Bin Liu

List of Publications by Year
in descending order

33 papers	1,059 citations	516710 16 h-index	414414 32 g-index
34 all docs	34 docs citations	34 times ranked	491 citing authors

#	ARTICLE	IF	CITATIONS
1	PreTP-Stack: Prediction of Therapeutic Peptides Based on the Stacked Ensemble Learing. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2023, 20, 1337-1344.	3.0	9
2	PHR-search: a search framework for protein remote homology detection based on the predicted protein hierarchical relationships. Briefings in Bioinformatics, 2022, , .	6.5	0
3	DeepIDP-2L: protein intrinsically disordered region prediction by combining convolutional attention network and hierarchical attention network. Bioinformatics, 2022, 38, 1252-1260.	4.1	18
4	PreRBP-TL: prediction of species-specific RNA-binding proteins based on transfer learning. Bioinformatics, 2022, 38, 2135-2143.	4.1	17
5	TPpred-ATMV: therapeutic peptide prediction by adaptive multi-view tensor learning model. Bioinformatics, 2022, 38, 2712-2718.	4.1	31
6	AMPpred-EL: An effective antimicrobial peptide prediction model based on ensemble learning. Computers in Biology and Medicine, 2022, 146, 105577.	7.0	12
7	iDRNA-ITF: identifying DNA- and RNA-binding residues in proteins based on induction and transfer framework. Briefings in Bioinformatics, 2022, 23, .	6.5	8
8	DeepDRBP-2L: A New Genome Annotation Predictor for Identifying DNA-Binding Proteins and RNA-Binding Proteins Using Convolutional Neural Network and Long Short-Term Memory. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1451-1463.	3.0	30
9	iLncRNAdis-FB: Identify lncRNA-Disease Associations by Fusing Biological Feature Blocks Through Deep Neural Network. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1946-1957.	3.0	37
10	Protein Fold Recognition by Combining Support Vector Machines and Pairwise Sequence Similarity Scores. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2008-2016.	3.0	13
11	Protein Fold Recognition Based on Auto-Weighted Multi-view Graph Embedding Learning Model. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1-1.	3.0	7
12	PL-search: a profile-link-based search method for protein remote homology detection. Briefings in Bioinformatics, 2021, 22, .	6.5	7
13	idenPC-MIIP: identify protein complexes from weighted PPI networks using mutual important interacting partner relation. Briefings in Bioinformatics, 2021, 22, 1972-1983.	6.5	15
14	FoldRec-C2C: protein fold recognition by combining cluster-to-cluster model and protein similarity network. Briefings in Bioinformatics, 2021, 22, .	6.5	50
15	MLDH-Fold: Protein fold recognition based on multi-view low-rank modeling. Neurocomputing, 2021, 421, 127-139.	5.9	11
16	SMI-BLAST: a novel supervised search framework based on PSI-BLAST for protein remote homology detection. Bioinformatics, 2021, 37, 913-920.	4.1	19
17	NCBRPred: predicting nucleic acid binding residues in proteins based on multilabel learning. Briefings in Bioinformatics, 2021, 22, .	6.5	21
18	iCircDA-LTR: identification of circRNAâ€"disease associations based on Learning to Rank. Bioinformatics, 2021, 37, 3302-3310.	4.1	21

#	ARTICLE	IF	CITATIONS
19	S2L-PSIBLAST: a supervised two-layer search framework based on PSI-BLAST for protein remote homology detection. Bioinformatics, 2021, 37, 4321-4327.	4.1	7
20	PreTP-EL: prediction of therapeutic peptides based on ensemble learning. Briefings in Bioinformatics, 2021, 22, .	6.5	31
21	BioSeq-BLM: a platform for analyzing DNA, RNAÂand protein sequences based on biological language models. Nucleic Acids Research, 2021, 49, e129-e129.	14.5	84
22	idenPC-CAP: Identify protein complexes from weighted RNA-protein heterogeneous interaction networks using co-assemble partner relation. Briefings in Bioinformatics, 2021, 22, .	6.5	12
23	Fold-LTR-TCP: protein fold recognition based on triadic closure principle. Briefings in Bioinformatics, 2020, 21, 2185-2193.	6.5	56
24	MotifCNN-fold: protein fold recognition based on fold-specific features extracted by motif-based convolutional neural networks. Briefings in Bioinformatics, 2020, 21, 2133-2141.	6.5	63
25	iDRBP_MMC: Identifying DNA-Binding Proteins and RNA-Binding Proteins Based on Multi-Label Learning Model and Motif-Based Convolutional Neural Network. Journal of Molecular Biology, 2020, 432, 5860-5875.	4.2	43
26	iPiDA-sHN: Identification of Piwi-interacting RNA-disease associations by selecting high quality negative samples. Computational Biology and Chemistry, 2020, 88, 107361.	2.3	16
27	ReFold-MAP: Protein remote homology detection and fold recognition based on features extracted from profiles. Analytical Biochemistry, 2020, 611, 114013.	2.4	3
28	sgRNA-PSM: Predict sgRNAs On-Target Activity Based on Position-Specific Mismatch. Molecular Therapy - Nucleic Acids, 2020, 20, 323-330.	5.1	13
29	Identification of Intrinsically Disordered Proteins and Regions by Length-Dependent Predictors Based on Conditional Random Fields. Molecular Therapy - Nucleic Acids, 2019, 17, 396-404.	5.1	13
30	BioSeq-Analysis2.0: an updated platform for analyzing DNA, RNA and protein sequences at sequence level and residue level based on machine learning approaches. Nucleic Acids Research, 2019, 47, e127-e127.	14.5	276
31	iPromoter-2L2.0: Identifying Promoters and Their Types by Combining Smoothing Cutting Window Algorithm and Sequence-Based Features. Molecular Therapy - Nucleic Acids, 2019, 18, 80-87.	5.1	65
32	Protein Remote Homology Detection and Fold Recognition Based on Sequence-Order Frequency Matrix. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 292-300.	3.0	21
33	ProtDet-CCH: Protein Remote Homology Detection by Combining Long Short-Term Memory and Ranking Methods. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1203-1210.	3.0	30