Fuyi Li

List of Publications by Year in descending order

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	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
2	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
3	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
4	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
5	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
6	PROSPERous: high-throughput prediction of substrate cleavage sites for 90 proteases with improved accuracy. Bioinformatics, 2018, 34, 684-687.	4.1	131
7	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
8	PREvaIL, 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
9	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
10	MULTiPly: a novel multi-layer predictor for discovering general and specific types of promoters. Bioinformatics, 2019, 35, 2957-2965.	4.1	109
11	DeepCleave: a deep learning predictor for caspase and matrix metalloprotease substrates and cleavage sites. Bioinformatics, 2020, 36, 1057-1065.	4.1	102
12	Large-scale comparative assessment of computational predictors for lysine post-translational modification sites. Briefings in Bioinformatics, 2019, 20, 2267-2290.	6.5	99
13	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
14	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
15	DeepTorrent: a deep learning-based approach for predicting DNA N4-methylcytosine sites. Briefings in Bioinformatics, 2021, 22, .	6.5	84
16	Procleave: Predicting Protease-specific Substrate Cleavage Sites by Combining Sequence and Structural Information. Genomics, Proteomics and Bioinformatics, 2020, 18, 52-64.	6.9	71
17	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
18	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

#	Article	IF	Citations
19	Comparative analysis and prediction of quorum-sensing peptides using feature representation learning and machine learning algorithms. Briefings in Bioinformatics, 2018, , .	6.5	60
20	Positive-unlabelled learning of glycosylation sites in the human proteome. BMC Bioinformatics, 2019, 20, 112.	2.6	60
21	PASSION: an ensemble neural network approach for identifying the binding sites of RBPs on circRNAs. Bioinformatics, 2020, 36, 4276-4282.	4.1	58
22	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
23	Comprehensive assessment of machine learning-based methods for predicting antimicrobial peptides. Briefings in Bioinformatics, 2021, 22, .	6.5	55
24	Computational identification of eukaryotic promoters based on cascaded deep capsule neural networks. Briefings in Bioinformatics, 2021, 22, .	6.5	44
25	Large-scale comparative review and assessment of computational methods for anti-cancer peptide identification. Briefings in Bioinformatics, 2021, 22, .	6.5	40
26	Inspector: a lysine succinylation predictor based on edited nearest-neighbor undersampling and adaptive synthetic oversampling. Analytical Biochemistry, 2020, 593, 113592.	2.4	40
27	Porpoise: a new approach for accurate prediction of RNA pseudouridine sites. Briefings in Bioinformatics, 2021, 22, .	6.5	39
28	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
29	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
30	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
31	Assessing the performance of computational predictors for estimating protein stability changes upon missense mutations. Briefings in Bioinformatics, 2021, 22, .	6.5	30
32	Positive-unlabeled learning in bioinformatics and computational biology: a brief review. Briefings in Bioinformatics, 2022, 23, .	6.5	26
33	PROSPECT: A web server for predicting protein histidine phosphorylation sites. Journal of Bioinformatics and Computational Biology, 2020, 18, 2050018.	0.8	25
34	The flagellotropic bacteriophage YSD1 targets Salmonella Typhi with a Chiâ€like protein tailÂfibre. Molecular Microbiology, 2019, 112, 1831-1846.	2.5	24
35	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
36	Characterization of the Src-regulated kinome identifies SGK1 as a key mediator of Src-induced transformation. Nature Communications, 2019, 10, 296.	12.8	23

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37	Systematic evaluation of machine learning methods for identifying humanâ€“pathogen proteinâ€“protein interactions. Briefings in Bioinformatics, 2021, 22, .	6.5	23
38	Staem5: A novel computational approach for accurate prediction of m5C site. Molecular Therapy - Nucleic Acids, 2021, 26, 1027-1034.	5.1	20
39	Predicting Proteolysis in Complex Proteomes Using Deep Learning. International Journal of Molecular Sciences, 2021, 22, 3071.	4.1	18
40	HEAL: an automated deep learning framework for cancer histopathology image analysis. Bioinformatics, 2021, 37, 4291-4295.	4.1	18
41	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
42	Computational analysis and prediction of PE_PGRS proteins using machine learning. Computational and Structural Biotechnology Journal, 2022, 20, 662-674.	4.1	12
43	Accurate multistage prediction of protein crystallization propensity using deep-cascade forest with sequence-based features. Briefings in Bioinformatics, 2021, 22, .	6.5	11
44	Critical assessment of computational tools for prokaryotic and eukaryotic promoter prediction. Briefings in Bioinformatics, 2022, 23, .	6.5	11
45	ASPIRER: a new computational approach for identifying non-classical secreted proteins based on deep learning. Briefings in Bioinformatics, 2022, 23, .	6.5	11
46	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
47	DeepBL: a deep learning-based approach for in silico discovery of beta-lactamases. Briefings in Bioinformatics, 2021, 22, .	6.5	9
48	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
49	DeepGenGrep: a general deep learning-based predictor for multiple genomic signals and regions. Bioinformatics, 2022, 38, 4053-4061.	4.1	6
50	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
51	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
52	Pippin: A random forest-based method for identifying presynaptic and postsynaptic neurotoxins. Journal of Bioinformatics and Computational Biology, 2020, 18, 2050008.	0.8	1