

# Pengmian Feng

## List of Publications by Year in descending order

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Version: 2024-02-01

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  | iRSpot-PseDNC: identify recombination spots with pseudo dinucleotide composition. <i>Nucleic Acids Research</i> , 2013, 41, e68-e68.   | 6.5 | 562       |
| 2  | iACP: a sequence-based tool for identifying anticancer peptides. <i>Oncotarget</i> , 2016, 7, 16895-16909.   | 0.8 | 354       |
| 3  | iRNA-Methyl: Identifying N6-methyladenosine sites using pseudo nucleotide composition. <i>Analytical Biochemistry</i> , 2015, 490, 26-33.  | 1.1 | 350       |
| 4  | 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       |
| 5  | 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       |
| 6  | iDNA4mC: identifying DNA N4-methylcytosine sites based on nucleotide chemical properties. <i>Bioinformatics</i> , 2017, 33, 3518-3523.   | 1.8 | 256       |
| 7  | 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       |
| 8  | iDNA6mA-PseKNC: Identifying DNA N6-methyladenosine sites by incorporating nucleotide physicochemical properties into PseKNC. <i>Genomics</i> , 2019, 111, 96-102.  | 1.3 | 234       |
| 9  | iRNA-AI: identifying the adenosine to inosine editing sites in RNA sequences. <i>Oncotarget</i> , 2017, 8, 4208-4217.  | 0.8 | 209       |
| 10 | iNuc-PhysChem: A Sequence-Based Predictor for Identifying Nucleosomes via Physicochemical Properties. <i>PLoS ONE</i> , 2012, 7, e47843.   | 1.1 | 181       |
| 11 | 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       |
| 12 | Identification of bacteriophage virion proteins by the ANOVA feature selection and analysis. <i>Molecular BioSystems</i> , 2014, 10, 2229-2235.  | 2.9 | 147       |
| 13 | Naïve 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       |
| 14 | Using deformation energy to analyze nucleosome positioning in genomes. <i>Genomics</i> , 2016, 107, 69-75.   | 1.3 | 104       |
| 15 | Identification of Antioxidants from Sequence Information Using Naïve Bayes. <i>Computational and Mathematical Methods in Medicine</i> , 2013, 2013, 1-5.   | 0.7 | 102       |
| 16 | iRNA-m7G: Identifying N7-methylguanosine Sites by Fusing Multiple Features. <i>Molecular Therapy - Nucleic Acids</i> , 2019, 18, 269-274.  | 2.3 | 85        |
| 17 | Recent Advances in Machine Learning Methods for Predicting Heat Shock Proteins. <i>Current Drug Metabolism</i> , 2019, 20, 224-228.  | 0.7 | 75        |
| 18 | Identifying N 6-methyladenosine sites in the Arabidopsis thaliana transcriptome. <i>Molecular Genetics and Genomics</i> , 2016, 291, 2225-2229.  | 1.0 | 58        |

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|----|--|-----|-----------|
| 19 | Identifying 2â€²-O-methylation sites by integrating nucleotide chemical properties and nucleotide compositions. <i>Genomics</i> , 2016, 107, 255-258.                        | 1.3 | 55        |
| 20 | Prediction of replication origins by calculating DNA structural properties. <i>FEBS Letters</i> , 2012, 586, 934-938.  | 1.3 | 53        |
| 21 | RAMPred: identifying the N1-methyladenosine sites in eukaryotic transcriptomes. <i>Scientific Reports</i> , 2016, 6, 31080.  | 1.6 | 50        |
| 22 | AOD: the antioxidant protein database. <i>Scientific Reports</i> , 2017, 7, 7449.  | 1.6 | 49        |
| 23 | Identifying RNA 5-methylcytosine sites via pseudo nucleotide compositions. <i>Molecular BioSystems</i> , 2016, 12, 3307-3311.  | 2.9 | 48        |
| 24 | PHYPred: a tool for identifying bacteriophage enzymes and hydrolases. <i>Virologica Sinica</i> , 2016, 31, 350-352.  | 1.2 | 47        |
| 25 | Computational Identification of Small Interfering RNA Targets in SARS-CoV-2. <i>Virologica Sinica</i> , 2020, 35, 359-361.   | 1.2 | 45        |
| 26 | iATP: A Sequence Based Method for Identifying Anti-tubercular Peptides. <i>Medicinal Chemistry</i> , 2020, 16, 620-625.  | 0.7 | 43        |
| 27 | Identifying Antioxidant Proteins by Using Optimal Dipeptide Compositions. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2016, 8, 186-191.                 | 2.2 | 42        |
| 28 | Iterative feature representation algorithm to improve the predictive performance of N7-methylguanosine sites. <i>Briefings in Bioinformatics</i> , 2021, 22, .               | 3.2 | 35        |
| 29 | Prediction of CpG island methylation status by integrating DNA physicochemical properties. <i>Genomics</i> , 2014, 104, 229-233.   | 1.3 | 33        |
| 30 | PAI: Predicting adenosine to inosine editing sites by using pseudo nucleotide compositions. <i>Scientific Reports</i> , 2016, 6, 35123.                                      | 1.6 | 32        |
| 31 | 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        |
| 32 | Predicting the Types of J-Proteins Using Clustered Amino Acids. <i>BioMed Research International</i> , 2014, 2014, 1-8.  | 0.9 | 30        |
| 33 | Prediction of DNase I Hypersensitive Sites by Using Pseudo Nucleotide Compositions. <i>Scientific World Journal</i> , The, 2014, 2014, 1-4.                                  | 0.8 | 26        |
| 34 | Identifying RNA N6-Methyladenosine Sites in Escherichia coli Genome. <i>Frontiers in Microbiology</i> , 2018, 9, 955.  | 1.5 | 24        |
| 35 | Classifying Included and Excluded Exons in Exon Skipping Event Using Histone Modifications. <i>Frontiers in Genetics</i> , 2018, 9, 433.                                     | 1.1 | 23        |
| 36 | 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        |

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|----|--|-----|-----------|
| 37 | Identification of D Modification Sites by Integrating Heterogeneous Features in <i>Saccharomyces cerevisiae</i> . <i>Molecules</i> , 2019, 24, 380.  | 1.7 | 15        |
| 38 | 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        |
| 39 | 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        |
| 40 | Exon skipping event prediction based on histone modifications. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2014, 6, 241-249.  | 2.2 | 10        |
| 41 | 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        |
| 42 | Benchmark data for identifying N <sup>6</sup> -methyladenosine sites in the <i>Saccharomyces cerevisiae</i> genome. <i>Data in Brief</i> , 2015, 5, 376-378.   | 0.5 | 9         |
| 43 | 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         |
| 44 | Recent Advances in Computational Methods for Identifying Anticancer Peptides. <i>Current Drug Targets</i> , 2019, 20, 481-487.   | 1.0 | 6         |
| 45 | DNA Physical Parameters Modulate Nucleosome Positioning in the <i>Saccharomyces cerevisiae</i> Genome. <i>Current Bioinformatics</i> , 2014, 9, 188-193.   | 0.7 | 6         |
| 46 | Recent Advances on Antioxidant Identification Based on Machine Learning Methods. <i>Current Drug Metabolism</i> , 2020, 21, 804-809.   | 0.7 | 5         |
| 47 | 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         |
| 48 | Comparison and Analysis of Computational Methods for Identifying N <sup>6</sup> -Methyladenosine Sites in <i>Saccharomyces cerevisiae</i> . <i>Current Pharmaceutical Design</i> , 2021, 27, 1219-1229.        | 0.9 | 1         |
| 49 | Identification of Pathologic and Prognostic Genes in Prostate Cancer Based on Database Mining. <i>Frontiers in Genetics</i> , 2022, 13, 854531.  | 1.1 | 1         |