

# Leyi Wei

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

85  
papers

4,320  
citations

39  
h-index

65  
g-index

92  
ext. papers

5,629  
ext. citations

7.2  
avg, IF

6.62  
L-index

#	Paper	IF	Citations
85	Gene2vec: gene subsequence embedding for prediction of mammalian -methyladenosine sites from mRNA. <i>Rna</i> , <b>2019</b> , 25, 205-218	5.8	279
84	DUNet: A deformable network for retinal vessel segmentation. <i>Knowledge-Based Systems</i> , <b>2019</b> , 178, 149-162	7.3	243
83	Improved prediction of protein-protein interactions using novel negative samples, features, and an ensemble classifier. <i>Artificial Intelligence in Medicine</i> , <b>2017</b> , 83, 67-74	7.4	174
82	Local-DPP: An improved DNA-binding protein prediction method by exploring local evolutionary information. <i>Information Sciences</i> , <b>2017</b> , 384, 135-144	7.7	172
81	Improved and Promising Identification of Human MicroRNAs by Incorporating a High-Quality Negative Set. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2014</b> , 11, 192-201	3	170
80	ACPred-FL: a sequence-based predictor using effective feature representation to improve the prediction of anti-cancer peptides. <i>Bioinformatics</i> , <b>2018</b> , 34, 4007-4016	7.2	162
79	A novel hierarchical selective ensemble classifier with bioinformatics application. <i>Artificial Intelligence in Medicine</i> , <b>2017</b> , 83, 82-90	7.4	154
78	Prediction of human protein subcellular localization using deep learning. <i>Journal of Parallel and Distributed Computing</i> , <b>2018</b> , 117, 212-217	4.4	152
77	Meta-4mCpred: A Sequence-Based Meta-Predictor for Accurate DNA 4mC Site Prediction Using Effective Feature Representation. <i>Molecular Therapy - Nucleic Acids</i> , <b>2019</b> , 16, 733-744	10.7	126
76	mAHTPred: a sequence-based meta-predictor for improving the prediction of anti-hypertensive peptides using effective feature representation. <i>Bioinformatics</i> , <b>2019</b> , 35, 2757-2765	7.2	126
75	Fast Prediction of Protein Methylation Sites Using a Sequence-Based Feature Selection Technique. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2019</b> , 16, 1264-1273	3	123
74	CPPred-RF: A Sequence-based Predictor for Identifying Cell-Penetrating Peptides and Their Uptake Efficiency. <i>Journal of Proteome Research</i> , <b>2017</b> , 16, 2044-2053	5.6	120
73	Deep-Resp-Forest: A deep forest model to predict anti-cancer drug response. <i>Methods</i> , <b>2019</b> , 166, 91-102.6	11.7	117
72	M6APred-EL: A Sequence-Based Predictor for Identifying N6-methyladenosine Sites Using Ensemble Learning. <i>Molecular Therapy - Nucleic Acids</i> , <b>2018</b> , 12, 635-644	10.7	116
71	Integration of deep feature representations and handcrafted features to improve the prediction of N6-methyladenosine sites. <i>Neurocomputing</i> , <b>2019</b> , 324, 3-9	5.4	106
70	Exploring sequence-based features for the improved prediction of DNA N4-methylcytosine sites in multiple species. <i>Bioinformatics</i> , <b>2019</b> , 35, 1326-1333	7.2	104
69	PhosPred-RF: A Novel Sequence-Based Predictor for Phosphorylation Sites Using Sequential Information Only. <i>IEEE Transactions on Nanobioscience</i> , <b>2017</b> , 16, 240-247	3.4	98

68	Developing a Multi-Dose Computational Model for Drug-Induced Hepatotoxicity Prediction Based on Toxicogenomics Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2019</b> , 16, 1231-1239	3	85
67	Empirical comparison and analysis of web-based cell-penetrating peptide prediction tools. <i>Briefings in Bioinformatics</i> , <b>2020</b> , 21, 408-420	13.4	83
66	Iterative feature representations improve N4-methylcytosine site prediction. <i>Bioinformatics</i> , <b>2019</b> , 35, 4930-4937	7.2	77
65	Enhanced Protein Fold Prediction Method Through a Novel Feature Extraction Technique. <i>IEEE Transactions on Nanobioscience</i> , <b>2015</b> , 14, 649-59	3.4	77
64	PEPred-Suite: improved and robust prediction of therapeutic peptides using adaptive feature representation learning. <i>Bioinformatics</i> , <b>2019</b> , 35, 4272-4280	7.2	68
63	An Improved Protein Structural Classes Prediction Method by Incorporating Both Sequence and Structure Information. <i>IEEE Transactions on Nanobioscience</i> , <b>2015</b> , 14, 339-349	3.4	66
62	Recent Progress in Machine Learning-Based Methods for Protein Fold Recognition. <i>International Journal of Molecular Sciences</i> , <b>2016</b> , 17,	6.3	63
61	SkipCPP-Pred: an improved and promising sequence-based predictor for predicting cell-penetrating peptides. <i>BMC Genomics</i> , <b>2017</b> , 18, 742	4.5	62
60	AtbPpred: A Robust Sequence-Based Prediction of Anti-Tubercular Peptides Using Extremely Randomized Trees. <i>Computational and Structural Biotechnology Journal</i> , <b>2019</b> , 17, 972-981	6.8	62
59	Identifying enhancer-promoter interactions with neural network based on pre-trained DNA vectors and attention mechanism. <i>Bioinformatics</i> , <b>2020</b> , 36, 1037-1043	7.2	58
58	A Review of DNA-binding Proteins Prediction Methods. <i>Current Bioinformatics</i> , <b>2019</b> , 14, 246-254	4.7	56
57	M6AMRFS: Robust Prediction of N6-Methyladenosine Sites With Sequence-Based Features in Multiple Species. <i>Frontiers in Genetics</i> , <b>2018</b> , 9, 495	4.5	53
56	Comparative analysis and prediction of quorum-sensing peptides using feature representation learning and machine learning algorithms. <i>Briefings in Bioinformatics</i> , <b>2018</b> ,	13.4	51
55	4mCpred-EL: An Ensemble Learning Framework for Identification of DNA -methylcytosine Sites in the Mouse Genome. <i>Cells</i> , <b>2019</b> , 8,	7.9	50
54	Identifying N-methyladenosine sites using multi-interval nucleotide pair position specificity and support vector machine. <i>Scientific Reports</i> , <b>2017</b> , 7, 46757	4.9	49
53	ACPred-Fuse: fusing multi-view information improves the prediction of anticancer peptides. <i>Briefings in Bioinformatics</i> , <b>2020</b> , 21, 1846-1855	13.4	48
52	Briefing in family characteristics of microRNAs and their applications in cancer research. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , <b>2014</b> , 1844, 191-7	4	46
51	Improved detection of DNA-binding proteins via compression technology on PSSM information. <i>PLoS ONE</i> , <b>2017</b> , 12, e0185587	3.7	45

50	Meta-GDBP: a high-level stacked regression model to improve anticancer drug response prediction. <i>Briefings in Bioinformatics</i> , <b>2020</b> , 21, 996-1005	13.4	44
49	CPPred-FL: a sequence-based predictor for large-scale identification of cell-penetrating peptides by feature representation learning. <i>Briefings in Bioinformatics</i> , <b>2018</b> ,	13.4	44
48	Computational prediction and interpretation of cell-specific replication origin sites from multiple eukaryotes by exploiting stacking framework. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,	13.4	42
47	A novel machine learning method for cytokine-receptor interaction prediction. <i>Combinatorial Chemistry and High Throughput Screening</i> , <b>2016</b> , 19, 144-52	1.3	39
46	Construction, Model-Based Analysis, and Characterization of a Promoter Library for Fine-Tuned Gene Expression in <i>Bacillus subtilis</i> . <i>ACS Synthetic Biology</i> , <b>2018</b> , 7, 1785-1797	5.7	38
45	SecProMTB: Support Vector Machine-Based Classifier for Secretory Proteins Using Imbalanced Data Sets Applied to <i>Mycobacterium tuberculosis</i> . <i>Proteomics</i> , <b>2019</b> , 19, e1900007	4.8	33
44	Computational approaches in detecting non- coding RNA. <i>Current Genomics</i> , <b>2013</b> , 14, 371-7	2.6	32
43	MiR-93-5p Promotes Cell Proliferation through Down-Regulating PPARGC1A in Hepatocellular Carcinoma Cells by Bioinformatics Analysis and Experimental Verification. <i>Genes</i> , <b>2018</b> , 9,	4.2	26
42	Research progress in protein posttranslational modification site prediction. <i>Briefings in Functional Genomics</i> , <b>2018</b> , 18, 220-229	4.9	24
41	mGOF-loc: A novel ensemble learning method for human protein subcellular localization prediction. <i>Neurocomputing</i> , <b>2016</b> , 217, 73-82	5.4	23
40	Identification of DNA-Binding Proteins Using Mixed Feature Representation Methods. <i>Molecules</i> , <b>2017</b> , 22,	4.8	23
39	MinE-RFE: determine the optimal subset from RFE by minimizing the subset-accuracy-defined energy. <i>Briefings in Bioinformatics</i> , <b>2020</b> , 21, 687-698	13.4	20
38	6mA-RicePred: A Method for Identifying DNA -Methyladenine Sites in the Rice Genome Based on Feature Fusion. <i>Frontiers in Plant Science</i> , <b>2020</b> , 11, 4	6.2	18
37	Computational Analysis of miRNA Target Identification. <i>Current Bioinformatics</i> , <b>2012</b> , 7, 512-525	4.7	17
36	PRISMOID: a comprehensive 3D structure database for post-translational modifications and mutations with functional impact. <i>Briefings in Bioinformatics</i> , <b>2020</b> , 21, 1069-1079	13.4	17
35	Iterative feature representation algorithm to improve the predictive performance of N7-methylguanosine sites. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,	13.4	16
34	EP3: an ensemble predictor that accurately identifies type III secreted effectors. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22, 1918-1928	13.4	15
33	Classification and gene selection of triple-negative breast cancer subtype embedding gene connectivity matrix in deep neural network. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,	13.4	15

32	iRNA5hmC: The First Predictor to Identify RNA 5-Hydroxymethylcytosine Modifications Using Machine Learning. <i>Frontiers in Bioengineering and Biotechnology</i> , <b>2020</b> , 8, 227	5.8	14
31	UltraPse: A Universal and Extensible Software Platform for Representing Biological Sequences. <i>International Journal of Molecular Sciences</i> , <b>2017</b> , 18,	6.3	14
30	Supervised Brain Tumor Segmentation Based on Gradient and Context-Sensitive Features. <i>Frontiers in Neuroscience</i> , <b>2019</b> , 13, 144	5.1	14
29	Fusing convolutional neural network features with hand-crafted features for osteoporosis diagnoses. <i>Neurocomputing</i> , <b>2020</b> , 385, 300-309	5.4	13
28	Predicting drug-induced hepatotoxicity based on biological feature maps and diverse classification strategies. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22, 428-437	13.4	12
27	Learning embedding features based on multi-sense-scaled attention architecture to improve the predictive performance of anticancer peptides. <i>Bioinformatics</i> , <b>2021</b> ,	7.2	11
26	Domain adaptation based self-correction model for COVID-19 infection segmentation in CT images. <i>Expert Systems With Applications</i> , <b>2021</b> , 176, 114848	7.8	11
25	Exploring local discriminative information from evolutionary profiles for cytokine receptor interaction prediction. <i>Neurocomputing</i> , <b>2016</b> , 217, 37-45	5.4	10
24	Integrative machine learning framework for the identification of cell-specific enhancers from the human genome. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,	13.4	10
23	Identifying Plant Pentatricopeptide Repeat Coding Gene/Protein Using Mixed Feature Extraction Methods. <i>Frontiers in Plant Science</i> , <b>2018</b> , 9, 1961	6.2	9
22	Identification of expression signatures for non-small-cell lung carcinoma subtype classification. <i>Bioinformatics</i> , <b>2020</b> , 36, 339-346	7.2	9
21	ATSE: a peptide toxicity predictor by exploiting structural and evolutionary information based on graph neural network and attention mechanism. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,	13.4	8
20	A Bioinformatics Tool for the Prediction of DNA N6-Methyladenine Modifications Based on Feature Fusion and Optimization Protocol. <i>Frontiers in Bioengineering and Biotechnology</i> , <b>2020</b> , 8, 502	5.8	6
19	Protein subcellular localization based on deep image features and criterion learning strategy. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,	13.4	6
18	Improved Identification of Cytokines Using Feature Selection Techniques. <i>Letters in Organic Chemistry</i> , <b>2017</b> , 14,	0.6	5
17	Identification of glioblastoma molecular subtype and prognosis based on deep MRI features. <i>Knowledge-Based Systems</i> , <b>2021</b> , 232, 107490	7.3	5
16	PepFormer: End-to-End Transformer-Based Siamese Network to Predict and Enhance Peptide Detectability Based on Sequence Only. <i>Analytical Chemistry</i> , <b>2021</b> , 93, 6481-6490	7.8	4
15	FEGS: a novel feature extraction model for protein sequences and its applications. <i>BMC Bioinformatics</i> , <b>2021</b> , 22, 297	3.6	4

14	LncPred-IEL: A Long Non-coding RNA Prediction Method using Iterative Ensemble Learning <b>2019</b> ,		4
13	Accelerating bioactive peptide discovery via mutual information-based meta-learning. <i>Briefings in Bioinformatics</i> , <b>2021</b> ,	13.4	3
12	Robust Feature Matching for Remote Sensing Image Registration via Guided Hyperplane Fitting. <i>IEEE Transactions on Geoscience and Remote Sensing</i> , <b>2021</b> , 1-14	8.1	3
11	A 2-Layer Web Server for Enzyme and Multifunctional Enzyme Identification. <i>Current Bioinformatics</i> , <b>2014</b> , 9, 2-7	4.7	2
10	ToxIBTL: prediction of peptide toxicity based on information bottleneck and transfer learning.. <i>Bioinformatics</i> , <b>2022</b> ,	7.2	2
9	PRISMOID: a comprehensive 3D structure database for post-translational modifications and mutations with functional impact		2
8	<b>2018</b> ,		2
7	PESA-Net: Permutation-Equivariant Split Attention Network for correspondence learning. <i>Information Fusion</i> , <b>2022</b> , 77, 81-89	16.7	2
6	Three-Dimensional Face Reconstruction Using Multi-View-Based Bilinear Model. <i>Sensors</i> , <b>2019</b> , 19,	3.8	1
5	Distant metastasis identification based on optimized graph representation of gene interaction patterns. <i>Briefings in Bioinformatics</i> , <b>2021</b> ,	13.4	1
4	IEEE Access Special Section Editorial: Feature Representation and Learning Methods With Applications in Large-Scale Biological Sequence Analysis. <i>IEEE Access</i> , <b>2021</b> , 9, 33110-33119	3.5	1
3	iDNA-ABT : advanced deep learning model for detecting DNA methylation with adaptive features and transductive information maximization. <i>Bioinformatics</i> , <b>2021</b> ,	7.2	1
2	Signaling Potential Therapeutic Herbal Medicine Prescription for Treating COVID-19 by Collaborative Filtering.. <i>Frontiers in Pharmacology</i> , <b>2021</b> , 12, 759479	5.6	0
1	Discriminant Affinity Matrix for Deterministic Motion Trajectory Segmentation. <i>IEEE Access</i> , <b>2019</b> , 7, 57200-57209	3.5	