

# Shengli Zhang

## List of Publications by Year in descending order

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Version: 2024-02-01

45  
papers

804  
citations

516710

16  
h-index

526287

27  
g-index

45  
all docs

45  
docs citations

45  
times ranked

425  
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	A novel protein structural classes prediction method based on predicted secondary structure. <i>Biochimie</i> , 2012, 94, 1166-1171.	2.6	57
3	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
4	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
5	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
6	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
7	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
8	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
9	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
10	iRSpot-DTS: Predict recombination spots by incorporating the dinucleotide-based sparse-cross covariance information into Chou's pseudo components. <i>Genomics</i> , 2019, 111, 1760-1770.	2.9	27
11	Use of information discrepancy measure to compare protein secondary structures. <i>Computational and Theoretical Chemistry</i> , 2009, 909, 102-106.	1.5	21
12	Identifying DNA-binding proteins based on multi-features and LASSO feature selection. <i>Biopolymers</i> , 2021, 112, e23419.	2.4	21
13	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
14	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
15	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
16	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
17	KD-KLNMF: Identification of lncRNAs subcellular localization with multiple features and nonnegative matrix factorization. <i>Analytical Biochemistry</i> , 2020, 610, 113995.	2.4	16
18	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

#	ARTICLE	IF	CITATIONS
19	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
20	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
21	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
22	Pep-CNN: An improved convolutional neural network for predicting therapeutic peptides. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2022, 221, 104490.	3.5	12
23	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
24	iPromoter-ET: Identifying promoters and their strength by extremely randomized trees-based feature selection. <i>Analytical Biochemistry</i> , 2021, 630, 114335.	2.4	11
25	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
26	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
27	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
28	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
29	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
30	Detrended cross-correlation coefficient: Application to predict apoptosis protein subcellular localization. <i>Mathematical Biosciences</i> , 2016, 282, 61-67.	1.9	7
31	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
32	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
33	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
34	iDHS-DASTS: identifying DNase I hypersensitive sites based on LASSO and stacking learning. <i>Molecular Omics</i> , 2021, 17, 130-141.	2.8	6
35	iR5hmSC: Identifying RNA 5-hydroxymethylcytosine with multiple features based on stacking learning. <i>Computational Biology and Chemistry</i> , 2021, 95, 107583.	2.3	6
36	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

#	ARTICLE	IF	CITATIONS
37	Accurate prediction of Gram-negative bacterial secreted protein types by fusing multiple statistical features from PSI-BLAST profile. SAR and QSAR in Environmental Research, 2018, 29, 469-481.	2.2	4
38	Application of Machine Learning Techniques in Drug-target Interactions Prediction. Current Pharmaceutical Design, 2021, 27, 2076-2087.	1.9	4
39	Integrating Second-order Moving Average and Over-sampling Algorithm to Predict Apoptosis Protein Subcellular Localization. Current Bioinformatics, 2020, 15, 517-527.	1.5	3
40	Identification of DNA N4-methylcytosine sites based on multi-source features and gradient boosting decision tree. Analytical Biochemistry, 2022, 652, 114746.	2.4	3
41	A Gram-Negative Bacterial Secreted Protein Types Prediction Method Based on PSI-BLAST Profile. BioMed Research International, 2016, 2016, 1-5.	1.9	1
42	Prediction of Protein Subcellular Localization by Using $\alpha$ -Order Factor and Principal Component Analysis. Letters in Organic Chemistry, 2017, 14, .	0.5	1
43	Application of Machine Learning Techniques to Predict Protein Phosphorylation Sites. Letters in Organic Chemistry, 2019, 16, 247-257.	0.5	1
44	Integrating LASSO Feature Selection and Soft Voting Classifier to Identify Origins of Replication Sites. Current Genomics, 2022, 23, 83-93.	1.6	1
45	Pathogenic Genes Selection Model of Genetic Disease based on Network Motifs Slicing Feedback. Current Proteomics, 2019, 16, 392-401.	0.3	0