

Wei Du

List of Publications by Year in descending order

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Version: 2024-02-01

43
papers

1,798
citations

567144

15
h-index

377752

34
g-index

44
all docs

44
docs citations

44
times ranked

4153
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | Long Noncoding RNA Identification: Comparing Machine Learning Based Tools for Long Noncoding Transcripts Discrimination. <i>BioMed Research International</i> , 2016, 2016, 1-14. | 0.9 | 1,176 |
| 2 | LncFinder: an integrated platform for long non-coding RNA identification utilizing sequence intrinsic composition, structural information and physicochemical property. <i>Briefings in Bioinformatics</i> , 2019, 20, 2009-2027. | 3.2 | 98 |
| 3 | Classifying Breast Cancer Subtypes Using Deep Neural Networks Based on Multi-Omics Data. <i>Genes</i> , 2020, 11, 888. | 1.0 | 52 |
| 4 | Incident: A Tool for Rapid Identification of Long Noncoding RNAs Utilizing Sequence Intrinsic Composition and Open Reading Frame Information. <i>International Journal of Genomics</i> , 2016, 2016, 1-11. | 0.8 | 43 |
| 5 | Urine-Based Biomarkers for Alzheimer's Disease Identified Through Coupling Computational and Experimental Methods. <i>Journal of Alzheimer's Disease</i> , 2018, 65, 421-431. | 1.2 | 37 |
| 6 | Classifying Breast Cancer Subtypes Using Multiple Kernel Learning Based on Omics Data. <i>Genes</i> , 2019, 10, 200. | 1.0 | 34 |
| 7 | Identification of Gene-Expression Signatures and Protein Markers for Breast Cancer Grading and Staging. <i>PLoS ONE</i> , 2015, 10, e0138213. | 1.1 | 30 |
| 8 | Using Machine Learning to Measure Relatedness Between Genes: A Multi-Features Model. <i>Scientific Reports</i> , 2019, 9, 4192. | 1.6 | 27 |
| 9 | Integrative analysis with expanded DNA methylation data reveals common key regulators and pathways in cancers. <i>Npj Genomic Medicine</i> , 2019, 4, 2. | 1.7 | 27 |
| 10 | A feature selection method based on multiple kernel learning with expression profiles of different types. <i>BioData Mining</i> , 2017, 10, 4. | 2.2 | 26 |
| 11 | Capsule-LPI: a LncRNA-protein interaction predicting tool based on a capsule network. <i>BMC Bioinformatics</i> , 2021, 22, 246. | 1.2 | 26 |
| 12 | Systematic analyses of glutamine and glutamate metabolisms across different cancer types. <i>Chinese Journal of Cancer</i> , 2017, 36, 88. | 4.9 | 24 |
| 13 | A novel multi-stage feature selection method for microarray expression data analysis. <i>International Journal of Data Mining and Bioinformatics</i> , 2013, 7, 58. | 0.1 | 19 |
| 14 | Predicting lncRNA-disease associations using network topological similarity based on deep mining heterogeneous networks. <i>Mathematical Biosciences</i> , 2019, 315, 108229. | 0.9 | 17 |
| 15 | HBFP: a new repository for human body fluid proteome. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2021, . | 1.4 | 17 |
| 16 | Pancreatic cancer biomarker detection by two support vector strategies for recursive feature elimination. <i>Biomarkers in Medicine</i> , 2019, 13, 105-121. | 0.6 | 16 |
| 17 | Identification of Essential Proteins Based on Ranking Edge-Weights in Protein-Protein Interaction Networks. <i>PLoS ONE</i> , 2014, 9, e108716. | 1.1 | 15 |
| 18 | Biodiversity and dynamics of cyanobacterial communities during blooms in temperate lake (Harsha) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 | 2.2 | 15 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 19 | LnLocation: Efficient Subcellular Location Prediction of Long Non-Coding RNA-Based Multi-Source Heterogeneous Feature Fusion. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7271. | 1.8 | 10 |
| 20 | CapsNet-SSP: multilane capsule network for predicting human saliva-secretory proteins. <i>BMC Bioinformatics</i> , 2020, 21, 237. | 1.2 | 9 |
| 21 | Computational Analysis of Specific MicroRNA Biomarkers for Noninvasive Early Cancer Detection. <i>BioMed Research International</i> , 2017, 2017, 1-9. | 0.9 | 7 |
| 22 | SecProCT: In Silico Prediction of Human Secretory Proteins Based on Capsule Network and Transformer. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9054. | 1.8 | 7 |
| 23 | Deep forest ensemble learning for classification of alignments of non-coding RNA sequences based on multi-view structure representations. <i>Briefings in Bioinformatics</i> , 2021, 22, . | 3.2 | 7 |
| 24 | Prokaryotic Phylogenies Inferred from Whole-Genome Sequence and Annotation Data. <i>BioMed Research International</i> , 2013, 2013, 1-15. | 0.9 | 6 |
| 25 | A Novel SVC Method Based on K-means. , 2008, , . | | 5 |
| 26 | Pancreatic cancer biomarker detection using recursive feature elimination based on Support Vector Machine and large margin distribution machine. , 2017, , . | | 5 |
| 27 | Parameter Selection of Support Vector Regression Based on a Novel Chaotic Immune Algorithm. , 2009, , . | | 4 |
| 28 | The method for breast cancer grade prediction and pathway analysis based on improved multiple kernel learning. <i>Journal of Bioinformatics and Computational Biology</i> , 2017, 15, 1650037. | 0.3 | 4 |
| 29 | A Novel Unsupervised Algorithm for Biological Process-based Analysis on Cancer. <i>Scientific Reports</i> , 2017, 7, 4671. | 1.6 | 4 |
| 30 | CyanoPATH: a knowledgebase of genome-scale functional repertoire for toxic cyanobacterial blooms. <i>Briefings in Bioinformatics</i> , 2021, 22, . | 3.2 | 4 |
| 31 | BAENET: A Brain Age Estimation Network with 3D Skipping and Outlier Constraint Loss. , 2020, , . | | 4 |
| 32 | De novo Prediction of Moonlighting Proteins Using Multimodal Deep Ensemble Learning. <i>Frontiers in Genetics</i> , 2021, 12, 630379. | 1.1 | 4 |
| 33 | Specific Biomarkers: Detection of Cancer Biomarkers Through High-Throughput Transcriptomics Data. <i>Cognitive Computation</i> , 2015, 7, 652-666. | 3.6 | 3 |
| 34 | DeepUEP: Prediction of Urine Excretory Proteins Using Deep Learning. <i>IEEE Access</i> , 2020, 8, 100251-100261. | 2.6 | 3 |
| 35 | DEEPSMP: A deep learning model for predicting the ectodomain shedding events of membrane proteins. <i>Journal of Bioinformatics and Computational Biology</i> , 2020, 18, 2050017. | 0.3 | 3 |
| 36 | Computational methods for recognition of cancer protein markers in saliva. <i>Mathematical Biosciences and Engineering</i> , 2020, 17, 2453-2469. | 1.0 | 3 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 37 | An improved normalized signal to noise ratio method for irrelevant genes removing. , 2010, , . | | 2 |
| 38 | LPInsider: a webserver for lncRNA-protein interaction extraction from the literature. BMC Bioinformatics, 2022, 23, 135. | 1.2 | 2 |
| 39 | The Application of Support Vector Machine to Operon Prediction. , 2008, , . | | 1 |
| 40 | Operon Prediction by Decision Tree Classifier Based on VPRSM. , 2009, , . | | 1 |
| 41 | DeepHBSP: A Deep Learning Framework for Predicting Human Blood-Secretory Proteins Using Transfer Learning. Journal of Computer Science and Technology, 2021, 36, 234-247. | 0.9 | 1 |
| 42 | Two modeling methods for near infrared spectroscopy nondestructive quantitative analysis of the protein contents in Cordyceps militaris mycelia powder. , 2010, , . | | 0 |
| 43 | Clustering methods based on rough estimate of cluster core. , 2010, , . | | 0 |