Pengmian Feng

List of Publications by Year
in descending order

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49

papers

4,609

citations

159585

30

h-index

197818

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g-index

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all docs

49

docs citations

49

times ranked

2057

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	Identification of Pathologic and Prognostic Genes in Prostate Cancer Based on Database Mining. Frontiers in Genetics, 2022, 13, 854531.	2.3	1
3	Iterative feature representation algorithm to improve the predictive performance of N7-methylguanosine sites. Briefings in Bioinformatics, 2021, 22, .	6.5	35
4	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
5	Comparison and Analysis of Computational Methods for Identifying N6-Methyladenosine Sites in Saccharomyces cerevisiae. Current Pharmaceutical Design, 2021, 27, 1219-1229.	1.9	1
6	Sequence based prediction of pattern recognition receptors by using feature selection technique. International Journal of Biological Macromolecules, 2020, 162, 931-934.	7.5	7
7	RNAWRE: a resource of writers, readers and erasers of RNA modifications. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	3.0	15
8	Computational Identification of Small Interfering RNA Targets in SARS-CoV-2. Virologica Sinica, 2020, 35, 359-361.	3.0	45
9	Recent Advances on Antioxidant Identification Based on Machine Learning Methods. Current Drug Metabolism, 2020, 21, 804-809.	1.2	5
10	iATP: A Sequence Based Method for Identifying Anti-tubercular Peptides. Medicinal Chemistry, 2020, 16, 620-625.	1.5	43
11	Recent Advances in Machine Learning Methods for Predicting Heat Shock Proteins. Current Drug Metabolism, 2019, 20, 224-228.	1.2	75
12	iRNA-m7G: Identifying N7-methylguanosine Sites by Fusing Multiple Features. Molecular Therapy - Nucleic Acids, 2019, 18, 269-274.	5.1	85
13	Identification of D Modification Sites by Integrating Heterogeneous Features in Saccharomyces cerevisiae. Molecules, 2019, 24, 380.	3.8	15
14	iDNA6mA-PseKNC: Identifying DNA N6-methyladenosine sites by incorporating nucleotide physicochemical properties into PseKNC. Genomics, 2019, 111, 96-102.	2.9	234
15	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
16	Recent Advances in Computational Methods for Identifying Anticancer Peptides. Current Drug Targets, 2019, 20, 481-487.	2.1	6
17	Classifying Included and Excluded Exons in Exon Skipping Event Using Histone Modifications. Frontiers in Genetics, 2018, 9, 433.	2.3	23
18	iRNA-3typeA: Identifying Three Types of Modification at RNAâ€™s Adenosine Sites. Molecular Therapy - Nucleic Acids, 2018, 11, 468-474.	5.1	173

#	ARTICLE	IF	CITATIONS
19	Identifying RNA N6-Methyladenosine Sites in Escherichia coli Genome. Frontiers in Microbiology, 2018, 9, 955.	3.5	24
20	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
21	iDNA4mC: identifying DNA N4-methylcytosine sites based on nucleotide chemical properties. Bioinformatics, 2017, 33, 3518-3523.	4.1	256
22	AOD: the antioxidant protein database. Scientific Reports, 2017, 7, 7449.	3.3	49
23	Predicting the Organelle Location of Noncoding RNAs Using Pseudo Nucleotide Compositions. Interdisciplinary Sciences, Computational Life Sciences, 2017, 9, 540-544.	3.6	19
24	iRNA-AI: identifying the adenosine to inosine editing sites in RNA sequences. Oncotarget, 2017, 8, 4208-4217.	1.8	209
25	iACP: a sequence-based tool for identifying anticancer peptides. Oncotarget, 2016, 7, 16895-16909.	1.8	354
26	PAI: Predicting adenosine to inosine editing sites by using pseudo nucleotide compositions. Scientific Reports, 2016, 6, 35123.	3.3	32
27	Identifying 2â€²-O-methylationation sites by integrating nucleotide chemical properties and nucleotide compositions. Genomics, 2016, 107, 255-258.	2.9	55
28	PHYPred: a tool for identifying bacteriophage enzymes and hydrolases. Virologica Sinica, 2016, 31, 350-352.	3.0	47
29	Identifying N 6-methyladenosine sites in the Arabidopsis thaliana transcriptome. Molecular Genetics and Genomics, 2016, 291, 2225-2229.	2.1	58
30	Identifying RNA 5-methylcytosine sites via pseudo nucleotide compositions. Molecular BioSystems, 2016, 12, 3307-3311.	2.9	48
31	RAMPred: identifying the N1-methyladenosine sites in eukaryotic transcriptomes. Scientific Reports, 2016, 6, 31080.	3.3	50
32	Using deformation energy to analyze nucleosome positioning in genomes. Genomics, 2016, 107, 69-75.	2.9	104
33	Identifying Antioxidant Proteins by Using Optimal Dipeptide Compositions. Interdisciplinary Sciences, Computational Life Sciences, 2016, 8, 186-191.	3.6	42
34	Benchmark data for identifying N 6 -methyladenosine sites in the Saccharomyces cerevisiae genome. Data in Brief, 2015, 5, 376-378.	1.0	9
35	iRNA-Methyl: Identifying N6-methyladenosine sites using pseudo nucleotide composition. Analytical Biochemistry, 2015, 490, 26-33.	2.4	350
36	Prediction of DNase I Hypersensitive Sites by Using Pseudo Nucleotide Compositions. Scientific World Journal, The, 2014, 2014, 1-4.	2.1	26

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37	Predicting the Types of J-Proteins Using Clustered Amino Acids. BioMed Research International, 2014, 2014, 1-8.	1.9	30
38	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
39	Exon skipping event prediction based on histone modifications. Interdisciplinary Sciences, Computational Life Sciences, 2014, 6, 241-249.	3.6	10
40	Identification of bacteriophage virion proteins by the ANOVA feature selection and analysis. Molecular BioSystems, 2014, 10, 2229-2235.	2.9	147
41	Prediction of CpG island methylation status by integrating DNA physicochemical properties. Genomics, 2014, 104, 229-233.	2.9	33
42	DNA Physical Parameters Modulate Nucleosome Positioning in the Saccharomyces cerevisiae Genome. Current Bioinformatics, 2014, 9, 188-193.	1.5	6
43	iHSP-PseRAAAC: Identifying the heat shock protein families using pseudo reduced amino acid alphabet composition. Analytical Biochemistry, 2013, 442, 118-125.	2.4	287
44	iRSpot-PseDNC: identify recombination spots with pseudo dinucleotide composition. Nucleic Acids Research, 2013, 41, e68-e68.	14.5	562
45	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
46	Identification of Antioxidants from Sequence Information Using NaÃ¯ve Bayes. Computational and Mathematical Methods in Medicine, 2013, 2013, 1-5.	1.3	102
47	iNuc-PhysChem: A Sequence-Based Predictor for Identifying Nucleosomes via Physicochemical Properties. PLoS ONE, 2012, 7, e47843.	2.5	181
48	Prediction of ketoacyl synthase family using reduced amino acid alphabets. Journal of Industrial Microbiology and Biotechnology, 2012, 39, 579-584.	3.0	31
49	Prediction of replication origins by calculating DNA structural properties. FEBS Letters, 2012, 586, 934-938.	2.8	53