

Zi Liu

List of Publications by Year in descending order

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Version: 2024-02-01

22
papers

2,547
citations

430442

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676716

22
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docs citations

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times ranked

1189
citing authors

#	ARTICLE	IF	CITATIONS
1	pSuc-Lys: Predict lysine succinylation sites in proteins with PseAAC and ensemble random forest approach. <i>Journal of Theoretical Biology</i> , 2016, 394, 223-230.	0.8	297
2	iPPI-Esml: An ensemble classifier for identifying the interactions of proteins by incorporating their physicochemical properties and wavelet transforms into PseAAC. <i>Journal of Theoretical Biology</i> , 2015, 377, 47-56.	0.8	265
3	iSuc-PseOpt: Identifying lysine succinylation sites in proteins by incorporating sequence-coupling effects into pseudo components and optimizing imbalanced training dataset. <i>Analytical Biochemistry</i> , 2016, 497, 48-56.	1.1	254
4	pRNAm-PC: Predicting N6-methyladenosine sites in RNA sequences via physical-chemical properties. <i>Analytical Biochemistry</i> , 2016, 497, 60-67.	1.1	247
5	iDNA-Methyl: Identifying DNA methylation sites via pseudo trinucleotide composition. <i>Analytical Biochemistry</i> , 2015, 474, 69-77.	1.1	246
6	iDrug-Target: predicting the interactions between drug compounds and target proteins in cellular networking via benchmark dataset optimization approach. <i>Journal of Biomolecular Structure and Dynamics</i> , 2015, 33, 2221-2233.	2.0	185
7	pSumo-CD: predicting sumoylation sites in proteins with covariance discriminant algorithm by incorporating sequence-coupled effects into general PseAAC. <i>Bioinformatics</i> , 2016, 32, 3133-3141.	1.8	177
8	iCar-PseCp: identify carbonylation sites in proteins by Monte Carlo sampling and incorporating sequence coupled effects into general PseAAC. <i>Oncotarget</i> , 2016, 7, 34558-34570.	0.8	176
9	iPPBS-Opt: A Sequence-Based Ensemble Classifier for Identifying Protein-Protein Binding Sites by Optimizing Imbalanced Training Datasets. <i>Molecules</i> , 2016, 21, 95.	1.7	142
10	Identification of protein-protein binding sites by incorporating the physicochemical properties and stationary wavelet transforms into pseudo amino acid composition. <i>Journal of Biomolecular Structure and Dynamics</i> , 2016, 34, 1946-1961.	2.0	120
11	iROS-gPseKNC: Predicting replication origin sites in DNA by incorporating dinucleotide position-specific propensity into general pseudo nucleotide composition. <i>Oncotarget</i> , 2016, 7, 34180-34189.	0.8	118
12	TargetM6A: Identifying N ⁶ -Methyladenosine Sites From RNA Sequences via Position-Specific Nucleotide Propensities and a Support Vector Machine. <i>IEEE Transactions on Nanobioscience</i> , 2016, 15, 674-682.	2.2	73
13	LS-align: an atom-level, flexible ligand structural alignment algorithm for high-throughput virtual screening. <i>Bioinformatics</i> , 2018, 34, 2209-2218.	1.8	62
14	Improving N6-methyladenosine site prediction with heuristic selection of nucleotide physical-chemical properties. <i>Analytical Biochemistry</i> , 2016, 508, 104-113.	1.1	43
15	Accurate RNA 5-methylcytosine site prediction based on heuristic physical-chemical properties reduction and classifier ensemble. <i>Analytical Biochemistry</i> , 2018, 550, 41-48.	1.1	43
16	iAFP-Ense: An Ensemble Classifier for Identifying Antifreeze Protein by Incorporating Grey Model and PSSM into PseAAC. <i>Journal of Membrane Biology</i> , 2016, 249, 845-854.	1.0	25
17	Improving prediction of extracellular matrix proteins using evolutionary information via a grey system model and asymmetric under-sampling technique. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2018, 174, 22-32.	1.8	25
18	Fusing hierarchical multi-scale local binary patterns and virtual mirror samples to perform face recognition. <i>Neural Computing and Applications</i> , 2015, 26, 2013-2026.	3.2	18

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19	A new sparse representation-based classification algorithm using iterative class elimination. <i>Neural Computing and Applications</i> , 2014, 24, 1627-1637.	3.2	10
20	iCataly-PseAAC: Identification of Enzymes Catalytic Sites Using Sequence Evolution Information with Grey Model GM (2,1). <i>Journal of Membrane Biology</i> , 2015, 248, 1033-1041.	1.0	10
21	Benchmark data for identifying DNA methylation sites via pseudo trinucleotide composition. <i>Data in Brief</i> , 2015, 4, 87-89.	0.5	8
22	Using idea of three-step sparse residuals measurement to perform discriminant analysis. <i>Soft Computing</i> , 2015, 19, 2355-2370.	2.1	3