

# Pengmian Feng

## List of Publications by Year in descending order

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49  
papers

4,609  
citations

159358

30  
h-index

197535

49  
g-index

49  
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 <i>Saccharomyces cerevisiae</i> . <i>Methods</i> , 2022, 203, 28-31.	1.9	11
2	Identification of Pathologic and Prognostic Genes in Prostate Cancer Based on Database Mining. <i>Frontiers in Genetics</i> , 2022, 13, 854531.	1.1	1
3	Iterative feature representation algorithm to improve the predictive performance of N7-methylguanosine sites. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	35
4	Classifying the superfamily of small heat shock proteins by using g-gap dipeptide compositions. <i>International Journal of Biological Macromolecules</i> , 2021, 167, 1575-1578.	3.6	2
5	Comparison and Analysis of Computational Methods for Identifying N6-Methyladenosine Sites in <i>Saccharomyces cerevisiae</i> . <i>Current Pharmaceutical Design</i> , 2021, 27, 1219-1229.	0.9	1
6	Sequence based prediction of pattern recognition receptors by using feature selection technique. <i>International Journal of Biological Macromolecules</i> , 2020, 162, 931-934.	3.6	7
7	RNAWRE: a resource of writers, readers and erasers of RNA modifications. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	15
8	Computational Identification of Small Interfering RNA Targets in SARS-CoV-2. <i>Virologica Sinica</i> , 2020, 35, 359-361.	1.2	45
9	Recent Advances on Antioxidant Identification Based on Machine Learning Methods. <i>Current Drug Metabolism</i> , 2020, 21, 804-809.	0.7	5
10	iATP: A Sequence Based Method for Identifying Anti-tubercular Peptides. <i>Medicinal Chemistry</i> , 2020, 16, 620-625.	0.7	43
11	Recent Advances in Machine Learning Methods for Predicting Heat Shock Proteins. <i>Current Drug Metabolism</i> , 2019, 20, 224-228.	0.7	75
12	iRNA-m7G: Identifying N7-methylguanosine Sites by Fusing Multiple Features. <i>Molecular Therapy - Nucleic Acids</i> , 2019, 18, 269-274.	2.3	85
13	Identification of D Modification Sites by Integrating Heterogeneous Features in <i>Saccharomyces cerevisiae</i> . <i>Molecules</i> , 2019, 24, 380.	1.7	15
14	iDNA6mA-PseKNC: Identifying DNA N6-methyladenosine sites by incorporating nucleotide physicochemical properties into PseKNC. <i>Genomics</i> , 2019, 111, 96-102.	1.3	234
15	Predicting Antimicrobial Peptides by Using Increment of Diversity with Quadratic Discriminant Analysis Method. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1309-1312.	1.9	10
16	Recent Advances in Computational Methods for Identifying Anticancer Peptides. <i>Current Drug Targets</i> , 2019, 20, 481-487.	1.0	6
17	Classifying Included and Excluded Exons in Exon Skipping Event Using Histone Modifications. <i>Frontiers in Genetics</i> , 2018, 9, 433.	1.1	23
18	iRNA-3typeA: Identifying Three Types of Modification at RNA's Adenosine Sites. <i>Molecular Therapy - Nucleic Acids</i> , 2018, 11, 468-474.	2.3	173

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19	Identifying RNA N6-Methyladenosine Sites in Escherichia coli Genome. <i>Frontiers in Microbiology</i> , 2018, 9, 955.	1.5	24
20	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.	2.3	259
21	iDNA4mC: Identifying DNA N4-methylcytosine sites based on nucleotide chemical properties. <i>Bioinformatics</i> , 2017, 33, 3518-3523.	1.8	256
22	AOD: the antioxidant protein database. <i>Scientific Reports</i> , 2017, 7, 7449.	1.6	49
23	Predicting the Organelle Location of Noncoding RNAs Using Pseudo Nucleotide Compositions. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2017, 9, 540-544.	2.2	19
24	iRNA-AI: identifying the adenosine to inosine editing sites in RNA sequences. <i>Oncotarget</i> , 2017, 8, 4208-4217.	0.8	209
25	iACP: a sequence-based tool for identifying anticancer peptides. <i>Oncotarget</i> , 2016, 7, 16895-16909.	0.8	354
26	PAI: Predicting adenosine to inosine editing sites by using pseudo nucleotide compositions. <i>Scientific Reports</i> , 2016, 6, 35123.	1.6	32
27	Identifying 2â€²-O-methylation sites by integrating nucleotide chemical properties and nucleotide compositions. <i>Genomics</i> , 2016, 107, 255-258.	1.3	55
28	PHYPred: a tool for identifying bacteriophage enzymes and hydrolases. <i>Virologica Sinica</i> , 2016, 31, 350-352.	1.2	47
29	Identifying N 6-methyladenosine sites in the Arabidopsis thaliana transcriptome. <i>Molecular Genetics and Genomics</i> , 2016, 291, 2225-2229.	1.0	58
30	Identifying RNA 5-methylcytosine sites via pseudo nucleotide compositions. <i>Molecular BioSystems</i> , 2016, 12, 3307-3311.	2.9	48
31	RAMPred: identifying the N1-methyladenosine sites in eukaryotic transcriptomes. <i>Scientific Reports</i> , 2016, 6, 31080.	1.6	50
32	Using deformation energy to analyze nucleosome positioning in genomes. <i>Genomics</i> , 2016, 107, 69-75.	1.3	104
33	Identifying Antioxidant Proteins by Using Optimal Dipeptide Compositions. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2016, 8, 186-191.	2.2	42
34	Benchmark data for identifying N 6 -methyladenosine sites in the Saccharomyces cerevisiae genome. <i>Data in Brief</i> , 2015, 5, 376-378.	0.5	9
35	iRNA-Methyl: Identifying N6-methyladenosine sites using pseudo nucleotide composition. <i>Analytical Biochemistry</i> , 2015, 490, 26-33.	1.1	350
36	Prediction of DNase I Hypersensitive Sites by Using Pseudo Nucleotide Compositions. <i>Scientific World Journal, The</i> , 2014, 2014, 1-4.	0.8	26

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37	Predicting the Types of J-Proteins Using Clustered Amino Acids. <i>BioMed Research International</i> , 2014, 2014, 1-8.	0.9	30
38	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.	1.1	245
39	Exon skipping event prediction based on histone modifications. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2014, 6, 241-249.	2.2	10
40	Identification of bacteriophage virion proteins by the ANOVA feature selection and analysis. <i>Molecular BioSystems</i> , 2014, 10, 2229-2235.	2.9	147
41	Prediction of CpG island methylation status by integrating DNA physicochemical properties. <i>Genomics</i> , 2014, 104, 229-233.	1.3	33
42	DNA Physical Parameters Modulate Nucleosome Positioning in the <i>Saccharomyces cerevisiae</i> Genome. <i>Current Bioinformatics</i> , 2014, 9, 188-193.	0.7	6
43	iHSP-PseRAAAC: Identifying the heat shock protein families using pseudo reduced amino acid alphabet composition. <i>Analytical Biochemistry</i> , 2013, 442, 118-125.	1.1	287
44	iRSpot-PseDNC: identify recombination spots with pseudo dinucleotide composition. <i>Nucleic Acids Research</i> , 2013, 41, e68-e68.	6.5	562
45	Na <sup>+</sup> -ve Bayes Classifier with Feature Selection to Identify Phage Virion Proteins. <i>Computational and Mathematical Methods in Medicine</i> , 2013, 2013, 1-6.	0.7	145
46	Identification of Antioxidants from Sequence Information Using Na <sup>+</sup> -ve Bayes. <i>Computational and Mathematical Methods in Medicine</i> , 2013, 2013, 1-5.	0.7	102
47	iNuc-PhysChem: A Sequence-Based Predictor for Identifying Nucleosomes via Physicochemical Properties. <i>PLoS ONE</i> , 2012, 7, e47843.	1.1	181
48	Prediction of ketoacyl synthase family using reduced amino acid alphabets. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2012, 39, 579-584.	1.4	31
49	Prediction of replication origins by calculating DNA structural properties. <i>FEBS Letters</i> , 2012, 586, 934-938.	1.3	53