

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

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38
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docs citations

38
times ranked

1129
citing authors

#	ARTICLE	IF	CITATIONS
1	Using the Concept of Chou's 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
2	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
3	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
4	PLMLA: prediction of lysine methylation and lysine acetylation by combining multiple features. <i>Molecular BioSystems</i> , 2012, 8, 1520.	2.9	81
5	PMeS: Prediction of Methylation Sites Based on Enhanced Feature Encoding Scheme. <i>PLoS ONE</i> , 2012, 7, e38772.	2.5	74
6	Position-Specific Analysis and Prediction for Protein Lysine Acetylation Based on Multiple Features. <i>PLoS ONE</i> , 2012, 7, e49108.	2.5	64
7	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
8	SuccFind: a novel succinylation sites online prediction tool via enhanced characteristic strategy. <i>Bioinformatics</i> , 2015, 31, 3748-3750.	4.1	58
9	Computational prediction of species-specific malonylation sites via enhanced characteristic strategy. <i>Bioinformatics</i> , 2017, 33, 1457-1463.	4.1	56
10	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
11	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
12	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
13	PredSulSite: Prediction of protein tyrosine sulfation sites with multiple features and analysis. <i>Analytical Biochemistry</i> , 2012, 428, 16-23.	2.4	39
14	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
15	ProAcePred: prokaryote lysine acetylation sites prediction based on elastic net feature optimization. <i>Bioinformatics</i> , 2018, 34, 3999-4006.	4.1	29
16	PSEA: Kinase-specific prediction and analysis of human phosphorylation substrates. <i>Scientific Reports</i> , 2014, 4, 4524.	3.3	27
17	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
18	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

#	ARTICLE	IF	CITATIONS
19	Systematic Analysis and Prediction of Pupylation Sites in Prokaryotic Proteins. PLoS ONE, 2013, 8, e74002.	2.5	24
20	Using support vector machines to identify protein phosphorylation sites in viruses. Journal of Molecular Graphics and Modelling, 2015, 56, 84-90.	2.4	24
21	A novel algorithm combining support vector machine with the discrete wavelet transform for the prediction of protein subcellular localization. Computers in Biology and Medicine, 2012, 42, 180-187.	7.0	20
22	PredHydroxy: computational prediction of protein hydroxylation site locations based on the primary structure. Molecular BioSystems, 2015, 11, 819-825.	2.9	20
23	Proteomic analysis and prediction of human phosphorylation sites in subcellular level reveal subcellular specificity. Bioinformatics, 2015, 31, 194-200.	4.1	19
24	Proteome-wide Analysis of Amino Acid Variations That Influence Protein Lysine Acetylation. Journal of Proteome Research, 2013, 12, 949-958.	3.7	17
25	Predicting homo-oligomers and hetero-oligomers by pseudo-amino acid composition: An approach from discrete wavelet transformation. Biochimie, 2011, 93, 1132-1138.	2.6	15
26	Computational Prediction and Analysis for Tyrosine Post-Translational Modifications via Elastic Net. Journal of Chemical Information and Modeling, 2018, 58, 1272-1281.	5.4	12
27	Computational prediction and analysis of species-specific fungi phosphorylation via feature optimization strategy. Briefings in Bioinformatics, 2020, 21, 595-608.	6.5	12
28	Progress and challenges in predicting protein methylation sites. Molecular BioSystems, 2015, 11, 2610-2619.	2.9	11
29	Systematic Analysis of the Genetic Variability That Impacts SUMO Conjugation and Their Involvement in Human Diseases. Scientific Reports, 2015, 5, 10900.	3.3	11
30	Computing Prediction and Functional Analysis of Prokaryotic Propionylation. Journal of Chemical Information and Modeling, 2017, 57, 2896-2904.	5.4	7
31	Site-specific Systematic Analysis of Lysine Modification Crosstalk. Proteomics, 2018, 18, e1700292.	2.2	6
32	PREDAIIP: Computational Prediction and Analysis for Anti-inflammatory Peptide via a Hybrid Feature Selection Technique. Current Bioinformatics, 2021, 16, .	1.5	6
33	A homology-based pipeline for global prediction of post-translational modification sites. Scientific Reports, 2016, 6, 25801.	3.3	4
34	OUP accepted manuscript. Briefings in Bioinformatics, 2021, , .	6.5	4
35	Proteomic analysis and prediction of amino acid variations that influence protein posttranslational modifications. Briefings in Bioinformatics, 2019, 20, 1597-1606.	6.5	3
36	DeepCLA: A Hybrid Deep Learning Approach for the Identification of Clathrin. Journal of Chemical Information and Modeling, 2021, 61, 516-524.	5.4	0