

Leyi Wei

List of Publications by Year in Descending Order

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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 | ToxIBTL: prediction of peptide toxicity based on information bottleneck and transfer learning.. <i>Bioinformatics</i> , 2022 , | 7.2 | 2 |
| 84 | PESA-Net: Permutation-Equivariant Split Attention Network for correspondence learning. <i>Information Fusion</i> , 2022 , 77, 81-89 | 16.7 | 2 |
| 83 | Computational prediction and interpretation of cell-specific replication origin sites from multiple eukaryotes by exploiting stacking framework. <i>Briefings in Bioinformatics</i> , 2021 , 22, | 13.4 | 42 |
| 82 | Distant metastasis identification based on optimized graph representation of gene interaction patterns. <i>Briefings in Bioinformatics</i> , 2021 , | 13.4 | 1 |
| 81 | Accelerating bioactive peptide discovery via mutual information-based meta-learning. <i>Briefings in Bioinformatics</i> , 2021 , | 13.4 | 3 |
| 80 | Iterative feature representation algorithm to improve the predictive performance of N7-methylguanosine sites. <i>Briefings in Bioinformatics</i> , 2021 , 22, | 13.4 | 16 |
| 79 | Protein subcellular localization based on deep image features and criterion learning strategy. <i>Briefings in Bioinformatics</i> , 2021 , 22, | 13.4 | 6 |
| 78 | 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, | 13.4 | 8 |
| 77 | PepFormer: End-to-End Transformer-Based Siamese Network to Predict and Enhance Peptide Detectability Based on Sequence Only. <i>Analytical Chemistry</i> , 2021 , 93, 6481-6490 | 7.8 | 4 |
| 76 | FEGS: a novel feature extraction model for protein sequences and its applications. <i>BMC Bioinformatics</i> , 2021 , 22, 297 | 3.6 | 4 |
| 75 | Integrative machine learning framework for the identification of cell-specific enhancers from the human genome. <i>Briefings in Bioinformatics</i> , 2021 , 22, | 13.4 | 10 |
| 74 | EP3: an ensemble predictor that accurately identifies type III secreted effectors. <i>Briefings in Bioinformatics</i> , 2021 , 22, 1918-1928 | 13.4 | 15 |
| 73 | Predicting drug-induced hepatotoxicity based on biological feature maps and diverse classification strategies. <i>Briefings in Bioinformatics</i> , 2021 , 22, 428-437 | 13.4 | 12 |
| 72 | Classification and gene selection of triple-negative breast cancer subtype embedding gene connectivity matrix in deep neural network. <i>Briefings in Bioinformatics</i> , 2021 , 22, | 13.4 | 15 |
| 71 | IEEE Access Special Section Editorial: Feature Representation and Learning Methods With Applications in Large-Scale Biological Sequence Analysis. <i>IEEE Access</i> , 2021 , 9, 33110-33119 | 3.5 | 1 |
| 70 | iDNA-ABT : advanced deep learning model for detecting DNA methylation with adaptive features and transductive information maximization. <i>Bioinformatics</i> , 2021 , | 7.2 | 1 |
| 69 | Learning embedding features based on multi-sense-scaled attention architecture to improve the predictive performance of anticancer peptides. <i>Bioinformatics</i> , 2021 , | 7.2 | 11 |

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| 68 | Domain adaptation based self-correction model for COVID-19 infection segmentation in CT images. <i>Expert Systems With Applications</i> , 2021 , 176, 114848 | 7.8 | 11 |
| 67 | Identification of glioblastoma molecular subtype and prognosis based on deep MRI features. <i>Knowledge-Based Systems</i> , 2021 , 232, 107490 | 7.3 | 5 |
| 66 | Robust Feature Matching for Remote Sensing Image Registration via Guided Hyperplane Fitting. <i>IEEE Transactions on Geoscience and Remote Sensing</i> , 2021 , 1-14 | 8.1 | 3 |
| 65 | Signaling Potential Therapeutic Herbal Medicine Prescription for Treating COVID-19 by Collaborative Filtering.. <i>Frontiers in Pharmacology</i> , 2021 , 12, 759479 | 5.6 | 0 |
| 64 | Identifying enhancer-promoter interactions with neural network based on pre-trained DNA vectors and attention mechanism. <i>Bioinformatics</i> , 2020 , 36, 1037-1043 | 7.2 | 58 |
| 63 | 6mA-RicePred: A Method for Identifying DNA -Methyladenine Sites in the Rice Genome Based on Feature Fusion. <i>Frontiers in Plant Science</i> , 2020 , 11, 4 | 6.2 | 18 |
| 62 | 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> , 2020 , 8, 502 | 5.8 | 6 |
| 61 | iRNA5hmC: The First Predictor to Identify RNA 5-Hydroxymethylcytosine Modifications Using Machine Learning. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020 , 8, 227 | 5.8 | 14 |
| 60 | Identification of expression signatures for non-small-cell lung carcinoma subtype classification. <i>Bioinformatics</i> , 2020 , 36, 339-346 | 7.2 | 9 |
| 59 | PRISMOID: a comprehensive 3D structure database for post-translational modifications and mutations with functional impact. <i>Briefings in Bioinformatics</i> , 2020 , 21, 1069-1079 | 13.4 | 17 |
| 58 | ACPred-Fuse: fusing multi-view information improves the prediction of anticancer peptides. <i>Briefings in Bioinformatics</i> , 2020 , 21, 1846-1855 | 13.4 | 48 |
| 57 | Fusing convolutional neural network features with hand-crafted features for osteoporosis diagnoses. <i>Neurocomputing</i> , 2020 , 385, 300-309 | 5.4 | 13 |
| 56 | Empirical comparison and analysis of web-based cell-penetrating peptide prediction tools. <i>Briefings in Bioinformatics</i> , 2020 , 21, 408-420 | 13.4 | 83 |
| 55 | Meta-GDBP: a high-level stacked regression model to improve anticancer drug response prediction. <i>Briefings in Bioinformatics</i> , 2020 , 21, 996-1005 | 13.4 | 44 |
| 54 | MinE-RFE: determine the optimal subset from RFE by minimizing the subset-accuracy-defined energy. <i>Briefings in Bioinformatics</i> , 2020 , 21, 687-698 | 13.4 | 20 |
| 53 | Meta-4mCpred: A Sequence-Based Meta-Predictor for Accurate DNA 4mC Site Prediction Using Effective Feature Representation. <i>Molecular Therapy - Nucleic Acids</i> , 2019 , 16, 733-744 | 10.7 | 126 |
| 52 | DUNet: A deformable network for retinal vessel segmentation. <i>Knowledge-Based Systems</i> , 2019 , 178, 149-162 | 7.3 | 243 |
| 51 | Iterative feature representations improve N4-methylcytosine site prediction. <i>Bioinformatics</i> , 2019 , 35, 4930-4937 | 7.2 | 77 |

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| 50 | PEPred-Suite: improved and robust prediction of therapeutic peptides using adaptive feature representation learning. <i>Bioinformatics</i> , 2019 , 35, 4272-4280 | 7.2 | 68 |
| 49 | Three-Dimensional Face Reconstruction Using Multi-View-Based Bilinear Model. <i>Sensors</i> , 2019 , 19, | 3.8 | 1 |
| 48 | 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 | 3 | 85 |
| 47 | Integration of deep feature representations and handcrafted features to improve the prediction of N6-methyladenosine sites. <i>Neurocomputing</i> , 2019 , 324, 3-9 | 5.4 | 106 |
| 46 | Discriminant Affinity Matrix for Deterministic Motion Trajectory Segmentation. <i>IEEE Access</i> , 2019 , 7, 57200-57209 | 3.5 | |
| 45 | 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 | 6.8 | 62 |
| 44 | SecProMTB: Support Vector Machine-Based Classifier for Secretory Proteins Using Imbalanced Data Sets Applied to Mycobacterium tuberculosis. <i>Proteomics</i> , 2019 , 19, e1900007 | 4.8 | 33 |
| 43 | Supervised Brain Tumor Segmentation Based on Gradient and Context-Sensitive Features. <i>Frontiers in Neuroscience</i> , 2019 , 13, 144 | 5.1 | 14 |
| 42 | 4mCpred-EL: An Ensemble Learning Framework for Identification of DNA -methylcytosine Sites in the Mouse Genome. <i>Cells</i> , 2019 , 8, | 7.9 | 50 |
| 41 | A Review of DNA-binding Proteins Prediction Methods. <i>Current Bioinformatics</i> , 2019 , 14, 246-254 | 4.7 | 56 |
| 40 | Deep-Resp-Forest: A deep forest model to predict anti-cancer drug response. <i>Methods</i> , 2019 , 166, 91-102. | 6 | 117 |
| 39 | LncPred-IEL: A Long Non-coding RNA Prediction Method using Iterative Ensemble Learning 2019 , | | 4 |
| 38 | Exploring sequence-based features for the improved prediction of DNA N4-methylcytosine sites in multiple species. <i>Bioinformatics</i> , 2019 , 35, 1326-1333 | 7.2 | 104 |
| 37 | mAHTPred: a sequence-based meta-predictor for improving the prediction of anti-hypertensive peptides using effective feature representation. <i>Bioinformatics</i> , 2019 , 35, 2757-2765 | 7.2 | 126 |
| 36 | Gene2vec: gene subsequence embedding for prediction of mammalian -methyladenosine sites from mRNA. <i>Rna</i> , 2019 , 25, 205-218 | 5.8 | 279 |
| 35 | Fast Prediction of Protein Methylation Sites Using a Sequence-Based Feature Selection Technique. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019 , 16, 1264-1273 | 3 | 123 |
| 34 | Research progress in protein posttranslational modification site prediction. <i>Briefings in Functional Genomics</i> , 2018 , 18, 220-229 | 4.9 | 24 |
| 33 | Identifying Plant Pentatricopeptide Repeat Coding Gene/Protein Using Mixed Feature Extraction Methods. <i>Frontiers in Plant Science</i> , 2018 , 9, 1961 | 6.2 | 9 |

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| 32 | Prediction of human protein subcellular localization using deep learning. <i>Journal of Parallel and Distributed Computing</i> , 2018 , 117, 212-217 | 4.4 | 152 |
| 31 | M6APred-EL: A Sequence-Based Predictor for Identifying N6-methyladenosine Sites Using Ensemble Learning. <i>Molecular Therapy - Nucleic Acids</i> , 2018 , 12, 635-644 | 10.7 | 116 |
| 30 | 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, | 4.2 | 26 |
| 29 | Comparative analysis and prediction of quorum-sensing peptides using feature representation learning and machine learning algorithms. <i>Briefings in Bioinformatics</i> , 2018 , | 13.4 | 51 |
| 28 | M6AMRFS: Robust Prediction of N6-Methyladenosine Sites With Sequence-Based Features in Multiple Species. <i>Frontiers in Genetics</i> , 2018 , 9, 495 | 4.5 | 53 |
| 27 | 2018 , | | 2 |
| 26 | CPPred-FL: a sequence-based predictor for large-scale identification of cell-penetrating peptides by feature representation learning. <i>Briefings in Bioinformatics</i> , 2018 , | 13.4 | 44 |
| 25 | ACPred-FL: a sequence-based predictor using effective feature representation to improve the prediction of anti-cancer peptides. <i>Bioinformatics</i> , 2018 , 34, 4007-4016 | 7.2 | 162 |
| 24 | 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 | 5.7 | 38 |
| 23 | Local-DPP: An improved DNA-binding protein prediction method by exploring local evolutionary information. <i>Information Sciences</i> , 2017 , 384, 135-144 | 7.7 | 172 |
| 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 | 3.4 | 98 |
| 21 | Improved prediction of protein-protein interactions using novel negative samples, features, and an ensemble classifier. <i>Artificial Intelligence in Medicine</i> , 2017 , 83, 67-74 | 7.4 | 174 |
| 20 | A novel hierarchical selective ensemble classifier with bioinformatics application. <i>Artificial Intelligence in Medicine</i> , 2017 , 83, 82-90 | 7.4 | 154 |
| 19 | Identifying N-methyladenosine sites using multi-interval nucleotide pair position specificity and support vector machine. <i>Scientific Reports</i> , 2017 , 7, 46757 | 4.9 | 49 |
| 18 | CPPred-RF: A Sequence-based Predictor for Identifying Cell-Penetrating Peptides and Their Uptake Efficiency. <i>Journal of Proteome Research</i> , 2017 , 16, 2044-2053 | 5.6 | 120 |
| 17 | SkipCPP-Pred: an improved and promising sequence-based predictor for predicting cell-penetrating peptides. <i>BMC Genomics</i> , 2017 , 18, 742 | 4.5 | 62 |
| 16 | UltraPse: A Universal and Extensible Software Platform for Representing Biological Sequences. <i>International Journal of Molecular Sciences</i> , 2017 , 18, | 6.3 | 14 |
| 15 | Identification of DNA-Binding Proteins Using Mixed Feature Representation Methods. <i>Molecules</i> , 2017 , 22, | 4.8 | 23 |

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| 14 | Improved detection of DNA-binding proteins via compression technology on PSSM information. <i>PLoS ONE</i> , 2017 , 12, e0185587 | 3.7 | 45 |
| 13 | Improved Identification of Cytokines Using Feature Selection Techniques. <i>Letters in Organic Chemistry</i> , 2017 , 14, | 0.6 | 5 |
| 12 | mGOF-loc: A novel ensemble learning method for human protein subcellular localization prediction. <i>Neurocomputing</i> , 2016 , 217, 73-82 | 5.4 | 23 |
| 11 | Exploring local discriminative information from evolutionary profiles for cytokine-receptor interaction prediction. <i>Neurocomputing</i> , 2016 , 217, 37-45 | 5.4 | 10 |
| 10 | A novel machine learning method for cytokine-receptor interaction prediction. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2016 , 19, 144-52 | 1.3 | 39 |
| 9 | Recent Progress in Machine Learning-Based Methods for Protein Fold Recognition. <i>International Journal of Molecular Sciences</i> , 2016 , 17, | 6.3 | 63 |
| 8 | Enhanced Protein Fold Prediction Method Through a Novel Feature Extraction Technique. <i>IEEE Transactions on Nanobioscience</i> , 2015 , 14, 649-59 | 3.4 | 77 |
| 7 | An Improved Protein Structural Classes Prediction Method by Incorporating Both Sequence and Structure Information. <i>IEEE Transactions on Nanobioscience</i> , 2015 , 14, 339-349 | 3.4 | 66 |
| 6 | Briefing in family characteristics of microRNAs and their applications in cancer research. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014 , 1844, 191-7 | 4 | 46 |
| 5 | Improved and Promising Identification of Human MicroRNAs by Incorporating a High-Quality Negative Set. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014 , 11, 192-201 | 3 | 170 |
| 4 | A 2-Layer Web Server for Enzyme and Multifunctional Enzyme Identification. <i>Current Bioinformatics</i> , 2014 , 9, 2-7 | 4.7 | 2 |
| 3 | Computational approaches in detecting non- coding RNA. <i>Current Genomics</i> , 2013 , 14, 371-7 | 2.6 | 32 |
| 2 | Computational Analysis of miRNA Target Identification. <i>Current Bioinformatics</i> , 2012 , 7, 512-525 | 4.7 | 17 |
| 1 | PRISMOID: a comprehensive 3D structure database for post-translational modifications and mutations with functional impact | | 2 |