

Bin Liu

List of Publications by Year in descending order

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Version: 2024-02-01

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	BioSeq-Analysis2.0: an updated platform for analyzing DNA, RNA and protein sequences at sequence level and residue level based on machine learning approaches. <i>Nucleic Acids Research</i> , 2019, 47, e127-e127.	14.5	276
2	BioSeq-BLM: a platform for analyzing DNA, RNA and protein sequences based on biological language models. <i>Nucleic Acids Research</i> , 2021, 49, e129-e129.	14.5	84
3	iPromoter-2L2.0: Identifying Promoters and Their Types by Combining Smoothing Cutting Window Algorithm and Sequence-Based Features. <i>Molecular Therapy - Nucleic Acids</i> , 2019, 18, 80-87.	5.1	65
4	MotifCNN-fold: protein fold recognition based on fold-specific features extracted by motif-based convolutional neural networks. <i>Briefings in Bioinformatics</i> , 2020, 21, 2133-2141.	6.5	63
5	Fold-LTR-TCP: protein fold recognition based on triadic closure principle. <i>Briefings in Bioinformatics</i> , 2020, 21, 2185-2193.	6.5	56
6	FoldRec-C2C: protein fold recognition by combining cluster-to-cluster model and protein similarity network. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	50
7	iDRBP_MMC: Identifying DNA-Binding Proteins and RNA-Binding Proteins Based on Multi-Label Learning Model and Motif-Based Convolutional Neural Network. <i>Journal of Molecular Biology</i> , 2020, 432, 5860-5875.	4.2	43
8	iLncRNADis-FB: Identify lncRNA-Disease Associations by Fusing Biological Feature Blocks Through Deep Neural Network. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 1946-1957.	3.0	37
9	PreTP-EL: prediction of therapeutic peptides based on ensemble learning. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	31
10	TPpred-ATMV: therapeutic peptide prediction by adaptive multi-view tensor learning model. <i>Bioinformatics</i> , 2022, 38, 2712-2718.	4.1	31
11	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. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 1451-1463.	3.0	30
12	ProtDet-CCH: Protein Remote Homology Detection by Combining Long Short-Term Memory and Ranking Methods. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1203-1210.	3.0	30
13	Protein Remote Homology Detection and Fold Recognition Based on Sequence-Order Frequency Matrix. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 292-300.	3.0	21
14	NCBRPred: predicting nucleic acid binding residues in proteins based on multilabel learning. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	21
15	iCircDA-LTR: identification of circRNA-disease associations based on Learning to Rank. <i>Bioinformatics</i> , 2021, 37, 3302-3310.	4.1	21
16	SMI-BLAST: a novel supervised search framework based on PSI-BLAST for protein remote homology detection. <i>Bioinformatics</i> , 2021, 37, 913-920.	4.1	19
17	DeepIDP-2L: protein intrinsically disordered region prediction by combining convolutional attention network and hierarchical attention network. <i>Bioinformatics</i> , 2022, 38, 1252-1260.	4.1	18
18	PreRBP-TL: prediction of species-specific RNA-binding proteins based on transfer learning. <i>Bioinformatics</i> , 2022, 38, 2135-2143.	4.1	17

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19	iPiDA-sHN: Identification of Piwi-interacting RNA-disease associations by selecting high quality negative samples. <i>Computational Biology and Chemistry</i> , 2020, 88, 107361.	2.3	16
20	idenPC-MIIP: identify protein complexes from weighted PPI networks using mutual important interacting partner relation. <i>Briefings in Bioinformatics</i> , 2021, 22, 1972-1983.	6.5	15
21	Identification of Intrinsically Disordered Proteins and Regions by Length-Dependent Predictors Based on Conditional Random Fields. <i>Molecular Therapy - Nucleic Acids</i> , 2019, 17, 396-404.	5.1	13
22	Protein Fold Recognition by Combining Support Vector Machines and Pairwise Sequence Similarity Scores. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 2008-2016.	3.0	13
23	sgRNA-PSM: Predict sgRNAs On-Target Activity Based on Position-Specific Mismatch. <i>Molecular Therapy - Nucleic Acids</i> , 2020, 20, 323-330.	5.1	13
24	idenPC-CAP: Identify protein complexes from weighted RNA-protein heterogeneous interaction networks using co-assemble partner relation. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	12
25	AMPpred-EL: An effective antimicrobial peptide prediction model based on ensemble learning. <i>Computers in Biology and Medicine</i> , 2022, 146, 105577.	7.0	12
26	MLDH-Fold: Protein fold recognition based on multi-view low-rank modeling. <i>Neurocomputing</i> , 2021, 421, 127-139.	5.9	11
27	PreTP-Stack: Prediction of Therapeutic Peptides Based on the Stacked Ensemble Learning. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2023, 20, 1337-1344.	3.0	9
28	iDRNA-ITF: identifying DNA- and RNA-binding residues in proteins based on induction and transfer framework. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	8
29	Protein Fold Recognition Based on Auto-Weighted Multi-view Graph Embedding Learning Model. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 1-1.	3.0	7
30	PL-search: a profile-link-based search method for protein remote homology detection. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	7
31	S2L-PSIBLAST: a supervised two-layer search framework based on PSI-BLAST for protein remote homology detection. <i>Bioinformatics</i> , 2021, 37, 4321-4327.	4.1	7
32	ReFold-MAP: Protein remote homology detection and fold recognition based on features extracted from profiles. <i>Analytical Biochemistry</i> , 2020, 611, 114013.	2.4	3
33	PHR-search: a search framework for protein remote homology detection based on the predicted protein hierarchical relationships. <i>Briefings in Bioinformatics</i> , 2022, .	6.5	0