Zi Liu

List of Publications by Year
in descending order

22	2,547	430442	676716
papers	citations	18 h-index	22 g-index

22	22	22	1189
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	LS-align: an atom-level, flexible ligand structural alignment algorithm for high-throughput virtual screening. Bioinformatics, 2018, 34, 2209-2218.	1.8	62
2	Accurate RNA 5-methylcytosine site prediction based on heuristic physical-chemical properties reduction and classifier ensemble. Analytical Biochemistry, 2018, 550, 41-48.	1.1	43
3	Improving prediction of extracellular matrix proteins using evolutionary information via a grey system model and asymmetric under-sampling technique. Chemometrics and Intelligent Laboratory Systems, 2018, 174, 22-32.	1.8	25
4	iROS-gPseKNC: Predicting replication origin sites in DNA by incorporating dinucleotide position-specific propensity into general pseudo nucleotide composition. Oncotarget, 2016, 7, 34180-34189.	0.8	118
5	iPPBS-Opt: A Sequence-Based Ensemble Classifier for Identifying Protein-Protein Binding Sites by Optimizing Imbalanced Training Datasets. Molecules, 2016, 21, 95.	1.7	142
6	iCar-PseCp: identify carbonylation sites in proteins by Monte Carlo sampling and incorporating sequence coupled effects into general PseAAC. Oncotarget, 2016, 7, 34558-34570.	0.8	176
7	pSumo-CD: predicting sumoylation sites in proteins with covariance discriminant algorithm by incorporating sequence-coupled effects into general PseAAC. Bioinformatics, 2016, 32, 3133-3141.	1.8	177
8	TargetM6A: Identifying N⁶-Methyladenosine Sites From RNA Sequences via Position-Specific Nucleotide Propensities and a Support Vector Machine. IEEE Transactions on Nanobioscience, 2016, 15, 674-682.	2.2	73
9	iAFP-Ense: An Ensemble Classifier for Identifying Antifreeze Protein by Incorporating Grey Model and PSSM into PseAAC. Journal of Membrane Biology, 2016, 249, 845-854.	1.0	25
10	Improving N6-methyladenosine site prediction with heuristic selection of nucleotide physicalâ€“chemical properties. Analytical Biochemistry, 2016, 508, 104-113.	1.1	43
11	pSuc-Lys: Predict lysine succinylation sites in proteins with PseAAC and ensemble random forest approach. Journal of Theoretical Biology, 2016, 394, 223-230.	0.8	297
12	pRNAm-PC: Predicting N6-methyladenosine sites in RNA sequences via physicalâ€“chemical properties. Analytical Biochemistry, 2016, 497, 60-67.	1.1	247
13	iSuc-PseOpt: Identifying lysine succinylation sites in proteins by incorporating sequence-coupling effects into pseudo components and optimizing imbalanced training dataset. Analytical Biochemistry, 2016, 497, 48-56.	1.1	254
14	Identification of protein-protein binding sites by incorporating the physicochemical properties and stationary wavelet transforms into pseudo amino acid composition. Journal of Biomolecular Structure and Dynamics, 2016, 34, 1946-1961.	2.0	120
15	iPPI-Esml: An ensemble classifier for identifying the interactions of proteins by incorporating their physicochemical properties and wavelet transforms into PseAAC. Journal of Theoretical Biology, 2015, 377, 47-56.	0.8	265
16	Benchmark data for identifying DNA methylation sites via pseudo trinucleotide composition. Data in Brief, 2015, 4, 87-89.	0.5	8
17	Using idea of three-step sparse residuals measurement to perform discriminant analysis. Soft Computing, 2015, 19, 2355-2370.	2.1	3
18	iDNA-Methyl: Identifying DNA methylation sites via pseudo trinucleotide composition. Analytical Biochemistry, 2015, 474, 69-77.	1.1	246

#	Article	IF	Citations
19	iCataly-PseAAC: Identification of Enzymes Catalytic Sites Using Sequence Evolution Information with Grey Model GM (2,1). Journal of Membrane Biology, 2015, 248, 1033-1041.	1.0	10
20	Fusing hierarchical multi-scale local binary patterns and virtual mirror samples to perform face recognition. Neural Computing and Applications, 2015, 26, 2013-2026.	3.2	18
21	iDrug-Target: predicting the interactions between drug compounds and target proteins in cellular networking via benchmark dataset optimization approach. Journal of Biomolecular Structure and Dynamics, 2015, 33, 2221-2233.	2.0	185
22	A new sparse representation-based classification algorithm using iterative class elimination. Neural Computing and Applications, 2014, 24, 1627-1637.	3.2	10