Jun Hu

List of Publications by Year
in descending order

34	1,035	471509 17	454955 30
papers	citations	h-index	g-index

34	34	34	859
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	ATPdock: a template-based method for ATP-specific proteinâ€“ligand docking. Bioinformatics, 2022, 38, 556-558.	4.1	5
2	Robust distance metric optimization driven GEPSVM classifier for pattern classification. Pattern Recognition, 2022, 129, 108779.	8.1	3
3	Improved Protein Secondary Structure Prediction Using Bidirectional Long Short-Term Memory Neural Network and Bootstrap Aggregating. , 2022, , .		1
4	Predicting RNA solvent accessibility from multi-scale context feature via multi-shot neural network. Analytical Biochemistry, 2022, 654, 114802.	2.4	3
5	Protein Structure Prediction Using Population-Based Algorithm Guided by Information Entropy. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 697-707.	3.0	6
6	TargetDBP+: Enhancing the Performance of Identifying DNA-Binding Proteins via Weighted Convolutional Features. Journal of Chemical Information and Modeling, 2021, 61, 505-515.	5.4	11
7	Accurate prediction of protein-ATP binding residues using position-specific frequency matrix. Analytical Biochemistry, 2021, 626, 114241.	2.4	6
8	Improved protein relative solvent accessibility prediction using deep multi-view feature learning framework. Analytical Biochemistry, 2021, 631, 114358.	2.4	1
9	Accurate multistage prediction of protein crystallization propensity using deep-cascade forest with sequence-based features. Briefings in Bioinformatics, 2021, 22, .	6.5	11
10	TargetMM: Accurate Missense Mutation Prediction by Utilizing Local and Global Sequence Information with Classifier Ensemble. Combinatorial Chemistry and High Throughput Screening, 2021, 25, 38-52.	1.1	5
11	Protein-DNA Binding Residue Prediction via Bagging Strategy and Sequence-based Cube-Format Feature. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	3.0	2
12	Two-Stage Distance Feature-based Optimization Algorithm for De novo Protein Structure Prediction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 2119-2130.	3.0	3
13	scTPA: a web tool for single-cell transcriptome analysis of pathway activation signatures. Bioinformatics, 2020, 36, 4217-4219.	4.1	21
14	Identification of ligand-binding residues using protein sequence profile alignment and query-specific support vector machine model. Analytical Biochemistry, 2020, 604, 113799.	2.4	4
15	Assembling multidomain protein structures through analogous global structural alignments. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 15930-15938.	7.1	104
16	Loop Enhanced Conformational Resampling Method for Protein Structure Prediction. IEEE Transactions on Nanobioscience, 2019, 18, 567-577.	3.3	0
17	ResPRE: high-accuracy protein contact prediction by coupling precision matrix with deep residual neural networks. Bioinformatics, 2019, 35, 4647-4655.	4.1	142
18	DNAPred: Accurate Identification of DNA-Binding Sites from Protein Sequence by Ensembled Hyperplane-Distance-Based Support Vector Machines. Journal of Chemical Information and Modeling, 2019, 59, 3057-3071.	5.4	53

#	Article	IF	Citations
19	TargetDBP: Accurate DNA-Binding Protein Prediction via Sequence-based Multi-View Feature Learning. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 17, 1-1.	3.0	28
20	Boosting Granular Support Vector Machines for the Accurate Prediction of Protein-Nucleotide Binding Sites. Combinatorial Chemistry and High Throughput Screening, 2019, 22, 455-469.	1.1	2
21	LS-align: an atom-level, flexible ligand structural alignment algorithm for high-throughput virtual screening. Bioinformatics, 2018, 34, 2209-2218.	4.1	62
22	ATPbind: Accurate Proteinâ€“ATP Binding Site Prediction by Combining Sequence-Profiling and Structure-Based Comparisons. Journal of Chemical Information and Modeling, 2018, 58, 501-510.	5.4	57
23	Predicting Protein-DNA Binding Residues by Weightedly Combining Sequence-Based Features and Boosting Multiple SVMs. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 1389-1398.	3.0	64
24	TargetCrys: protein crystallization prediction by fusing multi-view features with two-layered SVM. Amino Acids, 2016, 48, 2533-2547.	2.7	39
25	GPCRâ€“drug interactions prediction using random forest with drug-association-matrix-based post-processing procedure. Computational Biology and Chemistry, 2016, 60, 59-71.	2.3	29
26	KNN-based dynamic query-driven sample rescaling strategy for class imbalance learning. Neurocomputing, 2016, 191, 363-373.	5.9	20
27	Frontoâ€parallel building facades stitching. Electronics Letters, 2016, 52, 1524-1526.	1.0	0
28	TargetFreeze: Identifying Antifreeze Proteins via a Combination of Weights using Sequence Evolutionary Information and Pseudo Amino Acid Composition. Journal of Membrane Biology, 2015, 248, 1005-1014.	2.1	36
29	Constructing Query-Driven Dynamic Machine Learning Model With Application to Protein-Ligand Binding Sites Prediction. IEEE Transactions on Nanobioscience, 2015, 14, 45-58.	3.3	29
30	A New Supervised Over-Sampling Algorithm with Application to Protein-Nucleotide Binding Residue Prediction. PLoS ONE, 2014, 9, e107676.	2.5	37
31	Designing Template-Free Predictor for Targeting Protein-Ligand Binding Sites with Classifier Ensemble and Spatial Clustering. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 994-1008.	3.0	106
32	TargetATPsite: A templateâ€free method for ATPâ€binding sites prediction with residue evolution image sparse representation and classifier ensemble. Journal of Computational Chemistry, 2013, 34, 974-985.	3.3	64
33	Improving protein-ATP binding residues prediction by boosting SVMs with random under-sampling. Neurocomputing, 2013, 104, 180-190.	5.9	62
34	Learning protein multi-view features in complex space. Amino Acids, 2013, 44, 1365-1379.	2.7	19