

Shao-Ping Shi

List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

1,247
citations

361413

20
h-index

361022

35
g-index

38
all docs

38
docs citations

38
times ranked

1129
citing authors

#	ARTICLE	IF	CITATIONS
1	DeepCLA: A Hybrid Deep Learning Approach for the Identification of Clathrin. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 516-524.	5.4	0
2	OUP accepted manuscript. <i>Briefings in Bioinformatics</i> , 2021, , .	6.5	4
3	PREDAIIP: Computational Prediction and Analysis for Anti-inflammatory Peptide via a Hybrid Feature Selection Technique. <i>Current Bioinformatics</i> , 2021, 16, .	1.5	6
4	Computational prediction and analysis of species-specific fungi phosphorylation via feature optimization strategy. <i>Briefings in Bioinformatics</i> , 2020, 21, 595-608.	6.5	12
5	Proteomic analysis and prediction of amino acid variations that influence protein posttranslational modifications. <i>Briefings in Bioinformatics</i> , 2019, 20, 1597-1606.	6.5	3
6	PredGly: predicting lysine glycation sites for <i>Homo sapiens</i> based on XGboost feature optimization. <i>Bioinformatics</i> , 2019, 35, 2749-2756.	4.1	53
7	Prediction and functional analysis of prokaryote lysine acetylation site by incorporating six types of features into Chou's general PseAAC. <i>Journal of Theoretical Biology</i> , 2019, 461, 92-101.	1.7	27
8	Site-specific Systematic Analysis of Lysine Modification Crosstalk. <i>Proteomics</i> , 2018, 18, e1700292.	2.2	6
9	Computational Prediction and Analysis for Tyrosine Post-Translational Modifications via Elastic Net. <i>Journal of Chemical Information and Modeling</i> , 2018, 58, 1272-1281.	5.4	12
10	ProAcePred: prokaryote lysine acetylation sites prediction based on elastic net feature optimization. <i>Bioinformatics</i> , 2018, 34, 3999-4006.	4.1	29
11	Computational prediction of species-specific malonylation sites via enhanced characteristic strategy. <i>Bioinformatics</i> , 2017, 33, 1457-1463.	4.1	56
12	Computing Prediction and Functional Analysis of Prokaryotic Propionylation. <i>Journal of Chemical Information and Modeling</i> , 2017, 57, 2896-2904.	5.4	7
13	Accurate <i>in silico</i> prediction of species-specific methylation sites based on information gain feature optimization. <i>Bioinformatics</i> , 2016, 32, 3107-3115.	4.1	62
14	A homology-based pipeline for global prediction of post-translational modification sites. <i>Scientific Reports</i> , 2016, 6, 25801.	3.3	4
15	Progress and challenges in predicting protein methylation sites. <i>Molecular BioSystems</i> , 2015, 11, 2610-2619.	2.9	11
16	Using support vector machines to identify protein phosphorylation sites in viruses. <i>Journal of Molecular Graphics and Modelling</i> , 2015, 56, 84-90.	2.4	24
17	Systematic Analysis of the Genetic Variability That Impacts SUMO Conjugation and Their Involvement in Human Diseases. <i>Scientific Reports</i> , 2015, 5, 10900.	3.3	11
18	SuccFind: a novel succinylation sites online prediction tool via enhanced characteristic strategy. <i>Bioinformatics</i> , 2015, 31, 3748-3750.	4.1	58

#	ARTICLE	IF	CITATIONS
19	PredHydroxy: computational prediction of protein hydroxylation site locations based on the primary structure. <i>Molecular BioSystems</i> , 2015, 11, 819-825.	2.9	20
20	Proteomic analysis and prediction of human phosphorylation sites in subcellular level reveal subcellular specificity. <i>Bioinformatics</i> , 2015, 31, 194-200.	4.1	19
21	PSEA: Kinase-specific prediction and analysis of human phosphorylation substrates. <i>Scientific Reports</i> , 2014, 4, 4524.	3.3	27
22	Incorporating key position and amino acid residue features to identify general and species-specific Ubiquitin conjugation sites. <i>Bioinformatics</i> , 2013, 29, 1614-1622.	4.1	102
23	The prediction of palmitoylation site locations using a multiple feature extraction method. <i>Journal of Molecular Graphics and Modelling</i> , 2013, 40, 125-130.	2.4	31
24	Proteome-wide Analysis of Amino Acid Variations That Influence Protein Lysine Acetylation. <i>Journal of Proteome Research</i> , 2013, 12, 949-958.	3.7	17
25	Systematic Analysis and Prediction of Pupylation Sites in Prokaryotic Proteins. <i>PLoS ONE</i> , 2013, 8, e74002.	2.5	24
26	Identifying protein quaternary structural attributes by incorporating physicochemical properties into the general form of Chou's PseAAC via discrete wavelet transform. <i>Molecular BioSystems</i> , 2012, 8, 3178.	2.9	83
27	PLMLA: prediction of lysine methylation and lysine acetylation by combining multiple features. <i>Molecular BioSystems</i> , 2012, 8, 1520.	2.9	81
28	PredSulSite: Prediction of protein tyrosine sulfation sites with multiple features and analysis. <i>Analytical Biochemistry</i> , 2012, 428, 16-23.	2.4	39
29	A method to distinguish between lysine acetylation and lysine methylation from protein sequences. <i>Journal of Theoretical Biology</i> , 2012, 310, 223-230.	1.7	24
30	A novel algorithm combining support vector machine with the discrete wavelet transform for the prediction of protein subcellular localization. <i>Computers in Biology and Medicine</i> , 2012, 42, 180-187.	7.0	20
31	PMeS: Prediction of Methylation Sites Based on Enhanced Feature Encoding Scheme. <i>PLoS ONE</i> , 2012, 7, e38772.	2.5	74
32	Position-Specific Analysis and Prediction for Protein Lysine Acetylation Based on Multiple Features. <i>PLoS ONE</i> , 2012, 7, e49108.	2.5	64
33	Predicting homo-oligomers and hetero-oligomers by pseudo-amino acid composition: An approach from discrete wavelet transformation. <i>Biochimie</i> , 2011, 93, 1132-1138.	2.6	15
34	OligoPred: A web-server for predicting homo-oligomeric proteins by incorporating discrete wavelet transform into Chou's pseudo amino acid composition. <i>Journal of Molecular Graphics and Modelling</i> , 2011, 30, 129-134.	2.4	52
35	Identify submitochondria and subchloroplast locations with pseudo amino acid composition: Approach from the strategy of discrete wavelet transform feature extraction. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2011, 1813, 424-430.	4.1	42
36	Using the Concept of Chous Pseudo Amino Acid Composition to Predict Enzyme Family Classes: An Approach with Support Vector Machine Based on Discrete Wavelet Transform. <i>Protein and Peptide Letters</i> , 2010, 17, 715-722.	0.9	124