	31
32	Predicting the Types of J-Proteins Using Clustered Amino Acids. BioMed Research International, 2014, 2014, 1-8.	1.9	30
33	Prediction of DNase I Hypersensitive Sites by Using Pseudo Nucleotide Compositions. Scientific World Journal, The, 2014, 2014, 1-4.	2.1	26
34	Identifying RNA N6-Methyladenosine Sites in Escherichia coli Genome. Frontiers in Microbiology, 2018, 9, 955.	3.5	24
35	Classifying Included and Excluded Exons in Exon Skipping Event Using Histone Modifications. Frontiers in Genetics, 2018, 9, 433.	2.3	23
36	Predicting the Organelle Location of Noncoding RNAs Using Pseudo Nucleotide Compositions. Interdisciplinary Sciences, Computational Life Sciences, 2017, 9, 540-544.	3.6	19

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37	Identification of D Modification Sites by Integrating Heterogeneous Features in Saccharomyces cerevisiae. Molecules, 2019, 24, 380.	3.8	15
38	RNAWRE: a resource of writers, readers and erasers of RNA modifications. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	3.0	15
39	iRNA-m5U: A sequence based predictor for identifying 5-methyluridine modification sites in Saccharomyces cerevisiae. Methods, 2022, 203, 28-31.	3.8	11
40	Exon skipping event prediction based on histone modifications. Interdisciplinary Sciences, Computational Life Sciences, 2014, 6, 241-249.	3.6	10
41	Predicting Antimicrobial Peptides by Using Increment of Diversity with Quadratic Discriminant Analysis Method. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1309-1312.	3.0	10
42	Benchmark data for identifying N 6 -methyladenosine sites in the Saccharomyces cerevisiae genome. Data in Brief, 2015, 5, 376-378.	1.0	9
43	Sequence based prediction of pattern recognition receptors by using feature selection technique. International Journal of Biological Macromolecules, 2020, 162, 931-934.	7.5	7
44	Recent Advances in Computational Methods for Identifying Anticancer Peptides. Current Drug Targets, 2019, 20, 481-487.	2.1	6
45	DNA Physical Parameters Modulate Nucleosome Positioning in the Saccharomyces cerevisiae Genome. Current Bioinformatics, 2014, 9, 188-193.	1.5	6
46	Recent Advances on Antioxidant Identification Based on Machine Learning Methods. Current Drug Metabolism, 2020, 21, 804-809.	1.2	5
47	Classifying the superfamily of small heat shock proteins by using g-gap dipeptide compositions. International Journal of Biological Macromolecules, 2021, 167, 1575-1578.	7.5	2
48	Comparison and Analysis of Computational Methods for Identifying N6-Methyladenosine Sites in Saccharomyces cerevisiae. Current Pharmaceutical Design, 2021, 27, 1219-1229.	1.9	1
49	Identification of Pathologic and Prognostic Genes in Prostate Cancer Based on Database Mining. Frontiers in Genetics, 2022, 13, 854531.	2.3	1