

# Leyi Wei

## List of Publications by Year in descending order

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Version: 2024-02-01

91  
papers

6,709  
citations

70961

41  
h-index

62479

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.	4.0	535
2	Gene2vec: gene subsequence embedding for prediction of mammalian <i>N<sup>6</sup></i> -methyladenosine sites from mRNA. Rna, 2019, 25, 205-218.	1.6	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.	1.8	326
4	Local-DPP: An improved DNA-binding protein prediction method by exploring local evolutionary information. Information Sciences, 2017, 384, 135-144.	4.0	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.	3.8	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.	1.9	207
7	A novel hierarchical selective ensemble classifier with bioinformatics application. Artificial Intelligence in Medicine, 2017, 83, 82-90.	3.8	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.	1.8	186
9	Prediction of human protein subcellular localization using deep learning. Journal of Parallel and Distributed Computing, 2018, 117, 212-217.	2.7	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.	2.3	182
11	Deep-Resp-Forest: A deep forest model to predict anti-cancer drug response. Methods, 2019, 166, 91-102.	1.9	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.	1.8	168
13	M6APred-EL: A Sequence-Based Predictor for Identifying N6-methyladenosine Sites Using Ensemble Learning. Molecular Therapy - Nucleic Acids, 2018, 12, 635-644.	2.3	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.	1.9	163
15	Exploring sequence-based features for the improved prediction of DNA N4-methylcytosine sites in multiple species. Bioinformatics, 2019, 35, 1326-1333.	1.8	156
16	Integration of deep feature representations and handcrafted features to improve the prediction of N6-methyladenosine sites. Neurocomputing, 2019, 324, 3-9.	3.5	130
17	Identifying enhancer-promoter interactions with neural network based on pre-trained DNA vectors and attention mechanism. Bioinformatics, 2020, 36, 1037-1043.	1.8	127
18	Empirical comparison and analysis of web-based cell-penetrating peptide prediction tools. Briefings in Bioinformatics, 2020, 21, 408-420.	3.2	122

#	ARTICLE	IF	CITATIONS
19	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> , 2019, 16, 1231-1239.	1.9	120
20	PEPred-Suite: improved and robust prediction of therapeutic peptides using adaptive feature representation learning. <i>Bioinformatics</i> , 2019, 35, 4272-4280.	1.8	116
21	Iterative feature representations improve N4-methylcytosine site prediction. <i>Bioinformatics</i> , 2019, 35, 4930-4937.	1.8	113
22	PhosPred-RF: A Novel Sequence-Based Predictor for Phosphorylation Sites Using Sequential Information Only. <i>IEEE Transactions on Nanobioscience</i> , 2017, 16, 240-247.	2.2	112
23	ACPred-Fuse: fusing multi-view information improves the prediction of anticancer peptides. <i>Briefings in Bioinformatics</i> , 2020, 21, 1846-1855.	3.2	100
24	M6AMRFS: Robust Prediction of N6-Methyladenosine Sites With Sequence-Based Features in Multiple Species. <i>Frontiers in Genetics</i> , 2018, 9, 495.	1.1	90
25	AtbPpred: A Robust Sequence-Based Prediction of Anti-Tubercular Peptides Using Extremely Randomized Trees. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 972-981.	1.9	89
26	Enhanced Protein Fold Prediction Method Through a Novel Feature Extraction Technique. <i>IEEE Transactions on Nanobioscience</i> , 2015, 14, 649-659.	2.2	87
27	SkipCPP-Pred: an improved and promising sequence-based predictor for predicting cell-penetrating peptides. <i>BMC Genomics</i> , 2017, 18, 742.	1.2	85
28	An Improved Protein Structural Classes Prediction Method by Incorporating Both Sequence and Structure Information. <i>IEEE Transactions on Nanobioscience</i> , 2015, 14, 339-349.	2.2	80
29	A Review of DNA-binding Proteins Prediction Methods. <i>Current Bioinformatics</i> , 2019, 14, 246-254.	0.7	79
30	Identifying N6-methyladenosine sites using multi-interval nucleotide pair position specificity and support vector machine. <i>Scientific Reports</i> , 2017, 7, 46757.	1.6	77
31	4mCpred-EL: An Ensemble Learning Framework for Identification of DNA N4-methylcytosine Sites in the Mouse Genome. <i>Cells</i> , 2019, 8, 1332.	1.8	77
32	Recent Progress in Machine Learning-Based Methods for Protein Fold Recognition. <i>International Journal of Molecular Sciences</i> , 2016, 17, 2118.	1.8	73
33	Computational prediction and interpretation of cell-specific replication origin sites from multiple eukaryotes by exploiting stacking framework. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	73
34	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> , 2018, 7, 1785-1797.	1.9	67
35	Meta-GDBP: a high-level stacked regression model to improve anticancer drug response prediction. <i>Briefings in Bioinformatics</i> , 2020, 21, 996-1005.	3.2	63
36	Improved detection of DNA-binding proteins via compression technology on PSSM information. <i>PLoS ONE</i> , 2017, 12, e0185587.	1.1	63

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37	CPPred-FL: a sequence-based predictor for large-scale identification of cell-penetrating peptides by feature representation learning. <i>Briefings in Bioinformatics</i> , 2018, , .	3.2	62
38	Comparative analysis and prediction of quorum-sensing peptides using feature representation learning and machine learning algorithms. <i>Briefings in Bioinformatics</i> , 2018, , .	3.2	60
39	ToxIBTL: prediction of peptide toxicity based on information bottleneck and transfer learning. <i>Bioinformatics</i> , 2022, 38, 1514-1524.	1.8	54
40	Briefing in family characteristics of microRNAs and their applications in cancer research. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 191-197.	1.1	51
41	SecProMTB: Support Vector Machine-Based Classifier for Secretory Proteins Using Imbalanced Data Sets Applied to <i>Mycobacterium tuberculosis</i> . <i>Proteomics</i> , 2019, 19, 1900007.	1.3	43
42	ATSE: a peptide toxicity predictor by exploiting structural and evolutionary information based on graph neural network and attention mechanism. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	43
43	A novel machine learning method for cytokine-receptor interaction prediction. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2016, 19, 144-152.	0.6	43
44	Computational Approaches in Detecting Non- Coding RNA. <i>Current Genomics</i> , 2013, 14, 371-377.	0.7	41
45	Research progress in protein posttranslational modification site prediction. <i>Briefings in Functional Genomics</i> , 2019, 18, 220-229.	1.3	39
46	Integrative machine learning framework for the identification of cell-specific enhancers from the human genome. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	38
47	PRISMOID: a comprehensive 3D structure database for post-translational modifications and mutations with functional impact. <i>Briefings in Bioinformatics</i> , 2020, 21, 1069-1079.	3.2	38
48	Iterative feature representation algorithm to improve the predictive performance of N7-methylguanosine sites. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	35
49	Identification of DNA-Binding Proteins Using Mixed Feature Representation Methods. <i>Molecules</i> , 2017, 22, 1602.	1.7	34
50	6mA-RicePred: A Method for Identifying DNA N6-Methyladenine Sites in the Rice Genome Based on Feature Fusion. <i>Frontiers in Plant Science</i> , 2020, 11, 4.	1.7	34
51	Domain adaptation based self-correction model for COVID-19 infection segmentation in CT images. <i>Expert Systems With Applications</i> , 2021, 176, 114848.	4.4	34
52	MiR-93-5p Promotes Cell Proliferation through Down-Regulating PPARGC1A in Hepatocellular Carcinoma Cells by Bioinformatics Analysis and Experimental Verification. <i>Genes</i> , 2018, 9, 51.	1.0	31
53	Supervised Brain Tumor Segmentation Based on Gradient and Context-Sensitive Features. <i>Frontiers in Neuroscience</i> , 2019, 13, 144.	1.4	29
54	Accelerating bioactive peptide discovery via mutual information-based meta-learning. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	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.	3.2	28
56	mGOF-loc: A novel ensemble learning method for human protein subcellular localization prediction. Neurocomputing, 2016, 217, 73-82.	3.5	26
57	Identification of expression signatures for non-small-cell lung carcinoma subtype classification. Bioinformatics, 2020, 36, 339-346.	1.8	26
58	Fusing convolutional neural network features with hand-crafted features for osteoporosis diagnoses. Neurocomputing, 2020, 385, 300-309.	3.5	26
59	iRNA5hmC: The First Predictor to Identify RNA 5-Hydroxymethylcytosine Modifications Using Machine Learning. Frontiers in Bioengineering and Biotechnology, 2020, 8, 227.	2.0	26
60	EP3: an ensemble predictor that accurately identifies type III secreted effectors. Briefings in Bioinformatics, 2021, 22, 1918-1928.	3.2	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, .	3.2	26
62	Learning embedding features based on multisense-scaled attention architecture to improve the predictive performance of anticancer peptides. Bioinformatics, 2021, 37, 4684-4693.	1.8	26
63	Predicting proteinâ€‘peptide binding residues via interpretable deep learning. Bioinformatics, 2022, 38, 3351-3360.	1.8	24
64	iDNA-ABT: advanced deep learning model for detecting DNA methylation with adaptive features and transductive information maximization. Bioinformatics, 2021, 37, 4603-4610.	1.8	23
65	Computational Analysis of miRNA Target Identification. Current Bioinformatics, 2012, 7, 512-525.	0.7	20
66	Protein subcellular localization based on deep image features and criterion learning strategy. Briefings in Bioinformatics, 2021, 22, .	3.2	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.	3.2	20
68	Predicting drug-induced hepatotoxicity based on biological feature maps and diverse classification strategies. Briefings in Bioinformatics, 2021, 22, 428-437.	3.2	18
69	UltraPse: A Universal and Extensible Software Platform for Representing Biological Sequences. International Journal of Molecular Sciences, 2017, 18, 2400.	1.8	16
70	FEGS: a novel feature extraction model for protein sequences and its applications. BMC Bioinformatics, 2021, 22, 297.	1.2	16
71	Multi-scale deep learning for the imbalanced multi-label protein subcellular localization prediction based on immunohistochemistry images. Bioinformatics, 2022, 38, 2602-2611.	1.8	14
72	Identification of glioblastoma molecular subtype and prognosis based on deep MRI features. Knowledge-Based Systems, 2021, 232, 107490.	4.0	13

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73	PESA-Net: Permutation-Equivariant Split Attention Network for correspondence learning. Information Fusion, 2022, 77, 81-89.	11.7	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.	2.0	12
75	scIMC: a platform for benchmarking comparison and visualization analysis of scRNA-seq data imputation methods. Nucleic Acids Research, 2022, 50, 4877-4899.	6.5	12
76	Exploring local discriminative information from evolutionary profiles for cytokine-receptor interaction prediction. Neurocomputing, 2016, 217, 37-45.	3.5	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.	2.7	11
78	Identifying Plant Pentatricopeptide Repeat Coding Gene/Protein Using Mixed Feature Extraction Methods. Frontiers in Plant Science, 2018, 9, 1961.	1.7	10
79	PSSP-MVIRT: peptide secondary structure prediction based on a multi-view deep learning architecture. Briefings in Bioinformatics, 2021, 22, .	3.2	8
80	EOCSA: Predicting prognosis of Epithelial ovarian cancer with whole slide histopathological images. Expert Systems With Applications, 2022, 206, 117643.	4.4	8
81	Distant metastasis identification based on optimized graph representation of gene interaction patterns. Briefings in Bioinformatics, 2022, 23, .	3.2	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, .	0.2	5
84	Three-Dimensional Face Reconstruction Using Multi-View-Based Bilinear Model. Sensors, 2019, 19, 459.	2.1	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, .	1.2	3
87	A 2-Layer Web Server for Enzyme and Multifunctional Enzyme Identification. Current Bioinformatics, 2014, 9, 2-7.	0.7	2
88	Signaling Potential Therapeutic Herbal Medicine Prescription for Treating COVID-19 by Collaborative Filtering. Frontiers in Pharmacology, 2021, 12, 759479.	1.6	2
89	Discriminant Affinity Matrix for Deterministic Motion Trajectory Segmentation. IEEE Access, 2019, 7, 57200-57209.	2.6	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.	2.6	1

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