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	PESA-Net: Permutation-Equivariant Split Attention Network for correspondence learning. Information Fusion, 2022, 77, 81-89.	19.1	13
2	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
3	Accelerating bioactive peptide discovery via mutual information-based meta-learning. Briefings in Bioinformatics, 2022, 23, .	6.5	29
4	Distant metastasis identification based on optimized graph representation of gene interaction patterns. Briefings in Bioinformatics, 2022, 23, .	6.5	6
5	ToxIBTL: prediction of peptide toxicity based on information bottleneck and transfer learning. Bioinformatics, 2022, 38, 1514-1524.	4.1	54
6	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
7	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
8	Predicting protein–peptide binding residues via interpretable deep learning. Bioinformatics, 2022, 38, 3351-3360.	4.1	24
9	EOCSA: Predicting prognosis of Epithelial ovarian cancer with whole slide histopathological images. Expert Systems With Applications, 2022, 206, 117643.	7.6	8
10	Iterative feature representation algorithm to improve the predictive performance of N7-methylguanosine sites. Briefings in Bioinformatics, 2021, 22, .	6.5	35
11	Protein subcellular localization based on deep image features and criterion learning strategy. Briefings in Bioinformatics, 2021, 22, .	6.5	20
12	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
13	EP3: an ensemble predictor that accurately identifies type III secreted effectors. Briefings in Bioinformatics, 2021, 22, 1918-1928.	6.5	26
14	Predicting drug-induced hepatotoxicity based on biological feature maps and diverse classification strategies. Briefings in Bioinformatics, 2021, 22, 428-437.	6.5	18
15	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
16	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
17	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
18	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

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19	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
20	PSSP-MVIRT: peptide secondary structure prediction based on a multi-view deep learning architecture. Briefings in Bioinformatics, 2021, 22, .	6.5	8
21	FEGS: a novel feature extraction model for protein sequences and its applications. BMC Bioinformatics, 2021, 22, 297.	2.6	16
22	Integrative machine learning framework for the identification of cell-specific enhancers from the human genome. Briefings in Bioinformatics, 2021, 22, .	6.5	38
23	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
24	Domain adaptation based self-correction model for COVID-19 infection segmentation in CT images. Expert Systems With Applications, 2021, 176, 114848.	7.6	34
25	Better Performance with Transformer: CPPFormer in precise prediction of cell-Penetrating Peptides. Current Medicinal Chemistry, 2021, 28, .	2.4	3
26	Identification of glioblastoma molecular subtype and prognosis based on deep MRI features. Knowledge-Based Systems, 2021, 232, 107490.	7.1	13
27	Signaling Potential Therapeutic Herbal Medicine Prescription for Treating COVID-19 by Collaborative Filtering. Frontiers in Pharmacology, 2021, 12, 759479.	3.5	2
28	Identification of expression signatures for non-small-cell lung carcinoma subtype classification. Bioinformatics, 2020, 36, 339-346.	4.1	26
29	Identifying enhancer–promoter interactions with neural network based on pre-trained DNA vectors and attention mechanism. Bioinformatics, 2020, 36, 1037-1043.	4.1	127
30	Empirical comparison and analysis of web-based cell-penetrating peptide prediction tools. Briefings in Bioinformatics, 2020, 21, 408-420.	6.5	122
31	Meta-GDBP: a high-level stacked regression model to improve anticancer drug response prediction. Briefings in Bioinformatics, 2020, 21, 996-1005.	6.5	63
32	MinE-RFE: determine the optimal subset from RFE by minimizing the subset-accuracy–defined energy. Briefings in Bioinformatics, 2020, 21, 687-698.	6.5	28
33	ACPred-Fuse: fusing multi-view information improves the prediction of anticancer peptides. Briefings in Bioinformatics, 2020, 21, 1846-1855.	6.5	100
34	Fusing convolutional neural network features with hand-crafted features for osteoporosis diagnoses. Neurocomputing, 2020, 385, 300-309.	5.9	26
35	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
36	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

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37	iRNA5hmC: The First Predictor to Identify RNA 5-Hydroxymethylcytosine Modifications Using Machine Learning. Frontiers in Bioengineering and Biotechnology, 2020, 8, 227.	4.1	26
38	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
39	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
40	Integration of deep feature representations and handcrafted features to improve the prediction of N6-methyladenosine sites. Neurocomputing, 2019, 324, 3-9.	5.9	130
41	Discriminant Affinity Matrix for Deterministic Motion Trajectory Segmentation. IEEE Access, 2019, 7, 57200-57209.	4.2	1
42	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
43	SecProMTB: Support Vector Machineâ€Based Classifier for Secretory Proteins Using Imbalanced Data Sets Applied toMycobacterium tuberculosis. Proteomics, 2019, 19, 1900007.	2.2	43
44	Supervised Brain Tumor Segmentation Based on Gradient and Context-Sensitive Features. Frontiers in Neuroscience, 2019, 13, 144.	2.8	29
45	4mCpred-EL: An Ensemble Learning Framework for Identification of DNA N4-methylcytosine Sites in the Mouse Genome. Cells, 2019, 8, 1332.	4.1	77
46	Research progress in protein posttranslational modification site prediction. Briefings in Functional Genomics, 2019, 18, 220-229.	2.7	39
47	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
48	DUNet: A deformable network for retinal vessel segmentation. Knowledge-Based Systems, 2019, 178, 149-162.	7.1	535
49	Iterative feature representations improve N4-methylcytosine site prediction. Bioinformatics, 2019, 35, 4930-4937.	4.1	113
50	PEPred-Suite: improved and robust prediction of therapeutic peptides using adaptive feature representation learning. Bioinformatics, 2019, 35, 4272-4280.	4.1	116
51	Three-Dimensional Face Reconstruction Using Multi-View-Based Bilinear Model. Sensors, 2019, 19, 459.	3.8	4
52	Deep-Resp-Forest: A deep forest model to predict anti-cancer drug response. Methods, 2019, 166, 91-102.	3.8	182
53	Identification and Prediction of Key Nucleotide Sites Using Machine Learning in Bioinformatics: A Brief Overview. , 2019, , .		0
54	LncPred-IEL: A Long Non-coding RNA Prediction Method using Iterative Ensemble Learning. , 2019, , .		5

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55	Exploring sequence-based features for the improved prediction of DNA N4-methylcytosine sites in multiple species. Bioinformatics, 2019, 35, 1326-1333.	4.1	156
56	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
57	Gene2vec: gene subsequence embedding for prediction of mammalian N^6-methyladenosine sites from mRNA. Rna, 2019, 25, 205-218.	3.5	421
58	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
59	A Review of DNA-binding Proteins Prediction Methods. Current Bioinformatics, 2019, 14, 246-254.	1.5	79
60	Prediction of human protein subcellular localization using deep learning. Journal of Parallel and Distributed Computing, 2018, 117, 212-217.	4.1	184
61	Comparative analysis and prediction of quorum-sensing peptides using feature representation learning and machine learning algorithms. Briefings in Bioinformatics, 2018, , .	6.5	60
62	M6AMRFS: Robust Prediction of N6-Methyladenosine Sites With Sequence-Based Features in Multiple Species. Frontiers in Genetics, 2018, 9, 495.	2.3	90
63	Encoded Texture Features to Characterize Bone Radiograph Images. , 2018, , .		3
64	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
65	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
66	Construction, Model-Based Analysis, and Characterization of a Promoter Library for Fine-Tuned Gene Expression in *Bacillus subtilis*. ACS Synthetic Biology, 2018, 7, 1785-1797.	3.8	67
67	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
68	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
69	Identifying Plant Pentatricopeptide Repeat Coding Gene/Protein Using Mixed Feature Extraction Methods. Frontiers in Plant Science, 2018, 9, 1961.	3.6	10
70	Local-DPP: An improved DNA-binding protein prediction method by exploring local evolutionary information. Information Sciences, 2017, 384, 135-144.	6.9	226
71	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
72	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

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73	A novel hierarchical selective ensemble classifier with bioinformatics application. Artificial Intelligence in Medicine, 2017, 83, 82-90.	6.5	192
74	Identifying N6-methyladenosine sites using multi-interval nucleotide pair position specificity and support vector machine. Scientific Reports, 2017, 7, 46757.	3.3	77
75	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
76	Identification of DNA-Binding Proteins Using Mixed Feature Representation Methods. Molecules, 2017, 22, 1602.	3.8	34
77	SkipCPP-Pred: an improved and promising sequence-based predictor for predicting cell-penetrating peptides. BMC Genomics, 2017, 18, 742.	2.8	85
78	UltraPse: A Universal and Extensible Software Platform for Representing Biological Sequences. International Journal of Molecular Sciences, 2017, 18, 2400.	4.1	16
79	Improved detection of DNA-binding proteins via compression technology on PSSM information. PLoS ONE, 2017, 12, e0185587.	2.5	63
80	Improved Identification of Cytokines Using Feature Selection Techniques. Letters in Organic Chemistry, 2017, 14, .	0.5	5
81	Recent Progress in Machine Learning-Based Methods for Protein Fold Recognition. International Journal of Molecular Sciences, 2016, 17, 2118.	4.1	73
82	mGOF-loc: A novel ensemble learning method for human protein subcellular localization prediction. Neurocomputing, 2016, 217, 73-82.	5.9	26
83	Exploring local discriminative information from evolutionary profiles for cytokine–receptor interaction prediction. Neurocomputing, 2016, 217, 37-45.	5.9	11
84	A novel machine learning method for cytokine-receptor interaction prediction. Combinatorial Chemistry and High Throughput Screening, 2016, 19, 144-152.	1.1	43
85	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
86	Enhanced Protein Fold Prediction Method Through a Novel Feature Extraction Technique. IEEE Transactions on Nanobioscience, 2015, 14, 649-659.	3.3	87
87	A 2-Layer Web Server for Enzyme and Multifunctional Enzyme Identification. Current Bioinformatics, 2014, 9, 2-7.	1.5	2
88	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
89	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
90	Computational Approaches in Detecting Non- Coding RNA. Current Genomics, 2013, 14, 371-377.	1.6	41

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91	Computational Analysis of miRNA Target Identification. Current Bioinformatics, 2012, 7, 512-525.	1.5	20