

# Shengli Zhang

## List of Publications by Year in descending order

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526287

27  
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docs citations

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times ranked

425  
citing authors

| #  | ARTICLE   | IF  | CITATIONS |
|----|---|-----|-----------|
| 1  | M6A-GSMS: Computational identification of N <sup>6</sup> -methyladenosine sites with GBDT and stacking learning in multiple species. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 12380-12391. | 3.5 | 5         |
| 2  | Pep-CNN: An improved convolutional neural network for predicting therapeutic peptides. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2022, 221, 104490.  | 3.5 | 12        |
| 3  | iPro-GAN: A novel model based on generative adversarial learning for identifying promoters and their strength. <i>Computer Methods and Programs in Biomedicine</i> , 2022, 215, 106625.                             | 4.7 | 7         |
| 4  | Integrating LASSO Feature Selection and Soft Voting Classifier to Identify Origins of Replication Sites. <i>Current Genomics</i> , 2022, 23, 83-93.   | 1.6 | 1         |
| 5  | Accurate Prediction of Anti-hypertensive Peptides Based on Convolutional Neural Network and Gated Recurrent unit. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2022, 14, 879-894.               | 3.6 | 8         |
| 6  | Identification of DNA N4-methylcytosine sites based on multi-source features and gradient boosting decision tree. <i>Analytical Biochemistry</i> , 2022, 652, 114746.   | 2.4 | 3         |
| 7  | iDHS-DASTS: identifying DNase I hypersensitive sites based on LASSO and stacking learning. <i>Molecular Omics</i> , 2021, 17, 130-141.  | 2.8 | 6         |
| 8  | Identifying DNA-binding proteins based on multi-features and LASSO feature selection. <i>Biopolymers</i> , 2021, 112, e23419.   | 2.4 | 21        |
| 9  | PA-PseU: An incremental passive-aggressive based method for identifying RNA pseudouridine sites via Chou's 5-steps rule. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2021, 210, 104250.                | 3.5 | 13        |
| 10 | iORI-ENST: identifying origin of replication sites based on elastic net and stacking learning. <i>SAR and QSAR in Environmental Research</i> , 2021, 32, 317-331.   | 2.2 | 7         |
| 11 | i6mA-VC: A Multi-Classifer Voting Method for the Computational Identification of DNA N6-methyladenine Sites. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2021, 13, 413-425.                    | 3.6 | 10        |
| 12 | UMAP-DBP: An Improved DNA-Binding Proteins Prediction Method Based on Uniform Manifold Approximation and Projection. <i>Protein Journal</i> , 2021, 40, 562-575.  | 1.6 | 12        |
| 13 | Application of Machine Learning Techniques in Drug-target Interactions Prediction. <i>Current Pharmaceutical Design</i> , 2021, 27, 2076-2087.  | 1.9 | 4         |
| 14 | iPromoter-ET: Identifying promoters and their strength by extremely randomized trees-based feature selection. <i>Analytical Biochemistry</i> , 2021, 630, 114335.   | 2.4 | 11        |
| 15 | iR5hmC: Identifying RNA 5-hydroxymethylcytosine with multiple features based on stacking learning. <i>Computational Biology and Chemistry</i> , 2021, 95, 107583.   | 2.3 | 6         |
| 16 | iEnhancer-MFGBDT: Identifying enhancers and their strength by fusing multiple features and gradient boosting decision tree. <i>Mathematical Biosciences and Engineering</i> , 2021, 18, 8797-8814.                  | 1.9 | 9         |
| 17 | iDHS-DSAMS: Identifying DNase I hypersensitive sites based on the dinucleotide property matrix and ensemble bagged tree. <i>Genomics</i> , 2020, 112, 1282-1289.  | 2.9 | 12        |
| 18 | KD-KLNMF: Identification of lncRNAs subcellular localization with multiple features and nonnegative matrix factorization. <i>Analytical Biochemistry</i> , 2020, 610, 113995.                                       | 2.4 | 16        |

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|----|--|-----|-----------|
| 19 | Use Chou's 5-steps rule to identify DNase I hypersensitive sites via dinucleotide property matrix and extreme gradient boosting. <i>Molecular Genetics and Genomics</i> , 2020, 295, 1431-1442.                              | 2.1 | 19        |
| 20 | Integrating Second-order Moving Average and Over-sampling Algorithm to Predict Apoptosis Protein Subcellular Localization. <i>Current Bioinformatics</i> , 2020, 15, 517-527.  | 1.5 | 3         |
| 21 | Identifying DNase I hypersensitive sites using multi-features fusion and F-score features selection via Chou's 5-steps rule. <i>Biophysical Chemistry</i> , 2019, 253, 106227.   | 2.8 | 40        |
| 22 | Identification of amyloidogenic peptides via optimized integrated features space based on physicochemical properties and PSSM. <i>Analytical Biochemistry</i> , 2019, 583, 113362.   | 2.4 | 9         |
| 23 | iDHS-DMCAC: identifying DNase I hypersensitive sites with balanced dinucleotide-based detrending moving-average cross-correlation coefficient. <i>SAR and QSAR in Environmental Research</i> , 2019, 30, 429-445.            | 2.2 | 7         |
| 24 | Prediction of apoptosis protein subcellular localization via heterogeneous features and hierarchical extreme learning machine. <i>SAR and QSAR in Environmental Research</i> , 2019, 30, 209-228.                            | 2.2 | 16        |
| 25 | iRSpot-DTS: Predict recombination spots by incorporating the dinucleotide-based spare-cross covariance information into Chou's pseudo components. <i>Genomics</i> , 2019, 111, 1760-1770.                                    | 2.9 | 27        |
| 26 | Application of Machine Learning Techniques to Predict Protein Phosphorylation Sites. <i>Letters in Organic Chemistry</i> , 2019, 16, 247-257.  | 0.5 | 1         |
| 27 | Pathogenic Genes Selection Model of Genetic Disease based on Network Motifs Slicing Feedback. <i>Current Proteomics</i> , 2019, 16, 392-401.   | 0.3 | 0         |
| 28 | Accurate prediction of Gram-negative bacterial secreted protein types by fusing multiple statistical features from PSI-BLAST profile. <i>SAR and QSAR in Environmental Research</i> , 2018, 29, 469-481.                     | 2.2 | 4         |
| 29 | Prediction of Apoptosis Protein's Subcellular Localization by Fusing Two Different Descriptors Based on Evolutionary Information. <i>Acta Biotheoretica</i> , 2018, 66, 61-78.   | 1.5 | 11        |
| 30 | Prediction of protein subcellular localization with oversampling approach and Chou's general PseAAC. <i>Journal of Theoretical Biology</i> , 2018, 437, 239-250.   | 1.7 | 81        |
| 31 | Predicting apoptosis protein subcellular localization by integrating auto-cross correlation and PSSM into Chou's PseAAC. <i>Journal of Theoretical Biology</i> , 2018, 457, 163-169.   | 1.7 | 53        |
| 32 | Identify Gram-negative bacterial secreted protein types by incorporating different modes of PSSM into Chou's general PseAAC via Kullback-Leibler divergence. <i>Journal of Theoretical Biology</i> , 2018, 454, 22-29.       | 1.7 | 36        |
| 33 | Predict protein structural class by incorporating two different modes of evolutionary information into Chou's general pseudo amino acid composition. <i>Journal of Molecular Graphics and Modelling</i> , 2017, 78, 110-117. | 2.4 | 33        |
| 34 | Prediction of Protein Subcellular Localization by Using $\beta$ -Order Factor and Principal Component Analysis. <i>Letters in Organic Chemistry</i> , 2017, 14, .  | 0.5 | 1         |
| 35 | A Gram-Negative Bacterial Secreted Protein Types Prediction Method Based on PSI-BLAST Profile. <i>BioMed Research International</i> , 2016, 2016, 1-5.   | 1.9 | 1         |
| 36 | Detrended cross-correlation coefficient: Application to predict apoptosis protein subcellular localization. <i>Mathematical Biosciences</i> , 2016, 282, 61-67.  | 1.9 | 7         |

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|----|---|-----|-----------|
| 37 | Prediction of Protein Structural Classes for Low-Similarity Sequences Based on Consensus Sequence and Segmented PSSM. <i>Computational and Mathematical Methods in Medicine</i> , 2015, 2015, 1-9.                    | 1.3 | 16        |
| 38 | Accurate prediction of protein structural classes by incorporating PSSS and PSSM into Chou's general PseAAC. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2015, 142, 28-35.                               | 3.5 | 45        |
| 39 | Improving the prediction accuracy of protein structural class: Approached with alternating word frequency and normalized Lempel-Ziv complexity. <i>Journal of Theoretical Biology</i> , 2014, 341, 71-77.             | 1.7 | 20        |
| 40 | Using principal component analysis and support vector machine to predict protein structural class for low-similarity sequences via PSSM. <i>Journal of Biomolecular Structure and Dynamics</i> , 2012, 29, 1138-1146. | 3.5 | 55        |
| 41 | A novel protein structural classes prediction method based on predicted secondary structure. <i>Biochimie</i> , 2012, 94, 1166-1171.  | 2.6 | 57        |
| 42 | High-accuracy prediction of protein structural class for low-similarity sequences based on predicted secondary structure. <i>Biochimie</i> , 2011, 93, 710-714.   | 2.6 | 56        |
| 43 | A Complexity-based Method to Compare RNA Secondary Structures and its Application. <i>Journal of Biomolecular Structure and Dynamics</i> , 2010, 28, 247-258.   | 3.5 | 14        |
| 44 | Use of information discrepancy measure to compare protein secondary structures. <i>Computational and Theoretical Chemistry</i> , 2009, 909, 102-106.  | 1.5 | 21        |
| 45 | Feature analysis of protein structure by using discrete Fourier transform and continuous wavelet transform. <i>Journal of Mathematical Chemistry</i> , 2009, 46, 562-568.   | 1.5 | 8         |