Fuyi Li

List of Publications by Year in descending order

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Version: 2024-02-01

52 papers	3,452 citations	186265 28 h-index	175258 52 g-index
55 all docs	55 docs citations	55 times ranked	2172 citing authors

#	Article	IF	Citations
1	Positive-unlabeled learning in bioinformatics and computational biology: a brief review. Briefings in Bioinformatics, 2022, 23, .	6.5	26
2	Critical assessment of computational tools for prokaryotic and eukaryotic promoter prediction. Briefings in Bioinformatics, 2022, 23, .	6.5	11
3	Computational analysis and prediction of PE_PGRS proteins using machine learning. Computational and Structural Biotechnology Journal, 2022, 20, 662-674.	4.1	12
4	ASPIRER: a new computational approach for identifying non-classical secreted proteins based on deep learning. Briefings in Bioinformatics, 2022, 23, .	6.5	11
5	RBP-TSTL is a two-stage transfer learning framework for genome-scale prediction of RNA-binding proteins. Briefings in Bioinformatics, 2022, 23, .	6.5	6
6	PredPromoter-MF(2L): A Novel Approach of Promoter Prediction Based on Multi-source Feature Fusion and Deep Forest. Interdisciplinary Sciences, Computational Life Sciences, 2022, , .	3.6	3
7	iFeatureOmega:an integrative platform for engineering, visualization and analysis of features from molecular sequences, structural and ligand data sets. Nucleic Acids Research, 2022, 50, W434-W447.	14.5	24
8	DeepGenGrep: a general deep learning-based predictor for multiple genomic signals and regions. Bioinformatics, 2022, 38, 4053-4061.	4.1	6
9	Formator: Predicting Lysine Formylation Sites Based on the Most Distant Undersampling and Safe-Level Synthetic Minority Oversampling. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1937-1945.	3.0	17
10	DeepBL: a deep learning-based approach for in silico discovery of beta-lactamases. Briefings in Bioinformatics, 2021, 22, .	6.5	9
11	Computational identification of eukaryotic promoters based on cascaded deep capsule neural networks. Briefings in Bioinformatics, 2021, 22, .	6.5	44
12	A Deep Learning-Based Method for Identification of Bacteriophage-Host Interaction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1801-1810.	3.0	31
13	Large-scale comparative review and assessment of computational methods for anti-cancer peptide identification. Briefings in Bioinformatics, 2021, 22, .	6.5	40
14	Systematic evaluation of machine learning methods for identifying humanâ€“pathogen proteinâ€“protein interactions. Briefings in Bioinformatics, 2021, 22, .	6.5	23
15	Computational prediction and interpretation of both general and specific types of promoters in Escherichia coli by exploiting a stacked ensemble-learning framework. Briefings in Bioinformatics, 2021, 22, 2126-2140.	6.5	58
16	DeepTorrent: a deep learning-based approach for predicting DNA N4-methylcytosine sites. Briefings in Bioinformatics, 2021, 22, .	6.5	84
17	Anthem: a user customised tool for fast and accurate prediction of binding between peptides and HLA class I molecules. Briefings in Bioinformatics, 2021, 22, .	6.5	37
18	iLearnPlus:a comprehensive and automated machine-learning platform for nucleic acid and protein sequence analysis, prediction and visualization. Nucleic Acids Research, 2021, 49, e60-e60.	14.5	124

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19	Comprehensive assessment of machine learning-based methods for predicting antimicrobial peptides. Briefings in Bioinformatics, 2021, 22, .	6.5	55
20	Predicting Proteolysis in Complex Proteomes Using Deep Learning. International Journal of Molecular Sciences, 2021, 22, 3071.	4.1	18
21	Assessing the performance of computational predictors for estimating protein stability changes upon missense mutations. Briefings in Bioinformatics, 2021, 22, .	6.5	30
22	HEAL: an automated deep learning framework for cancer histopathology image analysis. Bioinformatics, 2021, 37, 4291-4295.	4.1	18
23	Porpoise: a new approach for accurate prediction of RNA pseudouridine sites. Briefings in Bioinformatics, 2021, 22, .	6.5	39
24	Accurate multistage prediction of protein crystallization propensity using deep-cascade forest with sequence-based features. Briefings in Bioinformatics, 2021, 22, .	6.5	11
25	Staem5: A novel computational approach for accurate prediction of m5C site. Molecular Therapy - Nucleic Acids, 2021, 26, 1027-1034.	5.1	20
26	BigFiRSt: A Software Program Using Big Data Technique for Mining Simple Sequence Repeats From Large-Scale Sequencing Data. Frontiers in Big Data, 2021, 4, 727216.	2.9	2
27	A comprehensive review and performance evaluation of bioinformatics tools for HLA class I peptide-binding prediction. Briefings in Bioinformatics, 2020, 21, 1119-1135.	6.5	127
28	iLearn: an integrated platform and meta-learner for feature engineering, machine-learning analysis and modeling of DNA, RNA and protein sequence data. Briefings in Bioinformatics, 2020, 21, 1047-1057.	6.5	294
29	DeepCleave: a deep learning predictor for caspase and matrix metalloprotease substrates and cleavage sites. Bioinformatics, 2020, 36, 1057-1065.	4.1	102
30	Comprehensive review and assessment of computational methods for predicting RNA post-transcriptional modification sites from RNA sequences. Briefings in Bioinformatics, 2020, 21, 1676-1696.	6.5	98
31	An Interpretable Prediction Model for Identifying N7-Methylguanosine Sites Based on XGBoost and SHAP. Molecular Therapy - Nucleic Acids, 2020, 22, 362-372.	5.1	93
32	Pippin: A random forest-based method for identifying presynaptic and postsynaptic neurotoxins. Journal of Bioinformatics and Computational Biology, 2020, 18, 2050008.	0.8	1
33	PASSION: an ensemble neural network approach for identifying the binding sites of RBPs on circRNAs. Bioinformatics, 2020, 36, 4276-4282.	4.1	58
34	Procleave: Predicting Protease-specific Substrate Cleavage Sites by Combining Sequence and Structural Information. Genomics, Proteomics and Bioinformatics, 2020, 18, 52-64.	6.9	71
35	PROSPECT: A web server for predicting protein histidine phosphorylation sites. Journal of Bioinformatics and Computational Biology, 2020, 18, 2050018.	0.8	25
36	Inspector: a lysine succinylation predictor based on edited nearest-neighbor undersampling and adaptive synthetic oversampling. Analytical Biochemistry, 2020, 593, 113592.	2.4	40

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37	PRISMOID: a comprehensive 3D structure database for post-translational modifications and mutations with functional impact. Briefings in Bioinformatics, 2020, 21, 1069-1079.	6.5	38
38	MULTiPly: a novel multi-layer predictor for discovering general and specific types of promoters. Bioinformatics, 2019, 35, 2957-2965.	4.1	109
39	The flagellotropic bacteriophage YSD1 targets Salmonella Typhi with a Chiâ€like protein tailÂfibre. Molecular Microbiology, 2019, 112, 1831-1846.	2.5	24
40	Characterization of the Src-regulated kinome identifies SGK1 as a key mediator of Src-induced transformation. Nature Communications, 2019, 10, 296.	12.8	23
41	Positive-unlabelled learning of glycosylation sites in the human proteome. BMC Bioinformatics, 2019, 20, 112.	2.6	60
42	SIMLIN: a bioinformatics tool for prediction of S-sulphenylation in theÂhuman proteome based on multi-stage ensemble-learning models. BMC Bioinformatics, 2019, 20, 602.	2.6	10
43	Twenty years of bioinformatics research for protease-specific substrate and cleavage site prediction: a comprehensive revisit and benchmarking of existing methods. Briefings in Bioinformatics, 2019, 20, 2150-2166.	6.5	70
44	Large-scale comparative assessment of computational predictors for lysine post-translational modification sites. Briefings in Bioinformatics, 2019, 20, 2267-2290.	6.5	99
45	iProt-Sub: a comprehensive package for accurately mapping and predicting protease-specific substrates and cleavage sites. Briefings in Bioinformatics, 2019, 20, 638-658.	6.5	166
46	iFeature: a Python package and web server for features extraction and selection from protein and peptide sequences. Bioinformatics, 2018, 34, 2499-2502.	4.1	481
47	PREvalL, an integrative approach for inferring catalytic residues using sequence, structural, and network features in a machine-learning framework. Journal of Theoretical Biology, 2018, 443, 125-137.	1.7	124
48	PROSPERous: high-throughput prediction of substrate cleavage sites for 90 proteases with improved accuracy. Bioinformatics, 2018, 34, 684-687.	4.1	131
49	Comparative analysis and prediction of quorum-sensing peptides using feature representation learning and machine learning algorithms. Briefings in Bioinformatics, 2018, , .	6.5	60
50	Quokka: a comprehensive tool for rapid and accurate prediction of kinase family-specific phosphorylation sites in the human proteome. Bioinformatics, 2018, 34, 4223-4231.	4.1	151
51	GlycoMinestruct: a new bioinformatics tool for highly accurate mapping of the human N-linked and O-linked glycoproteomes by incorporating structural features. Scientific Reports, 2016, 6, 34595.	3.3	69
52	GlycoMine: a machine learning-based approach for predicting N-, C- and O-linked glycosylation in the human proteome. Bioinformatics, 2015, 31, 1411-1419.	4.1	167