# List of Publications by Year in descending order



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|---|---|---|---|
| 68 papers | 7,101 citations | 61984 43 h-index | 110387 64 g-index |
| 69 all docs | 69 docs citations | 69 times ranked | 2639 citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | HGDTI: predicting drugâ€“target interaction by using information aggregation based on heterogeneous graph neural network. BMC Bioinformatics, 2022, 23, 126. | 2.6 | 11 |
| 2 | Identifying Pupylation Proteins and Sites by Incorporating Multiple Methods. Frontiers in Endocrinology, 2022, 13, 849549. | 3.5 | 1 |
| 3 | iPTT(2â€‰L)-CNN: A Two-Layer Predictor for Identifying Promoters and Their Types in Plant Genomes by Convolutional Neural Network. Computational and Mathematical Methods in Medicine, 2021, 2021, 1-9. | 1.3 | 3 |
| 4 | EMCBOW-GPCR: A method for identifying G-protein coupled receptors based on word embedding and wordbooks. Computational and Structural Biotechnology Journal, 2021, 19, 4961-4969. | 4.1 | 6 |
| 5 | iCDI-W2vCom: Identifying the Ion Channelâ€“Drug Interaction in Cellular Networking Based on word2vec and node2vec. Frontiers in Genetics, 2021, 12, 738274. | 2.3 | 6 |
| 6 | Boundary Focal Loss for Class Imbalanced Learning. , 2021, , . | | 0 |
| 7 | Identifying GPCR-drug interaction based on wordbook learning from sequences. BMC Bioinformatics, 2020, 21, 150. | 2.6 | 10 |
| 8 | BOW-GBDT: A GBDT Classifier Combining With Artificial Neural Network for Identifying GPCRâ€“Drug Interaction Based on Wordbook Learning From Sequences. Frontiers in Cell and Developmental Biology, 2020, 8, 623858. | 3.7 | 16 |
| 9 | pLoc_bal-mGpos: Predict subcellular localization of Gram-positive bacterial proteins by quasi-balancing training dataset and PseAAC. Genomics, 2019, 111, 886-892. | 2.9 | 87 |
| 10 | pLoc_bal-mAnimal: predict subcellular localization of animal proteins by balancing training dataset and PseAAC. Bioinformatics, 2019, 35, 398-406. | 4.1 | 89 |
| 11 | Identifying Acetylation Protein by Fusing Its PseAAC and Functional Domain Annotation. Frontiers in Bioengineering and Biotechnology, 2019, 7, 311. | 4.1 | 10 |
| 12 | pLoc_bal-mHum: Predict subcellular localization of human proteins by PseAAC and quasi-balancing training dataset. Genomics, 2019, 111, 1274-1282. | 2.9 | 63 |
| 13 | iPSW(2L)-PseKNC: A two-layer predictor for identifying promoters and their strength by hybrid features via pseudo K-tuple nucleotide composition. Genomics, 2019, 111, 1785-1793. | 2.9 | 60 |
| 14 | iPPI-PseAAC(CGR): Identify protein-protein interactions by incorporating chaos game representation into PseAAC. Journal of Theoretical Biology, 2019, 460, 195-203. | 1.7 | 88 |
| 15 | pLoc_bal-mVirus: Predict Subcellular Localization of Multi-Label Virus Proteins by Chou's General PseAAC and IHTS Treatment to Balance Training Dataset. Medicinal Chemistry, 2019, 15, 496-509. | 1.5 | 50 |
| 16 | pLoc_bal-mEuk: Predict Subcellular Localization of Eukaryotic Proteins by General PseAAC and Quasi-balancing Training Dataset. Medicinal Chemistry, 2019, 15, 472-485. | 1.5 | 44 |
| 17 | iAI-DSAE: A Computational Method for Adenosine to Inosine Editing Site Prediction. Letters in Organic Chemistry, 2019, 16, 347-355. | 0.5 | 1 |
| 18 | iKcr-PseEns: Identify lysine crotonylation sites in histone proteins with pseudo components and ensemble classifier. Genomics, 2018, 110, 239-246. | 2.9 | 127 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | pLoc_bal-mGneg: Predict subcellular localization of Gram-negative bacterial proteins by quasi-balancing training dataset and general PseAAC. Journal of Theoretical Biology, 2018, 458, 92-102. | 1.7 | 71 |
| 20 | PAI-SAE: Predicting Adenosine To Inosine Editing Sites Based On Hybrid Features By Using Spare Auto-Encoder. IOP Conference Series: Earth and Environmental Science, 2018, 170, 052018. | 0.3 | 3 |
| 21 | iATC-mISF: a multi-label classifier for predicting the classes of anatomical therapeutic chemicals. Bioinformatics, 2017, 33, 341-346. | 4.1 | 139 |
| 22 | iPhosâ€PseEvo: Identifying Human Phosphorylated Proteins by Incorporating Evolutionary Information into General PseAAC via Grey System Theory. Molecular Informatics, 2017, 36, 1600010. | 2.5 | 94 |
| 23 | iSS-PC: Identifying Splicing Sites via Physical-Chemical Properties Using Deep Sparse Auto-Encoder. Scientific Reports, 2017, 7, 8222. | 3.3 | 21 |
| 24 | An improved multilevel thresholding approach based modified bacterial foraging optimization. Applied Intelligence, 2017, 46, 214-226. | 5.3 | 45 |
| 25 | iRNAm5C-PseDNC: identifying RNA 5-methylcytosine sites by incorporating physical-chemical properties into pseudo dinucleotide composition. Oncotarget, 2017, 8, 41178-41188. | 1.8 | 191 |
| 26 | iDHSs-PseTNC: Identifying DNase I Hypersensitive Sites with Pseuo Trinucleotide Component by Deep Sparse Auto-encoder. Letters in Organic Chemistry, 2017, 14, . | 0.5 | 12 |
| 27 | iROS-gPseKNC: Predicting replication origin sites in DNA by incorporating dinucleotide position-specific propensity into general pseudo nucleotide composition. Oncotarget, 2016, 7, 34180-34189. | 1.8 | 118 |
| 28 | iPPBS-Opt: A Sequence-Based Ensemble Classifier for Identifying Protein-Protein Binding Sites by Optimizing Imbalanced Training Datasets. Molecules, 2016, 21, 95. | 3.8 | 142 |
| 29 | iHyd-PseCp: Identify hydroxyproline and hydroxylysine in proteins by incorporating sequence-coupled effects into general PseAAC. Oncotarget, 2016, 7, 44310-44321. | 1.8 | 150 |
| 30 | iCar-PseCp: identify carbonylation sites in proteins by Monte Carlo sampling and incorporating sequence coupled effects into general PseAAC. Oncotarget, 2016, 7, 34558-34570. | 1.8 | 176 |
| 31 | pSumo-CD: predicting sumoylation sites in proteins with covariance discriminant algorithm by incorporating sequence-coupled effects into general PseAAC. Bioinformatics, 2016, 32, 3133-3141. | 4.1 | 177 |
| 32 | Classifying Multifunctional Enzymes by Incorporating Three Different Models into Chouâ€™s General Pseudo Amino Acid Composition. Journal of Membrane Biology, 2016, 249, 551-557. | 2.1 | 32 |
| 33 | iAFP-Ense: An Ensemble Classifier for Identifying Antifreeze Protein by Incorporating Grey Model and PSSM into PseAAC. Journal of Membrane Biology, 2016, 249, 845-854. | 2.1 | 25 |
| 34 | pSuc-Lys: Predict lysine succinylation sites in proteins with PseAAC and ensemble random forest approach. Journal of Theoretical Biology, 2016, 394, 223-230. | 1.7 | 297 |
| 35 | pRNAm-PC: Predicting N6-methyladenosine sites in RNA sequences via physicalâ€“chemical properties. Analytical Biochemistry, 2016, 497, 60-67. | 2.4 | 247 |
| 36 | iSuc-PseOpt: Identifying lysine succinylation sites in proteins by incorporating sequence-coupling effects into pseudo components and optimizing imbalanced training dataset. Analytical Biochemistry, 2016, 497, 48-56. | 2.4 | 254 |

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|---|---|---|---|
| 37 | Identification of protein-protein binding sites by incorporating the physicochemical properties and stationary wavelet transforms into pseudo amino acid composition. Journal of Biomolecular Structure and Dynamics, 2016, 34, 1946-1961. | 3.5 | 120 |
| 38 | Predicting the Functional Types of Singleplex and Multiplex Eukaryotic Membrane Proteins via Different Models of Chouâ€™s Pseudo Amino Acid Compositions. Journal of Membrane Biology, 2016, 249, 23-29. | 2.1 | 24 |
| 39 | Prediction of Proteinâ€“Protein Interactions with Physicochemical Descriptors and Wavelet Transform via Random Forests. Journal of the Association for Laboratory Automation, 2016, 21, 368-377. | 2.8 | 13 |
| 40 | iPhos-PseEn: Identifying phosphorylation sites in proteins by fusing different pseudo components into an ensemble classifier. Oncotarget, 2016, 7, 51270-51283. | 1.8 | 142 |
| 41 | Benchmark data for identifying DNA methylation sites via pseudo trinucleotide composition. Data in Brief, 2015, 4, 87-89. | 1.0 | 8 |
| 42 | iCataly-PseAAC: Identification of Enzymes Catalytic Sites Using Sequence Evolution Information with Grey Model GM (2,1). Journal of Membrane Biology, 2015, 248, 1033-1041. | 2.1 | 10 |
| 43 | iMem-Seq: A Multi-label Learning Classifier for Predicting Membrane Proteins Types. Journal of Membrane Biology, 2015, 248, 745-752. | 2.1 | 19 |
| 44 | iUbiq-Lys: prediction of lysine ubiquitination sites in proteins by extracting sequence evolution information via a gray system model. Journal of Biomolecular Structure and Dynamics, 2015, 33, 1731-1742. | 3.5 | 149 |
| 45 | iDrug-Target: predicting the interactions between drug compounds and target proteins in cellular networking via benchmark dataset optimization approach. Journal of Biomolecular Structure and Dynamics, 2015, 33, 2221-2233. | 3.5 | 185 |
| 46 | iRSpot-TNCPseAAC: Identify Recombination Spots with Trinucleotide Composition and Pseudo Amino Acid Components. International Journal of Molecular Sciences, 2014, 15, 1746-1766. | 4.1 | 227 |
| 47 | iNR-Drug: Predicting the Interaction of Drugs with Nuclear Receptors in Cellular Networking. International Journal of Molecular Sciences, 2014, 15, 4915-4937. | 4.1 | 71 |
| 48 | iLoc-Animal: a multi-label learning classifier for predicting subcellular localization of animal proteins. Molecular BioSystems, 2013, 9, 634. | 2.9 | 245 |
| 49 | iAMP-2L: A two-level multi-label classifier for identifying antimicrobial peptides and their functional types. Analytical Biochemistry, 2013, 436, 168-177. | 2.4 | 442 |
| 50 | iCDI-PseFpt: Identify the channelâ€“drug interaction in cellular networking with PseAAC and molecular fingerprints. Journal of Theoretical Biology, 2013, 337, 71-79. | 1.7 | 113 |
| 51 | iEzy-Drug: A Web Server for Identifying the Interaction between Enzymes and Drugs in Cellular Networking. BioMed Research International, 2013, 2013, 1-13. | 1.9 | 73 |
| 52 | iGPCR-Drug: A Web Server for Predicting Interaction between GPCRs and Drugs in Cellular Networking. PLoS ONE, 2013, 8, e72234. | 2.5 | 106 |
| 53 | Predict Drug-Protein Interaction in Cellular Networking. Current Topics in Medicinal Chemistry, 2013, 13, 1707-1712. | 2.1 | 29 |
| 54 | Similarity-based spectral clustering ensemble selection. , 2012, , . | | 21 |

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| 55 | iLoc-Hum: using the accumulation-label scale to predict subcellular locations of human proteins with both single and multiple sites. Molecular BioSystems, 2012, 8, 629-641. | 2.9 | 335 |
| 56 | iLoc-Gpos: A Multi-Layer Classifier for Predicting the Subcellular Localization of Singleplex and Multiplex Gram-Positive Bacterial Proteins. Protein and Peptide Letters, 2012, 19, 4-14. | 0.9 | 138 |
| 57 | iNR-PhysChem: A Sequence-Based Predictor for Identifying Nuclear Receptors and Their Subfamilies via Physical-Chemical Property Matrix. PLoS ONE, 2012, 7, e30869. | 2.5 | 81 |
| 58 | iLoc-Plant: a multi-label classifier for predicting the subcellular localization of plant proteins with both single and multiple sites. Molecular BioSystems, 2011, 7, 3287. | 2.9 | 198 |
| 59 | A Multi-Label Classifier for Predicting the Subcellular Localization of Gram-Negative Bacterial Proteins with Both Single and Multiple Sites. PLoS ONE, 2011, 6, e20592. | 2.5 | 235 |
| 60 | iDNA-Prot: Identification of DNA Binding Proteins Using Random Forest with Grey Model. PLoS ONE, 2011, 6, e24756. | 2.5 | 255 |
| 61 | Quat-2L: a web-server for predicting protein quaternary structural attributes. Molecular Diversity, 2011, 15, 149-155. | 3.9 | 49 |
| 62 | Bagging-based spectral clustering ensemble selection. Pattern Recognition Letters, 2011, 32, 1456-1467. | 4.2 | 86 |
| 63 | iLoc-Virus: A multi-label learning classifier for identifying the subcellular localization of virus proteins with both single and multiple sites. Journal of Theoretical Biology, 2011, 284, 42-51. | 1.7 | 252 |
| 64 | iLoc-Euk: A Multi-Label Classifier for Predicting the Subcellular Localization of Singleplex and Multiplex Eukaryotic Proteins. PLoS ONE, 2011, 6, e18258. | 2.5 | 298 |
| 65 | NR-2L: A Two-Level Predictor for Identifying Nuclear Receptor Subfamilies Based on Sequence-Derived Features. PLoS ONE, 2011, 6, e23505. | 2.5 | 88 |
| 66 | Using AdaboostSVM to Predict the GPCR Functional Classes. International Conference on Bioinformatics and Biomedical Engineering: [proceedings] International Conference on Bioinformatics and Biomedical Engineering, 2010, , . | 0.0 | 0 |
| 67 | Predicting protein structural classes with pseudo amino acid composition: An approach using geometric moments of cellular automaton image. Journal of Theoretical Biology, 2008, 254, 691-696. | 1.7 | 126 |
| 68 | DTI-BERT: Identifying Drug-Target Interactions in Cellular Networking Based on BERT and Deep Learning Method. Frontiers in Genetics, 0, 13, . | 2.3 | 7 |