Leyi Wei

List of Publications by Year
in descending order

91 papers	6,709 citations	71102 41 h-index	62596 80 g-index
92 all docs	92 docs citations	92 times ranked	3418 citing authors

#	Article	IF	Citations
1	DUNet: A deformable network for retinal vessel segmentation. Knowledge-Based Systems, 2019, 178, 149-162.	7.1	535
2	Gene2vec: gene subsequence embedding for prediction of mammalian N^6-methyladenosine sites from mRNA. Rna, 2019, 25, 205-218.	3.5	421
3	ACPred-FL: a sequence-based predictor using effective feature representation to improve the prediction of anti-cancer peptides. Bioinformatics, 2018, 34, 4007-4016.	4.1	326
4	Local-DPP: An improved DNA-binding protein prediction method by exploring local evolutionary information. Information Sciences, 2017, 384, 135-144.	6.9	226
5	Improved prediction of protein–protein interactions using novel negative samples, features, and an ensemble classifier. Artificial Intelligence in Medicine, 2017, 83, 67-74.	6.5	220
6	Improved and Promising Identification of Human MicroRNAs by Incorporating a High-Quality Negative Set. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 192-201.	3.0	207
7	A novel hierarchical selective ensemble classifier with bioinformatics application. Artificial Intelligence in Medicine, 2017, 83, 82-90.	6.5	192
8	mAHTPred: a sequence-based meta-predictor for improving the prediction of anti-hypertensive peptides using effective feature representation. Bioinformatics, 2019, 35, 2757-2765.	4.1	186
9	Prediction of human protein subcellular localization using deep learning. Journal of Parallel and Distributed Computing, 2018, 117, 212-217.	4.1	184
10	Meta-4mCpred: A Sequence-Based Meta-Predictor for Accurate DNA 4mC Site Prediction Using Effective Feature Representation. Molecular Therapy - Nucleic Acids, 2019, 16, 733-744.	5.1	182
11	Deep-Resp-Forest: A deep forest model to predict anti-cancer drug response. Methods, 2019, 166, 91-102.	3.8	182
12	CPPred-RF: A Sequence-based Predictor for Identifying Cell-Penetrating Peptides and Their Uptake Efficiency. Journal of Proteome Research, 2017, 16, 2044-2053.	3.7	168
13	M6APred-EL: A Sequence-Based Predictor for Identifying N6-methyladenosine Sites Using Ensemble Learning. Molecular Therapy - Nucleic Acids, 2018, 12, 635-644.	5.1	167
14	Fast Prediction of Protein Methylation Sites Using a Sequence-Based Feature Selection Technique. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1264-1273.	3.0	163
15	Exploring sequence-based features for the improved prediction of DNA N4-methylcytosine sites in multiple species. Bioinformatics, 2019, 35, 1326-1333.	4.1	156
16	Integration of deep feature representations and handcrafted features to improve the prediction of N6-methyladenosine sites. Neurocomputing, 2019, 324, 3-9.	5.9	130
17	Identifying enhancer–promoter interactions with neural network based on pre-trained DNA vectors and attention mechanism. Bioinformatics, 2020, 36, 1037-1043.	4.1	127
18	Empirical comparison and analysis of web-based cell-penetrating peptide prediction tools. Briefings in Bioinformatics, 2020, 21, 408-420.	6.5	122

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19	Developing a Multi-Dose Computational Model for Drug-Induced Hepatotoxicity Prediction Based on Toxicogenomics Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1231-1239.	3.0	120
20	PEPred-Suite: improved and robust prediction of therapeutic peptides using adaptive feature representation learning. Bioinformatics, 2019, 35, 4272-4280.	4.1	116
21	Iterative feature representations improve N4-methylcytosine site prediction. Bioinformatics, 2019, 35, 4930-4937.	4.1	113
22	PhosPred-RF: A Novel Sequence-Based Predictor for Phosphorylation Sites Using Sequential Information Only. IEEE Transactions on Nanobioscience, 2017, 16, 240-247.	3.3	112
23	ACPred-Fuse: fusing multi-view information improves the prediction of anticancer peptides. Briefings in Bioinformatics, 2020, 21, 1846-1855.	6.5	100
24	M6AMRFS: Robust Prediction of N6-Methyladenosine Sites With Sequence-Based Features in Multiple Species. Frontiers in Genetics, 2018, 9, 495.	2.3	90
25	AtbPpred: A Robust Sequence-Based Prediction of Anti-Tubercular Peptides Using Extremely Randomized Trees. Computational and Structural Biotechnology Journal, 2019, 17, 972-981.	4.1	89
26	Enhanced Protein Fold Prediction Method Through a Novel Feature Extraction Technique. IEEE Transactions on Nanobioscience, 2015, 14, 649-659.	3.3	87
27	SkipCPP-Pred: an improved and promising sequence-based predictor for predicting cell-penetrating peptides. BMC Genomics, 2017, 18, 742.	2.8	85
28	An Improved Protein Structural Classes Prediction Method by Incorporating Both Sequence and Structure Information. IEEE Transactions on Nanobioscience, 2015, 14, 339-349.	3.3	80
29	A Review of DNA-binding Proteins Prediction Methods. Current Bioinformatics, 2019, 14, 246-254.	1.5	79
30	Identifying N6-methyladenosine sites using multi-interval nucleotide pair position specificity and support vector machine. Scientific Reports, 2017, 7, 46757.	3.3	77
31	4mCpred-EL: An Ensemble Learning Framework for Identification of DNA N4-methylcytosine Sites in the Mouse Genome. Cells, 2019, 8, 1332.	4.1	77
32	Recent Progress in Machine Learning-Based Methods for Protein Fold Recognition. International Journal of Molecular Sciences, 2016, 17, 2118.	4.1	73
33	Computational prediction and interpretation of cell-specific replication origin sites from multiple eukaryotes by exploiting stacking framework. Briefings in Bioinformatics, 2021, 22, .	6.5	73
34	Construction, Model-Based Analysis, and Characterization of a Promoter Library for Fine-Tuned Gene Expression in <i>Bacillus subtilis</i>. ACS Synthetic Biology, 2018, 7, 1785-1797.	3.8	67
35	Meta-GDBP: a high-level stacked regression model to improve anticancer drug response prediction. Briefings in Bioinformatics, 2020, 21, 996-1005.	6.5	63
36	Improved detection of DNA-binding proteins via compression technology on PSSM information. PLoS ONE, 2017, 12, e0185587.	2.5	63

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37	CPPred-FL: a sequence-based predictor for large-scale identification of cell-penetrating peptides by feature representation learning. Briefings in Bioinformatics, 2018, , .	6.5	62
38	Comparative analysis and prediction of quorum-sensing peptides using feature representation learning and machine learning algorithms. Briefings in Bioinformatics, 2018, , .	6.5	60
39	ToxIBTL: prediction of peptide toxicity based on information bottleneck and transfer learning. Bioinformatics, 2022, 38, 1514-1524.	4.1	54
40	Briefing in family characteristics of microRNAs and their applications in cancer research. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 191-197.	2.3	51
41	SecProMTB: Support Vector Machine€Based Classifier for Secretory Proteins Using Imbalanced Data Sets Applied toMycobacterium tuberculosis. Proteomics, 2019, 19, 1900007.	2.2	43
42	ATSE: a peptide toxicity predictor by exploiting structural and evolutionary information based on graph neural network and attention mechanism. Briefings in Bioinformatics, 2021, 22, .	6.5	43
43	A novel machine learning method for cytokine-receptor interaction prediction. Combinatorial Chemistry and High Throughput Screening, 2016, 19, 144-152.	1.1	43
44	Computational Approaches in Detecting Non- Coding RNA. Current Genomics, 2013, 14, 371-377.	1.6	41
45	Research progress in protein posttranslational modification site prediction. Briefings in Functional Genomics, 2019, 18, 220-229.	2.7	39
46	Integrative machine learning framework for the identification of cell-specific enhancers from the human genome. Briefings in Bioinformatics, 2021, 22, .	6.5	38
47	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
48	Iterative feature representation algorithm to improve the predictive performance of N7-methylguanosine sites. Briefings in Bioinformatics, 2021, 22, .	6.5	35
49	Identification of DNA-Binding Proteins Using Mixed Feature Representation Methods. Molecules, 2017, 22, 1602.	3.8	34
50	6mA-RicePred: A Method for Identifying DNA N6-Methyladenine Sites in the Rice Genome Based on Feature Fusion. Frontiers in Plant Science, 2020, 11, 4.	3.6	34
51	Domain adaptation based self-correction model for COVID-19 infection segmentation in CT images. Expert Systems With Applications, 2021, 176, 114848.	7.6	34
52	MiR-93-5p Promotes Cell Proliferation through Down-Regulating PPARGC1A in Hepatocellular Carcinoma Cells by Bioinformatics Analysis and Experimental Verification. Genes, 2018, 9, 51.	2.4	31
53	Supervised Brain Tumor Segmentation Based on Gradient and Context-Sensitive Features. Frontiers in Neuroscience, 2019, 13, 144.	2.8	29
54	Accelerating bioactive peptide discovery via mutual information-based meta-learning. Briefings in Bioinformatics, 2022, 23, .	6.5	29

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55	MinE-RFE: determine the optimal subset from RFE by minimizing the subset-accuracyâ€"defined energy. Briefings in Bioinformatics, 2020, 21, 687-698.	6.5	28
56	mGOF-loc: A novel ensemble learning method for human protein subcellular localization prediction. Neurocomputing, 2016, 217, 73-82.	5.9	26
57	Identification of expression signatures for non-small-cell lung carcinoma subtype classification. Bioinformatics, 2020, 36, 339-346.	4.1	26
58	Fusing convolutional neural network features with hand-crafted features for osteoporosis diagnoses. Neurocomputing, 2020, 385, 300-309.	5.9	26
59	iRNA5hmC: The First Predictor to Identify RNA 5-Hydroxymethylcytosine Modifications Using Machine Learning. Frontiers in Bioengineering and Biotechnology, 2020, 8, 227.	4.1	26
60	EP3: an ensemble predictor that accurately identifies type III secreted effectors. Briefings in Bioinformatics, 2021, 22, 1918-1928.	6.5	26
61	Classification and gene selection of triple-negative breast cancer subtype embedding gene connectivity matrix in deep neural network. Briefings in Bioinformatics, 2021, 22, .	6.5	26
62	Learning embedding features based on multisense-scaled attention architecture to improve the predictive performance of anticancer peptides. Bioinformatics, 2021, 37, 4684-4693.	4.1	26
63	Predicting proteinâ€"peptide binding residues via interpretable deep learning. Bioinformatics, 2022, 38, 3351-3360.	4.1	24
64	iDNA-ABT: advanced deep learning model for detecting DNA methylation with adaptive features and transductive information maximization. Bioinformatics, 2021, 37, 4603-4610.	4.1	23
65	Computational Analysis of miRNA Target Identification. Current Bioinformatics, 2012, 7, 512-525.	1.5	20
66	Protein subcellular localization based on deep image features and criterion learning strategy. Briefings in Bioinformatics, 2021, 22, .	6.5	20
67	PepFormer: End-to-End Transformer-Based Siamese Network to Predict and Enhance Peptide Detectability Based on Sequence Only. Analytical Chemistry, 2021, 93, 6481-6490.	6.5	20
68	Predicting drug-induced hepatotoxicity based on biological feature maps and diverse classification strategies. Briefings in Bioinformatics, 2021, 22, 428-437.	6.5	18
69	UltraPse: A Universal and Extensible Software Platform for Representing Biological Sequences. International Journal of Molecular Sciences, 2017, 18, 2400.	4.1	16
70	FEGS: a novel feature extraction model for protein sequences and its applications. BMC Bioinformatics, 2021, 22, 297.	2.6	16
71	Multi-scale deep learning for the imbalanced multi-label protein subcellular localization prediction based on immunohistochemistry images. Bioinformatics, 2022, 38, 2602-2611.	4.1	14
72	Identification of glioblastoma molecular subtype and prognosis based on deep MRI features. Knowledge-Based Systems, 2021, 232, 107490.	7.1	13

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73	PESA-Net: Permutation-Equivariant Split Attention Network for correspondence learning. Information Fusion, 2022, 77, 81-89.	19.1	13
74	A Bioinformatics Tool for the Prediction of DNA N6-Methyladenine Modifications Based on Feature Fusion and Optimization Protocol. Frontiers in Bioengineering and Biotechnology, 2020, 8, 502.	4.1	12
75	scIMC: a platform for benchmarking comparison and visualization analysis of scRNA-seq data imputation methods. Nucleic Acids Research, 2022, 50, 4877-4899.	14.5	12
76	Exploring local discriminative information from evolutionary profiles for cytokine–receptor interaction prediction. Neurocomputing, 2016, 217, 37-45.	5.9	11
77	Robust Feature Matching for Remote Sensing Image Registration via Guided Hyperplane Fitting. IEEE Transactions on Geoscience and Remote Sensing, 2022, 60, 1-14.	6.3	11
78	Identifying Plant Pentatricopeptide Repeat Coding Gene/Protein Using Mixed Feature Extraction Methods. Frontiers in Plant Science, 2018, 9, 1961.	3.6	10
79	PSSP-MVIRT: peptide secondary structure prediction based on a multi-view deep learning architecture. Briefings in Bioinformatics, 2021, 22, .	6.5	8
80	EOCSA: Predicting prognosis of Epithelial ovarian cancer with whole slide histopathological images. Expert Systems With Applications, 2022, 206, 117643.	7.6	8
81	Distant metastasis identification based on optimized graph representation of gene interaction patterns. Briefings in Bioinformatics, 2022, 23, .	6.5	6
82	LncPred-IEL: A Long Non-coding RNA Prediction Method using Iterative Ensemble Learning. , 2019, , .		5
83	Improved Identification of Cytokines Using Feature Selection Techniques. Letters in Organic Chemistry, 2017, 14, .	0.5	5
84	Three-Dimensional Face Reconstruction Using Multi-View-Based Bilinear Model. Sensors, 2019, 19, 459.	3.8	4
85	Encoded Texture Features to Characterize Bone Radiograph Images. , 2018, , .		3
86	Better Performance with Transformer: CPPFormer in precise prediction of cell-Penetrating Peptides. Current Medicinal Chemistry, 2021, 28, .	2.4	3
87	A 2-Layer Web Server for Enzyme and Multifunctional Enzyme Identification. Current Bioinformatics, 2014, 9, 2-7.	1.5	2
88	Signaling Potential Therapeutic Herbal Medicine Prescription for Treating COVID-19 by Collaborative Filtering. Frontiers in Pharmacology, 2021, 12, 759479.	3.5	2
89	Discriminant Affinity Matrix for Deterministic Motion Trajectory Segmentation. IEEE Access, 2019, 7, 57200-57209.	4.2	1
90	IEEE Access Special Section Editorial: Feature Representation and Learning Methods With Applications in Large-Scale Biological Sequence Analysis. IEEE Access, 2021, 9, 33110-33119.	4.2	1

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91	Identification and Prediction of Key Nucleotide Sites Using Machine Learning in Bioinformatics: A Brief Overview. , 2019, , .		0