

# Jun Hu

## List of Publications by Year in descending order

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34  
papers

1,035  
citations

471509

17  
h-index

454955

30  
g-index

34  
all docs

34  
docs citations

34  
times ranked

859  
citing authors

#	ARTICLE	IF	CITATIONS
1	ResPRE: high-accuracy protein contact prediction by coupling precision matrix with deep residual neural networks. <i>Bioinformatics</i> , 2019, 35, 4647-4655.	4.1	142
2	Designing Template-Free Predictor for Targeting Protein-Ligand Binding Sites with Classifier Ensemble and Spatial Clustering. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 994-1008.	3.0	106
3	Assembling multidomain protein structures through analogous global structural alignments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 15930-15938.	7.1	104
4	TargetATPsite: A template-free method for ATP-binding sites prediction with residue evolution image sparse representation and classifier ensemble. <i>Journal of Computational Chemistry</i> , 2013, 34, 974-985.	3.3	64
5	Predicting Protein-DNA Binding Residues by Weightedly Combining Sequence-Based Features and Boosting Multiple SVMs. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 1389-1398.	3.0	64
6	Improving protein-ATP binding residues prediction by boosting SVMs with random under-sampling. <i>Neurocomputing</i> , 2013, 104, 180-190.	5.9	62
7	LS-align: an atom-level, flexible ligand structural alignment algorithm for high-throughput virtual screening. <i>Bioinformatics</i> , 2018, 34, 2209-2218.	4.1	62
8	ATPbind: Accurate Protein-ATP Binding Site Prediction by Combining Sequence-Profiling and Structure-Based Comparisons. <i>Journal of Chemical Information and Modeling</i> , 2018, 58, 501-510.	5.4	57
9	DNAPred: Accurate Identification of DNA-Binding Sites from Protein Sequence by Ensembled Hyperplane-Distance-Based Support Vector Machines. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 3057-3071.	5.4	53
10	TargetCrys: protein crystallization prediction by fusing multi-view features with two-layered SVM. <i>Amino Acids</i> , 2016, 48, 2533-2547.	2.7	39
11	A New Supervised Over-Sampling Algorithm with Application to Protein-Nucleotide Binding Residue Prediction. <i>PLoS ONE</i> , 2014, 9, e107676.	2.5	37
12	TargetFreeze: Identifying Antifreeze Proteins via a Combination of Weights using Sequence Evolutionary Information and Pseudo Amino Acid Composition. <i>Journal of Membrane Biology</i> , 2015, 248, 1005-1014.	2.1	36
13	Constructing Query-Driven Dynamic Machine Learning Model With Application to Protein-Ligand Binding Sites Prediction. <i>IEEE Transactions on Nanobioscience</i> , 2015, 14, 45-58.	3.3	29
14	GPCR-drug interactions prediction using random forest with drug-association-matrix-based post-processing procedure. <i>Computational Biology and Chemistry</i> , 2016, 60, 59-71.	2.3	29
15	TargetDBP: Accurate DNA-Binding Protein Prediction via Sequence-based Multi-View Feature Learning. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 17, 1-1.	3.0	28
16	scTPA: a web tool for single-cell transcriptome analysis of pathway activation signatures. <i>Bioinformatics</i> , 2020, 36, 4217-4219.	4.1	21
17	KNN-based dynamic query-driven sample rescaling strategy for class imbalance learning. <i>Neurocomputing</i> , 2016, 191, 363-373.	5.9	20
18	Learning protein multi-view features in complex space. <i>Amino Acids</i> , 2013, 44, 1365-1379.	2.7	19

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19	TargetDBP+: Enhancing the Performance of Identifying DNA-Binding Proteins via Weighted Convolutional Features. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 505-515.	5.4	11
20	Accurate multistage prediction of protein crystallization propensity using deep-cascade forest with sequence-based features. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	11
21	Protein Structure Prediction Using Population-Based Algorithm Guided by Information Entropy. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 697-707.	3.0	6
22	Accurate prediction of protein-ATP binding residues using position-specific frequency matrix. <i>Analytical Biochemistry</i> , 2021, 626, 114241.	2.4	6
23	ATPdock: a template-based method for ATP-specific proteinâ€“ligand docking. <i>Bioinformatics</i> , 2022, 38, 556-558.	4.1	5
24	TargetMM: Accurate Missense Mutation Prediction by Utilizing Local and Global Sequence Information with Classifier Ensemble. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2021, 25, 38-52.	1.1	5
25	Identification of ligand-binding residues using protein sequence profile alignment and query-specific support vector machine model. <i>Analytical Biochemistry</i> , 2020, 604, 113799.	2.4	4
26	Two-Stage Distance Feature-based Optimization Algorithm for De novo Protein Structure Prediction. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 17, 2119-2130.	3.0	3
27	Robust distance metric optimization driven GEPSVM classifier for pattern classification. <i>Pattern Recognition</i> , 2022, 129, 108779.	8.1	3
28	Predicting RNA solvent accessibility from multi-scale context feature via multi-shot neural network. <i>Analytical Biochemistry</i> , 2022, 654, 114802.	2.4	3
29	Boosting Granular Support Vector Machines for the Accurate Prediction of Protein-Nucleotide Binding Sites. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2019, 22, 455-469.	1.1	2
30	Protein-DNA Binding Residue Prediction via Bagging Strategy and Sequence-based Cube-Format Feature. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, PP, 1-1.	3.0	2
31	Improved protein relative solvent accessibility prediction using deep multi-view feature learning framework. <i>Analytical Biochemistry</i> , 2021, 631, 114358.	2.4	1
32	Improved Protein Secondary Structure Prediction Using Bidirectional Long Short-Term Memory Neural Network and Bootstrap Aggregating. , 2022, , .		1
33	Loop Enhanced Conformational Resampling Method for Protein Structure Prediction. <i>IEEE Transactions on Nanobioscience</i> , 2019, 18, 567-577.	3.3	0
34	Frontoâ€“parallel building facades stitching. <i>Electronics Letters</i> , 2016, 52, 1524-1526.	1.0	0