# MiPred: classification of real and pseudo microRNA pre prediction model with combined features

## Nucleic Acids Research

35, W339-W344

Citation Report

| # | ARTICLE | IF | CITATIONS |
|---|---------|-----|-----------|
| 1 | Ab initio identification of human microRNAs based on structure motifs. BMC Bioinformatics, 2007, 8, 478. | 1.2 | 53 |
| 2 | A novel representation of RNA secondary structure based on element-contact graphs. BMC Bioinformatics, 2008, 9, 188. | 1.2 | 15 |
| 3 | MicroRNA-encoding long non-coding RNAs. BMC Genomics, 2008, 9, 236. | 1.2 | 60 |
| 4 | The rat mitochondrial Ori L encodes a novel small RNA resembling an ancestral tRNA. Biochemical and Biophysical Research Communications, 2008, 372, 634-638. | 1.0 | 21 |
| 5 | Identification of MicroRNA Precursors with Support Vector Machine and String Kernel. Genomics, Proteomics and Bioinformatics, 2008, 6, 121-128. | 3.0 | 17 |
| 6 | Application of massively parallel sequencing to microRNA profiling and discovery in human embryonic stem cells. Genome Research, 2008, 18, 610-621. | 2.4 | 964 |
| 7 | Sequence Analysis in Vicinity of Type 2 Diabetes Related SNP rs7903146. , 2008, , . | | 0 |
| 8 | A Novel Comparative Sequence Analysis Method for ncRNA Secondary Structure Prediction without Multiple Sequence Alignment. , 2008, , . | | 0 |
| 9 | An Improved Diverse Density Algorithm for Multiple Overlapped Instances. , 2008, , . | | 1 |
| 10 | Self Containment, a Property of Modular RNA Structures, Distinguishes microRNAs. PLoS Computational Biology, 2008, 4, e1000150. | 1.5 | 17 |
| 11 | Bioinformatics in China: A Personal Perspective. PLoS Computational Biology, 2008, 4, e1000020. | 1.5 | 18 |
| 12 | Structures of MicroRNA Precursors. , 2008, , 1-16. | | 8 |
| 13 | Computational Prediction of UV-responsible MicroRNA Genes in Vitis vinifera Genome. , 2008, , . | | 0 |
| 14 | Computational Prediction of Abiotic Stress Responsible MicroRNAs in Vitis vinifera Genome. , 2009, , . | | 1 |
| 15 | Novel and Homology Microrna Prediction by Using a Bayesian Network Based Program in Strongylocentrotus purpuratus Genome. , 2009, , . | | 0 |
| 16 | Predictor correlation impacts machine learning algorithms: implications for genomic studies. Bioinformatics, 2009, 25, 1884-1890. | 1.8 | 123 |
| 17 | *microPred*: effective classification of pre-miRNAs for human miRNA gene prediction. Bioinformatics, 2009, 25, 989-995. | 1.8 | 227 |
| 18 | miROrtho: computational survey of microRNA genes. Nucleic Acids Research, 2009, 37, D111-D117. | 6.5 | 65 |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 19 | An Ariadne's thread to the identification and annotation of noncoding RNAs in eukaryotes. Briefings in Bioinformatics, 2009, 10, 475-489. | 3.2 | 25 |
| 20 | In silico method for systematic analysis of feature importance in microRNA-mRNA interactions. BMC Bioinformatics, 2009, 10, 427. | 1.2 | 12 |
| 21 | Genic regions of a large salamander genome contain long introns and novel genes. BMC Genomics, 2009, 10, 19. | 1.2 | 81 |
| 22 | Alu-directed transcriptional regulation of some novel miRNAs. BMC Genomics, 2009, 10, 563. | 1.2 | 52 |
| 23 | Genome-wide computational identification of microRNAs and their targets in the deep-branching eukaryote Giardia lamblia. Computational Biology and Chemistry, 2009, 33, 391-396. | 1.1 | 22 |
| 24 | Predicting RNA secondary structure based on the class information and Hopfield network. Computers in Biology and Medicine, 2009, 39, 206-214. | 3.9 | 21 |
| 25 | In silico detection and characteristics of novel microRNA genes in the Equus caballus genome using an integrated ab initio and comparative genomic approach. Genomics, 2009, 94, 125-131. | 1.3 | 52 |
| 26 | Current tools for the identification of miRNA genes and their targets. Nucleic Acids Research, 2009, 37, 2419-2433. | 6.5 | 211 |
| 27 | Identification and characterization of novel amphioxus microRNAs by Solexa sequencing. Genome Biology, 2009, 10, R78. | 13.9 | 136 |
| 28 | A pre-microRNA classifier by structural and thermodynamic motifs. , 2009, , . | | 7 |
| 29 | Spectroscopic diagnosis of laryngeal carcinoma using near-infrared Raman spectroscopy and random recursive partitioning ensemble techniques. Analyst, The, 2009, 134, 1232. | 1.7 | 66 |
| 30 | miRanalyzer: a microRNA detection and analysis tool for next-generation sequencing experiments. Nucleic Acids Research, 2009, 37, W68-W76. | 6.5 | 283 |
| 31 | DuplexFinder: Predicting the miRNA miRNA* duplex from the animal precursors. International Journal of Bioinformatics Research and Applications, 2010, 6, 69. | 0.1 | 2 |
| 32 | Computational approaches for microRNA studies: a review. Mammalian Genome, 2010, 21, 1-12. | 1.0 | 152 |
| 33 | Computational RNomics: Structure identification and functional prediction of non-coding RNAs in silico. Science China Life Sciences, 2010, 53, 548-562. | 2.3 | 7 |
| 34 | Prediction of novel precursor miRNAs using a context-sensitive hidden Markov model (CSHMM). BMC Bioinformatics, 2010, 11, S29. | 1.2 | 53 |
| 35 | MiRenSVM: towards better prediction of microRNA precursors using an ensemble SVM classifier with multi-loop features. BMC Bioinformatics, 2010, 11, S11. | 1.2 | 78 |
| 36 | Correlation between sequence conservation and structural thermodynamics of microRNA precursors from human, mouse, and chicken genomes. BMC Evolutionary Biology, 2010, 10, 329. | 3.2 | 11 |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 37 | Origin and evolution of a placental-specific microRNA family in the human genome. BMC Evolutionary Biology, 2010, 10, 346. | 3.2 | 53 |
| 38 | Analysis of microRNA transcriptome by deep sequencing of small RNA libraries of peripheral blood. BMC Genomics, 2010, 11, 288. | 1.2 | 136 |
| 39 | Comprehensive survey of human brain microRNA by deep sequencing. BMC Genomics, 2010, 11, 409. | 1.2 | 142 |
| 40 | Impact on cell to plasma ratio of miR-92a in patients with acute leukemia: in vivo assessment of cell to plasma ratio of miR-92a. BMC Research Notes, 2010, 3, 347. | 0.6 | 55 |
| 41 | PMirP: A pre-microRNA prediction method based on structure–sequence hybrid features. Artificial Intelligence in Medicine, 2010, 49, 127-132. | 3.8 | 26 |
| 42 | Computational methodologies for studying non-coding RNAs relevant to central nervous system function and dysfunction. Brain Research, 2010, 1338, 131-145. | 1.1 | 8 |
| 43 | Expression of two novel transcripts in the mouse definitive endoderm. Gene Expression Patterns, 2010, 10, 127-134. | 0.3 | 21 |
| 44 | A DNA transposon-based approach to functional screening in neural stem cells. Journal of Biotechnology, 2010, 150, 11-21. | 1.9 | 8 |
| 45 | New syntax to describe local continuous structure-sequence information for recognizing new pre-miRNAs. Journal of Theoretical Biology, 2010, 264, 578-584. | 0.8 | 5 |
| 46 | MicroRNA identity and abundance in porcine skeletal muscles determined by deep sequencing. Animal Genetics, 2010, 41, 159-168. | 0.6 | 144 |
| 47 | Computational Identification and Characterization of Putative miRNAs in Nasonia Species. International Journal of Insect Science, 2010, 2, IJIS.S4197. | 1.7 | 0 |
| 48 | Computational Identification of Putative miRNAs from <i>Felis Catus</i>. Biomedical Engineering and Computational Biology, 2010, 2, BECB.S5233. | 0.8 | 2 |
| 49 | MIReNA: finding microRNAs with high accuracy and no learning at genome scale and from deep sequencing data. Bioinformatics, 2010, 26, 2226-2234. | 1.8 | 141 |
| 50 | Genome-Wide Identification of Orthologs of miR-1302 Genes in Placental Mammals. International Conference on Bioinformatics and Biomedical Engineering: [proceedings] International Conference on Bioinformatics and Biomedical Engineering, 2010, , . | 0.0 | 0 |
| 51 | Two-stage clustering based effective sample selection for classification of pre-miRNAs. , 2010, , . | | 0 |
| 52 | MicroRNA transcriptome in the newborn mouse ovaries determined by massive parallel sequencing. Molecular Human Reproduction, 2010, 16, 463-471. | 1.3 | 122 |
| 53 | Sequence and Structure Analysis of Noncoding RNAs. Methods in Molecular Biology, 2010, 609, 285-306. | 0.4 | 20 |
| 54 | Characterization of an Ultra-Conserved Putative <i>cis</i>-Regulatory Module at the Mammalian Telomerase Reverse Transcriptase Gene. DNA and Cell Biology, 2010, 29, 499-508. | 0.9 | 6 |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 55 | MiRNA features for automated classification. , 2010, , . | | 0 |
| 56 | Identifying essential features for the classification of real and pseudo microRNAs precursors using fuzzy decision trees. , 2010, , . | | 4 |
| 57 | Feature Selection Based on Genetic Algorithm for Classification of Pre-miRNAs. , 2010, , . | | 1 |
| 58 | Identification of microRNA precursors based on random forest with network-level representation method of stem-loop structure. BMC Bioinformatics, 2011, 12, 165. | 1.2 | 33 |
| 59 | MicroRNAs as Post-Transcriptional Machines and their Interplay with Cellular Networks. Advances in Experimental Medicine and Biology, 2011, 722, 59-74. | 0.8 | 78 |
| 60 | Identification and analysis of novel microRNAs from fragile sites of human cervical cancer: Computational and experimental approach. Genomics, 2011, 97, 333-340. | 1.3 | 20 |
| 61 | Predicting human microRNA precursors based on an optimized feature subset generated by GA–SVM. Genomics, 2011, 98, 73-78. | 1.3 | 53 |
| 62 | Genome-wide identification of novel microRNAs and their target genes in the human parasite Schistosoma mansoni. Genomics, 2011, 98, 96-111. | 1.3 | 83 |
| 63 | A MicroRNA Catalog of Swine Umbilical Vein Endothelial Cells Identified by Deep Sequencing. Agricultural Sciences in China, 2011, 10, 1467-1474. | 0.6 | 1 |
| 64 | Genetic algorithm-based efficient feature selection for classification of pre-miRNAs. Genetics and Molecular Research, 2011, 10, 588-603. | 0.3 | 16 |
| 65 | Solexa Sequencing of Novel and Differentially Expressed MicroRNAs in Testicular and Ovarian Tissues in Holstein Cattle. International Journal of Biological Sciences, 2011, 7, 1016-1026. | 2.6 | 157 |
| 66 | MicroRNA Genes Derived from Repetitive Elements and Expanded by Segmental Duplication Events in Mammalian Genomes. PLoS ONE, 2011, 6, e17666. | 1.1 | 77 |
| 67 | MicroRNAs Associated with Metastatic Prostate Cancer. PLoS ONE, 2011, 6, e24950. | 1.1 | 183 |
| 68 | MicroRNAs of rat articular cartilage at different developmental stages identified by Solexa sequencing. Osteoarthritis and Cartilage, 2011, 19, 1237-1245. | 0.6 | 29 |
| 69 | The use of classification trees for bioinformatics. Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery, 2011, 1, 55-63. | 4.6 | 103 |
| 70 | The discovery approaches and detection methods of microRNAs. Molecular Biology Reports, 2011, 38, 4125-4135. | 1.0 | 53 |
| 71 | Finding Cancer-Associated miRNAs: Methods and Tools. Molecular Biotechnology, 2011, 49, 97-107. | 1.3 | 7 |
| 72 | Identification and functional annotation of novel microRNAs in the proximal sciatic nerve after sciatic nerve transection. Science China Life Sciences, 2011, 54, 806-812. | 2.3 | 29 |

| # | ARTICLE | IF | CITATIONS |
|---|---------|-----|-----------|
| 73 | Recent acquisition of imprinting at the rodent Sfmbt2 locus correlates with insertion of a large block of miRNAs. BMC Genomics, 2011, 12, 204. | 1.2 | 50 |
| 74 | Evolutionary conserved microRNAs are ubiquitously expressed compared to tick-specific miRNAs in the cattle tick Rhipicephalus (Boophilus) microplus. BMC Genomics, 2011, 12, 328. | 1.2 | 33 |
| 75 | MicroRNA-mediated gene regulation plays a minor role in the transcriptomic plasticity of cold-acclimated Zebrafish brain tissue. BMC Genomics, 2011, 12, 605. | 1.2 | 35 |
| 76 | Genome‐wide approaches in the study of microRNA biology. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2011, 3, 491-512. | 6.6 | 26 |
| 77 | MicroRNA identity and abundance in developing swine adipose tissue as determined by solexa sequencing. Journal of Cellular Biochemistry, 2011, 112, 1318-1328. | 1.2 | 128 |
| 78 | mirExplorer: Detecting microRNAs from genome and next generation sequencing data using the AdaBoost method with transition probability matrix and combined features. RNA Biology, 2011, 8, 922-934. | 1.5 | 24 |
| 79 | An Overview of Computational Approaches for Prediction of miRNA Genes and their Targets. Current Bioinformatics, 2011, 6, 129-143. | 0.7 | 8 |
| 80 | Computational and experimental identification of mirtrons in *Drosophila melanogaster* and *Caenorhabditis elegans*. Genome Research, 2011, 21, 286-300. | 2.4 | 71 |
| 81 | Genomic and Proteomic Analysis of Invertebrate Iridovirus Type 9. Journal of Virology, 2011, 85, 7900-7911. | 1.5 | 42 |
| 82 | Identification and Differential Expression of MicroRNAs during Metamorphosis of the Japanese Flounder (Paralichthys olivaceus). PLoS ONE, 2011, 6, e22957. | 1.1 | 120 |
| 83 | Prediction of novel pre-microRNAs with high accuracy through boosting and SVM. Bioinformatics, 2011, 27, 1436-1437. | 1.8 | 26 |
| 84 | *PlantMiRNAPred*: efficient classification of real and pseudo plant pre-miRNAs. Bioinformatics, 2011, 27, 1368-1376. | 1.8 | 70 |
| 85 | A fast ab-initio method for predicting miRNA precursors in genomes. Nucleic Acids Research, 2012, 40, e80-e80. | 6.5 | 50 |
| 86 | Identification of miRNAs in sorghum by using bioinformatics approach. Plant Signaling and Behavior, 2012, 7, 246-259. | 1.2 | 38 |
| 87 | A prediction model for COPD readmissions: catching up, catching our breath, and improving a national problem. Journal of Community Hospital Internal Medicine Perspectives, 2012, 2, 9915. | 0.4 | 50 |
| 88 | Deep sequencing of virus-infected cells reveals HIV-encoded small RNAs. Nucleic Acids Research, 2012, 40, 414-427. | 6.5 | 123 |
| 89 | Computational methods for ab initio detection of microRNAs. Frontiers in Genetics, 2012, 3, 209. | 1.1 | 32 |
| 90 | Predicting MicroRNAs. , 2012, , 189-207. | | 1 |

| # | ARTICLE | IF | CITATIONS |
|---|---------|-----|-----------|
| 91 | A Living Fossil in the Genome of a Living Fossil: Harbinger Transposons in the Coelacanth Genome. Molecular Biology and Evolution, 2012, 29, 985-993. | 3.5 | 36 |
| 92 | Sequencing and analysis of the complete genome of Rana grylio virus (RGV). Archives of Virology, 2012, 157, 1559-1564. | 0.9 | 53 |
| 93 | Systematic analysis revealed better performance of random forest algorithm coupled with complex network features in predicting microRNA precursors. Chemometrics and Intelligent Laboratory Systems, 2012, 118, 317-323. | 1.8 | 7 |
| 94 | Classification of Real and Pseudo pre-miRNAs in Plant Species. Procedia Computer Science, 2012, 11, 17-23. | 1.2 | 3 |
| 95 | A Robust Feature Selection Method for Novel Pre-microRNA Identification Using a Combination of Nucleotide-Structure Triplets. , 2012, , . | | 3 |
| 96 | Random forests for genomic data analysis. Genomics, 2012, 99, 323-329. | 1.3 | 635 |
| 97 | Analysis of serum genome-wide microRNAs for breast cancer detection. Clinica Chimica Acta, 2012, 413, 1058-1065. | 0.5 | 120 |
| 98 | Differential expression patterns of conserved miRNAs and isomiRs during Atlantic halibut development. BMC Genomics, 2012, 13, 11. | 1.2 | 80 |
| 99 | High-throughput sequencing of small RNAs and analysis of differentially expressed microRNAs associated with pistil development in Japanese apricot. BMC Genomics, 2012, 13, 371. | 1.2 | 64 |
| 100 | The prediction of the porcine pre-microRNAs in genome-wide based on support vector machine (SVM) and homology searching. BMC Genomics, 2012, 13, 729. | 1.2 | 3 |
| 101 | Bioinformatic identification of cassava miRNAs differentially expressed in response to infection by Xanthomonas axonopodis pv. manihotis. BMC Plant Biology, 2012, 12, 29. | 1.6 | 57 |
| 102 | Target Prediction Algorithms and Bioinformatics Resources for miRNA Studies. , 2012, , 29-48. | | 1 |
| 103 | A Catalogue of Glioblastoma and Brain MicroRNAs Identified by Deep Sequencing. OMICS A Journal of Integrative Biology, 2012, 16, 690-699. | 1.0 | 51 |
| 104 | Methods for Identifying Small RNA Genes. Advances in Insect Physiology, 2012, , 155-194. | 1.1 | 0 |
| 105 | A Global Characterization and Identification of Multifunctional Enzymes. PLoS ONE, 2012, 7, e38979. | 1.1 | 53 |
| 106 | Insect MicroRNAs. , 2012, , 30-56. | | 22 |
| 107 | Integrated Sequence-Structure Motifs Suffice to Identify microRNA Precursors. PLoS ONE, 2012, 7, e32797. | 1.1 | 29 |
| 108 | Experimental Verification of a Predicted Intronic MicroRNA in Human NGFR Gene with a Potential Pro-Apoptotic Function. PLoS ONE, 2012, 7, e35561. | 1.1 | 29 |

| # | Article | IF | Citations |
|---|---------|----|-----------| 
| 109 | Prediction of Conserved Precursors of miRNAs and Their Mature Forms by Integrating Position-Specific Structural Features. PLoS ONE, 2012, 7, e44314. | 1.1 | 12 |
| 110 | miR-BAG: Bagging Based Identification of MicroRNA Precursors. PLoS ONE, 2012, 7, e45782. | 1.1 | 23 |
| 111 | MicroRNA Prediction Using a Fixed-Order Markov Model Based on the Secondary Structure Pattern. PLoS ONE, 2012, 7, e48236. | 1.1 | 28 |
| 112 | Plant MicroRNA Prediction by Supervised Machine Learning Using C5.0 Decision Trees. Journal of Nucleic Acids, 2012, 2012, 1-10. | 0.8 | 22 |
| 113 | Benchmark comparison of ab initio microRNA identification methods and software. Genetics and Molecular Research, 2012, 11, 4525-4538. | 0.3 | 9 |
| 114 | MicroRNA profiles and their control of male gametophyte development in rice. Plant Molecular Biology, 2012, 80, 85-102. | 2.0 | 40 |
| 115 | MicroRNA Expression Profiling and Discovery. , 2012, , 191-208. | | 0 |
| 116 | Evaluation of online miRNA resources for biomedical applications. Genes To Cells, 2012, 17, 11-27. | 0.5 | 29 |
| 117 | SoMART: a web server for plant miRNA, tasiRNA and target gene analysis. Plant Journal, 2012, 70, 891-901. | 2.8 | 71 |
| 118 | Identification and functional analysis of novel micro€nas in rat dorsal root ganglia after sciatic nerve resection. Journal of Neuroscience Research, 2012, 90, 791-801. | 1.3 | 19 |
| 119 | 25S€"18S rDNA IGS of Capsicum: molecular structure and comparison. Plant Systematics and Evolution, 2012, 298, 313-321. | 0.3 | 10 |
| 120 | Data mining in the Life Sciences with Random Forest: a walk in the park or lost in the jungle?. Briefings in Bioinformatics, 2013, 14, 315-326. | 3.2 | 324 |
| 121 | MicroRNA Cancer Regulation. Advances in Experimental Medicine and Biology, 2013, , . | 0.8 | 17 |
| 122 | Computational prediction of the localization of microRNAs within their pre-miRNA. Nucleic Acids Research, 2013, 41, 7200-7211. | 6.5 | 75 |
| 123 | A MicroRNA Encoded by Autographa californica Nucleopolyhedrovirus Regulates Expression of Viral Gene ODV-E25. Journal of Virology, 2013, 87, 13029-13034. | 1.5 | 31 |
| 124 | An integrative bioinformatics pipeline for the genomewide identification of novel porcine microRNA genes. Journal of Genetics, 2013, 92, 587-593. | 0.4 | 2 |
| 125 | The Training Set Selection Methods of microRNA Precursors Prediction Based on Machine Learning Approaches. , 2013, , . | | 1 |
| 126 | Analysis of the microRNA transcriptome and expression of different isomiRs in human peripheral blood mononuclear cells. BMC Research Notes, 2013, 6, 390. | 0.6 | 22 |

| # | Article | IF | Citations |
|---|---------|----|-----------|
| 127 | MicroRNA identification using linear dimensionality reduction with explicit feature mapping. BMC Proceedings, 2013, 7, S8. | 1.8 | 5 |
| 128 | Identification and characterization of microRNAs in the developing maize endosperm. Genomics, 2013, 102, 472-478. | 1.3 | 24 |
| 129 | Identification and characterization of novel microRNA candidates from deep sequencing. Clinica Chimica Acta, 2013, 415, 239-244. | 0.5 | 11 |
| 130 | Detecting miRNAs in deep-sequencing data: a software performance comparison and evaluation. Briefings in Bioinformatics, 2013, 14, 36-45. | 3.2 | 38 |
| 131 | Prediction of pre-miRNA with multiple stem-loops using pruning algorithm. Computers in Biology and Medicine, 2013, 43, 409-416. | 3.9 | 14 |
| 132 | Identification of dysregulated microRNAs in lymphocytes from children with Down syndrome. Gene, 2013, 530, 278-286. | 1.0 | 27 |
| 133 | Bioinformatics, Non-coding RNAs and Its Possible Application in Personalized Medicine. Advances in Experimental Medicine and Biology, 2013, 774, 21-37. | 0.8 | 8 |
| 134 | Identification and expression levels of pig miRNAs in skeletal muscle. Livestock Science, 2013, 154, 45-54. | 0.6 | 6 |
| 135 | The fuzzy Laplacianclassifier. Neurocomputing, 2013, 111, 43-53. | 3.5 | 4 |
| 136 | Data mining for microrna gene prediction: On the impact of class imbalance and feature number for microrna gene prediction. , 2013, , . |  | 12 |
| 137 | Band smearing of PCR amplified bacterial 16S rRNA genes: Dependence on initial PCR target diversity. Journal of Microbiological Methods, 2013, 95, 186-194. | 0.7 | 4 |
| 138 | Mining of miRNAs in pomegranate (Punica granatumL.) by pyrosequencing of part of the genome. Journal of Horticultural Science and Biotechnology, 2013, 88, 735-742. | 0.9 | 6 |
| 139 | Identification of Novel MicroRNAs in Primates by Using the Synteny Information and Small RNA Deep Sequencing Data. International Journal of Molecular Sciences, 2013, 14, 20820-20832. | 1.8 | 1 |
| 140 | Explaining microbial phenotypes on a genomic scale: GWAS for microbes. Briefings in Functional Genomics, 2013, 12, 366-380. | 1.3 | 57 |
| 141 | MicroRNAs -the Next Generation Therapeutic Targets in Human Diseases. Theranostics, 2013, 3, 930-942. | 4.6 | 68 |
| 142 | Heterogeneous ensemble approach with discriminative features and modified-SMOTEbagging for pre-miRNA classification. Nucleic Acids Research, 2013, 41, e21-e21. | 6.5 | 63 |
| 143 | miR-Explore: Predicting MicroRNA Precursors by Class Grouping and Secondary Structure Positional Alignment. Bioinformatics and Biology Insights, 2013, 7, BBI.S10758. | 1.0 | 2 |
| 144 | <i>AB INITIO</i> HUMAN miRNA AND PRE-miRNA PREDICTION. Journal of Bioinformatics and Computational Biology, 2013, 11, 1343009. | 0.3 | 3 |

| # | Article | IF | Citations |
|---|---------|----|-----------| 
| 145 | Profiling of differentially expressed microRNA and the bioinformatic target gene analyses in bovine fast- and slow-type muscles by massively parallel sequencing1. Journal of Animal Science, 2013, 91, 90-103. | 0.2 | 48 |
| 146 | Can MiRBase Provide Positive Data for Machine Learning for the Detection of MiRNA Hairpins?. Journal of Integrative Bioinformatics, 2013, 10, 1-11. | 1.0 | 18 |
| 147 | HuntMi: an efficient and taxon-specific approach in pre-miRNA identification. BMC Bioinformatics, 2013, 14, 83. | 1.2 | 67 |
| 148 | MicroRNA discovery by similarity search to a database of RNA-seq profiles. Frontiers in Genetics, 2013, 4, 133. | 1.1 | 8 |
| 149 | A novel over-sampling method and its application to miRNA prediction. Journal of Biomedical Science and Engineering, 2013, 06, 236-248. | 0.2 | 4 |
| 150 | Identification and Profiling of microRNAs and Their Target Genes from Developing Caprine Skeletal Muscle. PLoS ONE, 2014, 9, e96857. | 1.1 | 44 |
| 151 | Virus versus Host Plant MicroRNAs: Who Determines the Outcome of the Interaction?. PLoS ONE, 2014, 9, e98263. | 1.1 | 16 |
| 152 | Prediction of MicroRNA Precursors Using Parsimonious Feature Sets. Cancer Informatics, 2014, 13s1, CIN.S13877. | 0.9 | 2 |
| 153 | Improving Classification Accuracy based on Random Forest Model with Uncorrelated High Performing Trees. International Journal of Computer Applications, 2014, 101, 26-30. | 0.2 | 25 |
| 154 | Improving the chances of successful protein structure determination with a random forest classifier. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 627-635. | 2.5 | 46 |
| 155 | Network-based sub-network signatures unveil the potential for acute myeloid leukemia therapy. Molecular BioSystems, 2014, 10, 3290-3297. | 2.9 | 4 |
| 156 | Exploration of microRNAs in porcine milk exosomes. BMC Genomics, 2014, 15, 100. | 1.2 | 140 |
| 157 | Features in Identification Approaches for MicroRNA Precursors Based on Machine Learning. , 2014, , . | | 0 |
| 158 | miRdentify: high stringency miRNA predictor identifies several novel animal miRNAs. Nucleic Acids Research, 2014, 42, e124-e124. | 6.5 | 21 |
| 159 | The discriminant power of RNA features for pre-miRNA recognition. BMC Bioinformatics, 2014, 15, 124. | 1.2 | 40 |
| 160 | Ensemble-based classification approach for micro-RNA mining applied on diverse metagenomic sequences. BMC Research Notes, 2014, 7, 286. | 0.6 | 4 |
| 161 | Prediction of plant pre-microRNAs and their microRNAs in genome-scale sequences using structure-sequence features and support vector machine. BMC Bioinformatics, 2014, 15, 423. | 1.2 | 27 |
| 162 | Fast selection of miRNA candidates based on large-scale pre-computed MFE sets of randomized sequences. BMC Research Notes, 2014, 7, 34. | 0.6 | 8 |

| # | ARTICLE | IF | CITATIONS |
|---|---------|----|-----------|
| 163 | Systematic characterization of small RNAome during zebrafish early developmental stages. BMC Genomics, 2014, 15, 117. | 1.2 | 27 |
| 164 | Identification and characterization of the microRNA transcriptome of a moth orchid Phalaenopsis aphrodite. Plant Molecular Biology, 2014, 84, 529-548. | 2.0 | 38 |
| 165 | Identification and validation of sugarcane streak mosaic virus-encoded microRNAs and their targets in sugarcane. Plant Cell Reports, 2014, 33, 265-276. | 2.8 | 29 |
| 166 | Identification of miRNAs and their target genes in developing maize ears by combined small RNA and degradome sequencing. BMC Genomics, 2014, 15, 25. | 1.2 | 94 |
| 167 | BosFinder: a novell pre-microRNA gene prediction algorithm in<i>Bos taurus</i>. Animal Genetics, 2014, 45, 479-484. | 0.6 | 3 |
| 168 | miRClassify: An advanced web server for miRNA family classification and annotation. Computers in Biology and Medicine, 2014, 45, 157-160. | 3.9 | 101 |
| 169 | An integrated evolutionary analysis of miRNAâ€"lncRNA in mammals. Molecular Biology Reports, 2014, 41, 201-207. | 1.0 | 25 |
| 170 | Identification of Ebola virus microRNAs and their putative pathological function. Science China Life Sciences, 2014, 57, 973-981. | 2.3 | 50 |
| 171 | MicroRNA Prediction Based on Sample Classification Imbalance. Applied Mechanics and Materials, 2014, 577, 1252-1257. | 0.2 | 0 |
| 172 | Isolation of New Micro RNAs from the Diamondback Moth (Lepidoptera: Yponomeutidae) Genome by a Computational Method. Florida Entomologist, 2014, 97, 877-885. | 0.2 | 4 |
| 173 | Identification and Characterization of MicroRNAs in the Spleen of Common Carp Immune Organ. Journal of Cellular Biochemistry, 2014, 115, 1768-1778. | 1.2 | 38 |
| 174 | Machine Learningâ€"Based Differential Network Analysis: A Study of Stress-Responsive Transcriptomes in <i>Arabidopsis</i>. Plant Cell, 2014, 26, 520-537. | 3.1 | 104 |
| 175 | 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 |
| 176 | Hypoxic signature of microRNAs in glioblastoma: insights from small RNA deep sequencing. BMC Genomics, 2014, 15, 686. | 1.2 | 122 |
| 177 | Evidence for the biogenesis of more than 1,000 novel human microRNAs. Genome Biology, 2014, 15, R57. | 13.9 | 222 |
| 178 | Computational identification of human long intergenic non-coding RNAs using a GAâ€"SVM algorithm. Gene, 2014, 533, 94-99. | 1.0 | 34 |
| 179 | Gene selection for cancer identification: a decision tree model empowered by particle swarm optimization algorithm. BMC Bioinformatics, 2014, 15, 49. | 1.2 | 99 |
| 181 | An efficient algorithm coupled with synthetic minority over-sampling technique to classify imbalanced PubChem BioAssay data. Analytica Chimica Acta, 2014, 806, 117-127. | 2.6 | 50 |

| # | ARTICLE | IF | CITATIONS |
|---|---------|-----|-----------|
| 182 | Computational Prediction of miRNA Genes from Small RNA Sequencing Data. Frontiers in Bioengineering and Biotechnology, 2015, 3, 7. | 2.0 | 37 |
| 183 | Evolutionary conservation and function of the human embryonic stem cell specific miR-302/367 cluster. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2015, 16, 83-98. | 0.4 | 20 |
| 184 | Identification and characterization of microRNAs from in vitro-grown pear shoots infected with Apple stem grooving virus in response to high temperature using small RNA sequencing. BMC Genomics, 2015, 16, 945. | 1.2 | 22 |
| 185 | RBRIdent: An algorithm for improved identification of RNA-binding residues in proteins from primary sequences. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1068-1077. | 1.5 | 12 |
| 186 | Identification and Characterization of Cyprinid Herpesvirus-3 (CyHV-3) Encoded MicroRNAs. PLoS ONE, 2015, 10, e0125434. | 1.1 | 22 |
| 187 | The Precision-Recall Plot Is More Informative than the ROC Plot When Evaluating Binary Classifiers on Imbalanced Datasets. PLoS ONE, 2015, 10, e0118432. | 1.1 | 2,354 |
| 188 | Improved Pre-miRNA Classification by Reducing the Effect of Class Imbalance. BioMed Research International, 2015, 2015, 1-12. | 0.9 | 5 |
| 189 | A Complex Genome-MicroRNA Interplay in Human Mitochondria. BioMed Research International, 2015, 2015, 1-13. | 0.9 | 37 |
| 190 | <i>miRBoost</i>: boosting support vector machines for microRNA precursor classification. Rna, 2015, 21, 775-785. | 1.6 | 34 |
| 191 | Improving MiRNA prediction accuracy by deep learning strategies. , 2015, , . | | 0 |
| 192 | Genome-wide discovery of miRNAs using ensembles of machine learning algorithms and logistic regression. International Journal of Data Mining and Bioinformatics, 2015, 13, 338. | 0.1 | 2 |
| 193 | Characterization of Novel Transcripts in Pseudorabies Virus. Viruses, 2015, 7, 2727-2744. | 1.5 | 46 |
| 194 | miRNA-dis: microRNA precursor identification based on distance structure status pairs. Molecular BioSystems, 2015, 11, 1194-1204. | 2.9 | 66 |
| 195 | ViralmiR: a support-vector-machine-based method for predicting viral microRNA precursors. BMC Bioinformatics, 2015, 16, S9. | 1.2 | 23 |
| 196 | A novel member of the let-7 microRNA family is associated with developmental transitions in filarial nematode parasites. BMC Genomics, 2015, 16, 331. | 1.2 | 25 |
| 197 | Identification and Diagnostic Performance of a Small RNA within the PCA3 and BMCC1 Gene Locus That Potentially Targets mRNA. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 268-275. | 1.1 | 10 |
| 198 | Genome-wide identification and characterization of teleost-specific microRNAs within zebrafish. Gene, 2015, 561, 181-189. | 1.0 | 8 |
| 199 | What variables are important in predicting bovine viral diarrhea virus? A random forest approach. Veterinary Research, 2015, 46, 85. | 1.1 | 54 |

| # | Article | IF | Citations |
|---|---------|----|-----------| 
| 200 | miRNAfe: A comprehensive tool for feature extraction in microRNA prediction. BioSystems, 2015, 138, 1-5. | 0.9 | 37 |
| 201 | An integrative approach to identify hexaploid wheat miRNAome associated with development and tolerance to abiotic stress. BMC Genomics, 2015, 16, 339. | 1.2 | 25 |
| 202 | A framework for improving microRNA prediction in non-human genomes. Nucleic Acids Research, 2015, 43, gkv698. | 6.5 | 29 |
| 203 | Prediction of Pre-miRNA with Multiple Stem-Loops Using Feedforward Neural Network. Lecture Notes in Computer Science, 2015, , 554-562. | 1.0 | 1 |
| 204 | Viral Small-RNA Analysis of Bombyx mori Larval Midgut during Persistent and Pathogenic Cytoplasmic Polyhedrosis Virus Infection. Journal of Virology, 2015, 89, 11473-11486. | 1.5 | 47 |
| 205 | Discovering MicroRNAs and Their Targets in Plants. Critical Reviews in Plant Sciences, 2015, 34, 553-571. | 2.7 | 12 |
| 206 | Temporal expression profiling of novel Spodoptera litura nucleopolyhedrovirus-encoded microRNAs upon infection of Sf21 cells. Journal of General Virology, 2015, 96, 688-700. | 1.3 | 16 |
| 207 | Prediction of Ebolavirus Genomes Encoded MicroRNA-Like Small RNAs Using Bioinformatics Approaches. , 0, , . | | 1 |
| 208 | miRQuest: integration of tools on a Web server for microRNA research. Genetics and Molecular Research, 2016, 15, . | 0.3 | 7 |
| 209 | Comparison of Kernel and Decision Tree-based Algorithms for the Prediction of microRNAs Associated with Cancer. Current Bioinformatics, 2016, 11, 143-151. | 0.7 | 5 |
| 210 | Feature Selection Has a Large Impact on One-Class Classification Accuracy for MicroRNAs in Plants. Advances in Bioinformatics, 2016, 2016, 1-6. | 5.7 | 17 |
| 211 | The Role of Highly-Resolved Gust Speed in Simulations of Storm Damage in Forests at the Landscape Scale: A Case Study from Southwest Germany. Atmosphere, 2016, 7, 7. | 1.0 | 17 |
| 212 | A Review of Computational Methods for Finding Non-Coding RNA Genes. Genes, 2016, 7, 113. | 1.0 | 22 |
| 213 | Automatic learning of pre-miRNAs from different species. BMC Bioinformatics, 2016, 17, 224. | 1.2 | 6 |
| 214 | Alternative Oxidase Gene Family in Hypericum perforatum L.: Characterization and Expression at the Post-germinative Phase. Frontiers in Plant Science, 2016, 7, 1043. | 1.7 | 12 |
| 215 | BP Neural Network Could Help Improve Pre-miRNA Identification in Various Species. BioMed Research International, 2016, 2016, 1-11. | 0.9 | 33 |
| 216 | Enhanced Viral Precursor MicroRNA Identification with Structural Robustness Features in Back-Propagation Neural Network. , 2016, , . | | 0 |
| 217 | Improving classification of mature microRNA by solving class imbalance problem. Scientific Reports, 2016, 6, 25941. | 1.6 | 11 |

| # | ARTICLE | IF | CITATIONS |
|---|---------|----|-----------|
| 218 | iDHS-EL: identifying DNase I hypersensitive sites by fusing three different modes of pseudo nucleotide composition into an ensemble learning framework. Bioinformatics, 2016, 32, 2411-2418. | 1.8 | 196 |
| 219 | Ebola virus encodes a miR-155 analog to regulate importin-α5 expression. Cellular and Molecular Life Sciences, 2016, 73, 3733-3744. | 2.4 | 29 |
| 220 | A multiobjective based automatic framework for classifying cancer-microRNA biomarkers. Gene Reports, 2016, 4, 91-103. | 0.4 | 5 |
| 221 | MicroRNA discovery in the human parasite Echinococcus multilocularis from genome-wide data. Genomics, 2016, 107, 274-280. | 1.3 | 12 |
| 222 | Computational identification and characterization of novel microRNA in the mammary gland of dairy goat (Capra hircus). Journal of Genetics, 2016, 95, 625-637. | 0.4 | 2 |
| 223 | Well-characterized sequence features of eukaryote genomes and implications for ab initio gene prediction. Computational and Structural Biotechnology Journal, 2016, 14, 298-303. | 1.9 | 12 |
| 224 | Non-coding RNAs and Inter-kingdom Communication. , 2016, , . | | 5 |
| 225 | plantMirP: an efficient computational program for the prediction of plant pre-miRNA by incorporating knowledge-based energy features. Molecular BioSystems, 2016, 12, 3124-3131. | 2.9 | 15 |
| 226 | ERK Activation Globally Downregulates miRNAs through Phosphorylating Exportin-5. Cancer Cell, 2016, 30, 723-736. | 7.7 | 125 |
| 227 | Characterization and Small RNA Content of Extracellular Vesicles in Follicular Fluid of Developing Bovine Antral Follicles. Scientific Reports, 2016, 6, 25486. | 1.6 | 106 |
| 229 | iMiRNA-SSF: Improving the Identification of MicroRNA Precursors by Combining Negative Sets with Different Distributions. Scientific Reports, 2016, 6, 19062. | 1.6 | 65 |
| 230 | Data on differentially expressed microRNAs in the liver between nonalcoholic fatty liver disease and normal Wistar rat using Solexa sequencing. Data in Brief, 2016, 8, 280-285. | 0.5 | 1 |
| 231 | Gene-set activity toolbox (GAT): A platform for microarray-based cancer diagnosis using an integrative gene-set analysis approach. Journal of Bioinformatics and Computational Biology, 2016, 14, 1650015. | 0.3 | 5 |
| 232 | iMiRNA-PseDPC: microRNA precursor identification with a pseudo distance-pair composition approach. Journal of Biomolecular Structure and Dynamics, 2016, 34, 223-235. | 2.0 | 120 |
| 233 | Identification and profiling of microRNAs in the ovaries of polytocous and monotocous goats during estrus. Theriogenology, 2016, 85, 769-780. | 0.9 | 21 |
| 234 | Identification and differential expression of microRNAs associated with fat deposition in the liver of Wistar rats with nonalcoholic fatty liver disease. Gene, 2016, 585, 1-8. | 1.0 | 7 |
| 235 | Feature based quality assessment of DNA sequencing chromatograms. Applied Soft Computing Journal, 2016, 41, 420-427. | 4.1 | 5 |
| 237 | OP-Triplet-ELM: Identification of real and pseudo microRNA precursors using extreme learning machine with optimal features. Journal of Bioinformatics and Computational Biology, 2016, 14, 1650006. | 0.3 | 1 |

| # | ARTICLE | IF | CITATIONS |
|---|---------|----|-----------|
| 238 | Identification of microRNA-like RNAs from Curvularia lunata associated with maize leaf spot by bioinformation analysis and deep sequencing. Molecular Genetics and Genomics, 2016, 291, 587-596. | 1.0 | 18 |
| 239 | Non-coding RNA identification based on topology secondary structure and reading frame in organelle genome level. Genomics, 2016, 107, 9-15. | 1.3 | 16 |
| 240 | Differential expression of miRNAs related to caste differentiation in the honey bee, Apis mellifera. Apidologie, 2016, 47, 495-508. | 0.9 | 18 |
| 241 | iRSpot-GAEnsC: identifing recombination spots via ensemble classifier and extending the concept of Chou's PseAAC to formulate DNA samples. Molecular Genetics and Genomics, 2016, 291, 285-296. | 1.0 | 120 |
| 242 | High Class-Imbalance in pre-miRNA Prediction: A Novel Approach Based on deepSOM. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 1316-1326. | 1.9 | 28 |
| 243 | Classification of otoliths of fishes common in the Santa Barbara Basin based on morphology and chemical composition. Canadian Journal of Fisheries and Aquatic Sciences, 2017, 74, 1195-1207. | 0.7 | 5 |
| 244 | V-ELMpiRNAPred: Identification of human piRNAs by the voting-based extreme learning machine (V-ELM) with a new hybrid feature. Journal of Bioinformatics and Computational Biology, 2017, 15, 1650046. | 0.3 | 8 |
| 245 | Identification of microRNA precursors using reduced and hybrid features. Molecular BioSystems, 2017, 13, 1640-1645. | 2.9 | 8 |
| 247 | Exploring MicroRNA::Target Regulatory Interactions by Computing Technologies. Methods in Molecular Biology, 2017, 1617, 123-131. | 0.4 | 0 |
| 248 | A compilation of Web-based research tools for miRNA analysis. Briefings in Functional Genomics, 2017, 16, 249-273. | 1.3 | 32 |
| 249 | An improved method for identification of small non-coding RNAs in bacteria using support vector machine. Scientific Reports, 2017, 7, 46070. | 1.6 | 14 |
| 250 | In Silico Prediction of RNA Secondary Structure. Methods in Molecular Biology, 2017, 1543, 145-168. | 0.4 | 7 |
| 251 | Identification and characterization of microRNAs in the muscle of Schizothorax prenanti. Fish Physiology and Biochemistry, 2017, 43, 1055-1064. | 0.9 | 3 |
| 252 | MicroRNA categorization using sequence motifs and k-mers. BMC Bioinformatics, 2017, 18, 170. | 1.2 | 25 |
| 253 | On the performance of pre-microRNA detection algorithms. Nature Communications, 2017, 8, 330. | 5.8 | 47 |
| 254 | Variable importance-weighted Random Forests. Quantitative Biology, 2017, 5, 338-351. | 0.3 | 35 |
| 255 | Distinguishing the disease-associated SNPs based on composition frequency analysis. Interdisciplinary Sciences, Computational Life Sciences, 2017, 9, 459-467. | 2.2 | 4 |
| 256 | Circulating microRNA as candidates for early embryonic viability in cattle. Molecular Reproduction and Development, 2017, 84, 731-743. | 1.0 | 59 |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 257 | A framework for the targeted selection of herbs with similar efficacy by exploiting drug repositioning technique and curated biomedical knowledge. Journal of Ethnopharmacology, 2017, 208, 117-128. | 2.0 | 4 |
| 258 | Detection and comparison of microRNAs in the caprine mammary gland tissues of colostrum and common milk stages. BMC Genetics, 2017, 18, 38. | 2.7 | 60 |
| 259 | Prediction of microRNAs involved in immune system diseases through network based features. Journal of Biomedical Informatics, 2017, 65, 34-45. | 2.5 | 9 |
| 260 | Structure-based QSAR, molecule design and bioassays of protease-activated receptor 1 inhibitors. Journal of Biomolecular Structure and Dynamics, 2017, 35, 2853-2867. | 2.0 | 11 |
| 261 | The Landscape of Extreme Genomic Variation in the Highly Adaptable Atlantic Killifish. Genome Biology and Evolution, 2017, 9, 659-676. | 1.1 | 43 |
| 262 | Extreme learning machine prediction under high class imbalance in bioinformatics. , 2017, , . | | 1 |
| 263 | Categorization of species based on their microRNAs employing sequence motifs, information-theoretic sequence feature extraction, and k-mers. Eurasip Journal on Advances in Signal Processing, 2017, 2017, . | 1.0 | 11 |
| 264 | Identification of Plant Precursor miRNAs using Structural Robustness and Secondary Structures Features. , 2017, , . | | 0 |
| 265 | Transcriptome Analysis of Nonâ€Coding RNAs in Livestock Species: Elucidating the Ambiguity. , 2017, , . | | 3 |
| 266 | Assessing the Potential of Land Use Modification to Mitigate Ambient NO2 and Its Consequences for Respiratory Health. International Journal of Environmental Research and Public Health, 2017, 14, 750. | 1.2 | 13 |
| 267 | Epigenetics in Chronic Pain. , 2017, , 185-226. | | 1 |
| 268 | A Review on Recent Computational Methods for Predicting Noncoding RNAs. BioMed Research International, 2017, 2017, 1-14. | 0.9 | 25 |
| 269 | A novel method to identify pre-microRNA in various species knowledge base on various species. Journal of Biomedical Semantics, 2017, 8, 30. | 0.9 | 8 |
| 270 | AdaBoost Algorithm with Random Forests for Plant and Animal Precursor MicroRNAs Classification. , 2017, , . | | 0 |
| 271 | Application of the Random Forest model for chlorophyll-a forecasts in fresh and brackish water bodies in Japan, using multivariate long-term databases. Journal of Hydroinformatics, 2018, 20, 206-220. | 1.1 | 51 |
| 272 | In silico identification of microRNAs and their targets associated with coconut embryogenic calli. Agri Gene, 2018, 7, 59-65. | 1.9 | 15 |
| 273 | Contingent valuation of health and mood impacts of PM2.5 in Beijing, China. Science of the Total Environment, 2018, 630, 1269-1282. | 3.9 | 43 |
| 274 | Predicting the prolonged length of stay of general surgery patients: a supervised learning approach. International Transactions in Operational Research, 2018, 25, 75-90. | 1.8 | 28 |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 275 | Computational Approaches and Related Tools to Identify MicroRNAs in a Species: A Bird's Eye View. Interdisciplinary Sciences, Computational Life Sciences, 2018, 10, 616-635. | 2.2 | 12 |
| 276 | An ensemble of decision trees with random vector functional link networks for multi-class classification. Applied Soft Computing Journal, 2018, 70, 1146-1153. | 4.1 | 63 |
| 277 | Machine Learning-Based State-of-the-Art Methods for the Classification of RNA-Seq Data. Lecture Notes in Computational Vision and Biomechanics, 2018, , 133-172. | 0.5 | 24 |
| 278 | Systematic miRNome profiling reveals differential microRNAs in transgenic maize metabolism. Environmental Sciences Europe, 2018, 30, 37. | 2.6 | 0 |
| 279 | Identification of pre-microRNAs by characterizing their sequence order evolution information and secondary structure graphs. BMC Bioinformatics, 2018, 19, 521. | 1.2 | 8 |
| 280 | New 3D graphical representation for RNA structure analysis and its application in the pre-miRNA identification of plants. RSC Advances, 2018, 8, 30833-30841. | 1.7 | 6 |
| 281 | Intelligent computational method for discrimination of anticancer peptides by incorporating sequential and evolutionary profiles information. Chemometrics and Intelligent Laboratory Systems, 2018, 182, 158-165. | 1.8 | 48 |
| 282 | Distinguishing mirtrons from canonical miRNAs with data exploration and machine learning methods. Scientific Reports, 2018, 8, 7560. | 1.6 | 34 |
| 283 | Cancer Diagnosis Through IsomiR Expression with Machine Learning Method. Current Bioinformatics, 2018, 13, 57-63. | 0.7 | 138 |
| 284 | Micro-RNAs involved in cellular proliferation have altered expression profiles in granulosa of young women with diminished ovarian reserve. Journal of Assisted Reproduction and Genetics, 2018, 35, 1777-1786. | 1.2 | 38 |
| 285 | Identification and characterization of microRNA in the lung tissue of pigs with different susceptibilities to PCV2 infection. Veterinary Research, 2018, 49, 18. | 1.1 | 24 |
| 286 | Predicting novel microRNA: a comprehensive comparison of machine learning approaches. Briefings in Bioinformatics, 2019, 20, 1607-1620. | 3.2 | 31 |
| 287 | Trends in the development of miRNA bioinformatics tools. Briefings in Bioinformatics, 2019, 20, 1836-1852. | 3.2 | 361 |
| 288 | Prediction of Coding and Non-Coding RNA. , 2019, , 230-240. | | 4 |
| 289 | Steroid metabolomics: machine learning and multidimensional diagnostics for adrenal cortical tumors, hyperplasias, and related disorders. Current Opinion in Endocrine and Metabolic Research, 2019, 8, 40-49. | 0.6 | 8 |
| 290 | Towards a Physiological Scale of Vocal Fold Agent-Based Models of Surgical Injury and Repair: Sensitivity Analysis, Calibration and Verification. Applied Sciences (Switzerland), 2019, 9, 2974. | 1.3 | 9 |
| 291 | iRO-PsekGCC: Identify DNA Replication Origins Based on Pseudo k-Tuple GC Composition. Frontiers in Genetics, 2019, 10, 842. | 1.1 | 31 |
| 292 | miRWoods: Enhanced precursor detection and stacked random forests for the sensitive detection of microRNAs. PLoS Computational Biology, 2019, 15, e1007309. | 1.5 | 8 |

| # | ARTICLE | IF | CITATIONS |
|---|---------|----|-----------|
| 293 | Emotional Decision-Making Biases Prediction in Cyber-Physical Systems. Big Data and Cognitive Computing, 2019, 3, 49. | 2.9 | 1 |
| 294 | Selecting Essential MicroRNAs Using a Novel Voting Method. Molecular Therapy - Nucleic Acids, 2019, 18, 16-23. | 2.3 | 31 |
| 295 | Differential expression of novel MicroRNAs from developing fetal heart of Gallus gallus domesticus implies a role in cardiac development. Molecular and Cellular Biochemistry, 2019, 462, 157-165. | 1.4 | 1 |
| 296 | Genome-wide hairpins datasets of animals and plants for novel miRNA prediction. Data in Brief, 2019, 25, 104209. | 0.5 | 6 |
| 297 | CL-PMI: A Precursor MicroRNA Identification Method Based on Convolutional and Long Short-Term Memory Networks. Frontiers in Genetics, 2019, 10, 967. | 1.1 | 7 |
| 298 | An Inhaler Tracking System Based on Acoustic Analysis: Hardware and Software. IEEE Transactions on Instrumentation and Measurement, 2019, 68, 4472-4480. | 2.4 | 9 |
| 299 | Discovery of MicroRNAs from Batrachuperus yenyuanensis Using Deep Sequencing and Prediction of Their Targets. Biochemistry (Moscow), 2019, 84, 380-389. | 0.7 | 1 |
| 300 | AcMNPV-miR-3 is a miRNA encoded by Autographa californica nucleopolyhedrovirus and regulates the viral infection by targeting ac101. Virus Research, 2019, 267, 49-58. | 1.1 | 12 |
| 301 | Computational identification of hepatitis E virusâ€‌encoded microRNAs and their targets in human. Journal of Medical Virology, 2019, 91, 1545-1552. | 2.5 | 8 |
| 302 | Development of species specific putative miRNA and its target prediction tool in wheat (Triticum) Tj ETQq1 1 0.784314 rgBT /Overloc | 1.6 | 7 |
| 303 | Improved Pre-miRNAs Identification Through Mutual Information of Pre-miRNA Sequences and Structures. Frontiers in Genetics, 2019, 10, 119. | 1.1 | 28 |
| 304 | Small RNA (sRNA) expression in the chorioallantois, endometrium and serum of mares following experimental induction of placentitis. Reproduction, Fertility and Development, 2019, 31, 1144. | 0.1 | 8 |
| 305 | Nucleotide-level Convolutional Neural Networks for Pre-miRNA Classification. Scientific Reports, 2019, 9, 628. | 1.6 | 14 |
| 306 | Identification and characterization of salt-tolerance relative miRNAs in Procambarus clarkii by high-throughput sequencing. ExRNA, 2019, 1, . | 1.0 | 2 |
| 307 | Fast and accurate microRNA search using CNN. BMC Bioinformatics, 2019, 20, 646. | 1.2 | 8 |
| 308 | MicroRNA prediction based on 3D graphical representation of RNA secondary structures. Turkish Journal of Biology, 2019, 43, 274-280. | 2.1 | 4 |
| 309 | Fuzzy based algorithms to predict MicroRNA regulated protein interaction pathways and ranking estimation in Arabidopsis thaliana. Gene, 2019, 692, 170-175. | 1.0 | 2 |
| 310 | Computational Prediction of Functional MicroRNAâ€‌mRNA Interactions. Methods in Molecular Biology, 2019, 1912, 175-196. | 0.4 | 21 |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 311 | Computational Resources for Prediction and Analysis of Functional miRNA and Their Targetome. Methods in Molecular Biology, 2019, 1912, 215-250. | 0.4 | 27 |
| 312 | Prediction of membrane protein types by exploring local discriminative information from evolutionary profiles. Analytical Biochemistry, 2019, 564-565, 123-132. | 1.1 | 21 |
| 313 | Three-Level Hepatotoxicity Prediction System Based on Adverse Hepatic Effects. Molecular Pharmaceutics, 2019, 16, 393-408. | 2.3 | 19 |
| 314 | BioSeq-Analysis: a platform for DNA, RNA and protein sequence analysis based on machine learning approaches. Briefings in Bioinformatics, 2019, 20, 1280-1294. | 3.2 | 251 |
| 315 | Bioinformatics prediction and experimental validation of a novel microRNA: hsaâ€miRâ€B43 within human <i>CDH4</i> gene with a potential metastasisâ€related function in breast cancer. Journal of Cellular Biochemistry, 2020, 121, 1307-1316. | 1.2 | 7 |
| 316 | milRNApredictor: Genome-free prediction of fungi milRNAs by incorporating k-mer scheme and distance-dependent pair potential. Genomics, 2020, 112, 2233-2240. | 1.3 | 6 |
| 317 | Complexity measures of the mature miRNA for improving pre-miRNAs prediction. Bioinformatics, 2020, 36, 2319-2327. | 1.8 | 9 |
| 318 | A networkâ€based predictive gene expression signature for recurrence risks in stage II colorectal cancer. Cancer Medicine, 2020, 9, 179-193. | 1.3 | 16 |
| 319 | Discovery and annotation of novel microRNAs in the porcine genome by using a semi-supervised transductive learning approach. Genomics, 2020, 112, 2107-2118. | 1.3 | 5 |
| 320 | Identification of milRNAs and their target genes in Ganoderma lucidum by high-throughput sequencing and degradome analysis. Fungal Genetics and Biology, 2020, 136, 103313. | 0.9 | 18 |
| 321 | Urban flood risk mapping using data-driven geospatial techniques for a flood-prone case area in Iran. Hydrology Research, 2020, 51, 127-142. | 1.1 | 39 |
| 322 | Prediction of Recombination Spots Using Novel Hybrid Feature Extraction Method via Deep Learning Approach. Frontiers in Genetics, 2020, 11, 539227. | 1.1 | 15 |
| 323 | Multi-branch Convolutional Neural Network for Identification of Small Non-coding RNA genomic loci. Scientific Reports, 2020, 10, 9486. | 1.6 | 21 |
| 324 | binomialRF: interpretable combinatoric efficiency of random forests to identify biomarker interactions. BMC Bioinformatics, 2020, 21, 374. | 1.2 | 3 |
| 325 | Popular Computational Tools Used for miRNA Prediction and Their Future Development Prospects. Interdisciplinary Sciences, Computational Life Sciences, 2020, 12, 395-413. | 2.2 | 10 |
| 326 | Support Vector Machine Based on Localized Multiple Kernel Learning in pre-microRNA Classification. , 2020, , . | | 1 |
| 327 | miRNAFinder: A pre-microRNA classifier for plants and analysis of feature impact. , 2020, , . | | 1 |
| 328 | Prediction and experimental confirmation of banana bract mosaic virus encoding miRNAs and their targets. ExRNA, 2020, 2, . | 1.0 | 6 |

| # | Article | IF | Citations |
|---|---------|----|-----------| 
| 329 | A Day in the Life: Identification of Developmentally Regulated MicroRNAs in the Colorado Potato Beetle (Leptinotarsa decemlineata; Coleoptera: Chrysomelidae). Journal of Economic Entomology, 2020, 113, 1445-1454. | 0.8 | 4 |
| 330 | Integrating Household Travel Survey and Social Media Data to Improve the Quality of OD Matrix: A Comparative Case Study. IEEE Transactions on Intelligent Transportation Systems, 2020, , 1-9. | 4.7 | 16 |
| 331 | Tweaking microRNA-mediated gene regulation for crop improvement. , 2020, , 45-66. | | 3 |
| 332 | Deep neural networks for human microRNA precursor detection. BMC Bioinformatics, 2020, 21, 17. | 1.2 | 18 |
| 333 | Named Entity Recognition for Sensitive Data Discovery in Portuguese. Applied Sciences (Switzerland), 2020, 10, 2303. | 1.3 | 19 |
| 334 | Heavy metal contamination prediction using ensemble model: Case study of Bay sedimentation, Australia. Journal of Hazardous Materials, 2021, 403, 123492. | 6.5 | 68 |
| 335 | Prediction of Piwi-Interacting RNAs and Their Functions via Convolutional Neural Network. IEEE Access, 2021, 9, 54233-54240. | 2.6 | 2 |
| 336 | Identification of miRNAs encoded by Autographa californica nucleopolyhedrovirus. Journal of General Virology, 2021, 102, . | 1.3 | 4 |
| 337 | Prediction of donation return rate in young donors using machine‒learning models. ISBT Science Series, 2021, 16, 119-126. | 1.1 | 1 |
| 338 | Computationally predicted SARS-COV-2 encoded microRNAs target NFKB, JAK/STAT and TGFB signaling pathways. Gene Reports, 2021, 22, 101012. | 0.4 | 58 |
| 339 | The stacking strategy-based hybrid framework for identifying non-coding RNAs. Briefings in Bioinformatics, 2021, 22, . | 3.2 | 28 |
| 340 | MicroRNA annotation in plants: current status and challenges. Briefings in Bioinformatics, 2021, 22, . | 3.2 | 10 |
| 341 | Improving the performance of precision poverty alleviation based on big data mining and machine learning. Journal of Intelligent and Fuzzy Systems, 2021, 40, 6617-6628. | 0.8 | 1 |
| 342 | iT4SE-EP: Accurate Identification of Bacterial Type IV Secreted Effectors by Exploring Evolutionary Features from Two PSI-BLAST Profiles. Molecules, 2021, 26, 2487. | 1.7 | 2 |
| 343 | Classification of Precursor MicroRNAs from Different Species Based on K-mer Distance Features. Algorithms, 2021, 14, 132. | 1.2 | 0 |
| 344 | Deep Multiple Kernel Learning for Prediction of MicroRNA Precursors. Scientific Programming, 2021, 2021, 1-9. | 0.5 | 1 |
| 345 | A hybrid CNN-LSTM model for pre-miRNA classification. Scientific Reports, 2021, 11, 14125. | 1.6 | 36 |
| 346 | Estimation of modified expansive soil CBR with multivariate adaptive regression splines, random forest and gradient boosting machine. Innovative Infrastructure Solutions, 2021, 6, 1. | 1.1 | 26 |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 347 | Computational Detection of Pre-microRNAs. Methods in Molecular Biology, 2022, 2257, 167-174. | 0.4 | 1 |
| 348 | Computational Methods for Predicting Mature microRNAs. Methods in Molecular Biology, 2022, 2257, 175-185. | 0.4 | 2 |
| 349 | Analysis and prediction of nucleation mechanisms in a bi-component powder bed with wettability differentials. Powder Technology, 2021, 390, 209-218. | 2.1 | 3 |
| 350 | Deep Learning for the discovery of new pre-miRNAs: Helping the fight against COVID-19. Machine Learning With Applications, 2021, 6, 100150. | 3.0 | 11 |
| 351 | On the prediction of isolation, release, and decease states for COVID-19 patients: A case study in South Korea. ISA Transactions, 2021, , . | 3.1 | 4 |
| 352 | Machine Learning Methods for MicroRNA Gene Prediction. Methods in Molecular Biology, 2014, 1107, 177-187. | 0.4 | 28 |
| 353 | Computational and Bioinformatics Methods for MicroRNA Gene Prediction. Methods in Molecular Biology, 2014, 1107, 157-175. | 0.4 | 13 |
| 354 | Prediction and Classification of Real and Pseudo MicroRNA Precursors via Data Fuzzification and Fuzzy Decision Trees. Lecture Notes in Computer Science, 2009, , 323-334. | 1.0 | 5 |
| 355 | ncRNA-Class Web Tool: Non-coding RNA Feature Extraction and Pre-miRNA Classification Web Tool. International Federation for Information Processing, 2012, , 632-641. | 0.4 | 2 |
| 356 | Systematic Genome-wide Screening and Prediction of microRNAs in EBOV During the 2014 Ebolavirus Outbreak. Scientific Reports, 2015, 5, 9912. | 1.6 | 44 |
| 359 | Cross-Mapping Events in miRNAs Reveal Potential miRNA-Mimics and Evolutionary Implications. PLoS ONE, 2011, 6, e20517. | 1.1 | 25 |
| 360 | MaturePred: Efficient Identification of MicroRNAs within Novel Plant Pre-miRNAs. PLoS ONE, 2011, 6, e27422. | 1.1 | 61 |
| 361 | Identification of Novel and Differentially Expressed MicroRNAs of Dairy Goat Mammary Gland Tissues Using Solexa Sequencing and Bioinformatics. PLoS ONE, 2012, 7, e49463. | 1.1 | 70 |
| 362 | RFMirTarget: Predicting Human MicroRNA Target Genes with a Random Forest Classifier. PLoS ONE, 2013, 8, e70153. | 1.1 | 34 |
| 363 | Recipe for a Busy Bee: MicroRNAs in Honey Bee Caste Determination. PLoS ONE, 2013, 8, e81661. | 1.1 | 60 |
| 364 | Effective Identification of Gram-Negative Bacterial Type III Secreted Effectors Using Position-Specific Residue Conservation Profiles. PLoS ONE, 2013, 8, e84439. | 1.1 | 27 |
| 365 | Identification of Real MicroRNA Precursors with a Pseudo Structure Status Composition Approach. PLoS ONE, 2015, 10, e0121501. | 1.1 | 193 |
| 366 | Identify Beta-Hairpin Motifs with Quadratic Discriminant Algorithm Based on the Chemical Shifts. PLoS ONE, 2015, 10, e0139280. | 1.1 | 10 |

| # | ARTICLE | IF | CITATIONS |
|---|---------|----|-----------|
| 367 | Expression of microRNAs in Horse Plasma and Their Characteristic Nucleotide Composition. PLoS ONE, 2016, 11, e0146374. | 1.1 | 16 |
| 368 | qiRNApredictor: A Novel Computational Program for the Prediction of qiRNAs in Neurospora crassa. PLoS ONE, 2016, 11, e0159487. | 1.1 | 1 |
| 369 | Identification and Characterization of Microsatellite Loci in Maqui (Aristotelia chilensis [Molina]) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 6 | 1.1 | 17 |
| 370 | Integrated Strategy Improves the Prediction Accuracy of miRNA in Large Dataset. PLoS ONE, 2016, 11, e0168392. | 1.1 | 9 |
| 371 | Computational Approaches in Detecting Non- Coding RNA. Current Genomics, 2013, 14, 371-377. | 0.7 | 41 |
| 372 | ESDA: An Improved Approach to Accurately Identify Human snoRNAs for Precision Cancer Therapy. Current Bioinformatics, 2020, 15, 34-40. | 0.7 | 10 |
| 373 | Using the Chou's Pseudo Component to Predict the ncRNA Locations Based on the Improved K-Nearest Neighbor (iKNN) Classifier. Current Bioinformatics, 2020, 15, 563-573. | 0.7 | 6 |
| 374 | Can MiRBase provide positive data for machine learning for the detection of MiRNA hairpins?. Journal of Integrative Bioinformatics, 2013, 10, 215. | 1.0 | 19 |
| 377 | PremipreD: Precursor miRNA Prediction by Support Vector Machine Approach. Trends in Bioinformatics, 2018, 11, 17-24. | 0.3 | 3 |
| 378 | Novel MicroRNAs and Targets Prediction in PRRS Virus Genome. Journal of Convergence Information Technology, 2010, 5, 207-215. | 0.1 | 5 |
| 379 | Performance and Evaluation of MicroRNA Gene Identification Tools. Journal of Proteomics and Bioinformatics, 2009, 02, 336-343. | 0.4 | 4 |
| 380 | Sequence Motif-Based One-Class Classifiers Can Achieve Comparable Accuracy to Two-Class Learners for Plant microRNA Detection. Journal of Biomedical Science and Engineering, 2015, 08, 684-694. | 0.2 | 13 |
| 381 | Accurate Plant MicroRNA Prediction Can Be Achieved Using Sequence Motif Features. Journal of Intelligent Learning Systems and Applications, 2016, 08, 9-22. | 0.4 | 8 |
| 382 | Effective sample selection for classification of pre-miRNAs. Genetics and Molecular Research, 2011, 10, 506-518. | 0.3 | 6 |
| 383 | Identification and Function Prediction of Novel MicroRNAs in Laoshan Dairy Goats. Asian-Australasian Journal of Animal Sciences, 2013, 26, 309-315. | 2.4 | 11 |
| 384 | Ssa miRNAs DB: online repository of in silico predicted miRNAs in salmo salar. Bioinformation, 2012, 8, 284-286. | 0.2 | 6 |
| 385 | RAmiRNA: Software suite for generation of SVM-based prediction models of mature miRNAs. Bioinformation, 2012, 8, 581-585. | 0.2 | 1 |
| 386 | Computational identification and characterization of putative miRNAs in Heliothis virescens. Bioinformation, 2013, 9, 79-83. | 0.2 | 16 |

| # | Article | IF | Citations |
|---|---------|----|-----------| 
| 387 | Computational identification of putative miRNAs and their target genes in pathogenic amoeba Naegleria fowleri. Bioinformation, 2015, 11, 550-557. | 0.2 | 3 |
| 388 | Delineating the impact of machine learning elements in pre-microRNA detection. PeerJ, 2017, 5, e3131. | 0.9 | 13 |
| 389 | Identification of microRNA precursors with new sequence-structure features. Journal of Biomedical Science and Engineering, 2009, 02, 626-631. | 0.2 | 2 |
| 390 | A novel stepwise support vector machine (SVM) method based on optimal feature combination for predicting miRNA precursors. African Journal of Biotechnology, 2011, 10, . | 0.3 | 1 |
| 391 | RFMirTarget: A Random Forest Classifier for Human miRNA Target Gene Prediction. Lecture Notes in Computer Science, 2012, , 97-108. | 1.0 | 2 |
| 392 | Bioinformatics analysis on structural features of microRNA precursors in insects. European Journal of Entomology, 2013, 110, 13-20. | 1.2 | 2 |
| 393 | Comparison of Four Ab Initio MicroRNA Prediction Tools. , 2013, , . | | 3 |
| 394 | Machine Learning with Special Emphasis on Support Vector Machines (SVMs) in Systems Biology: A Plant Perspective. , 2014, , 273-281. | | 0 |
| 395 | GenoScan: Genomic Scanner for Putative miRNA Precursors. Lecture Notes in Computer Science, 2014, , 266-277. | 1.0 | 0 |
| 396 | A Rule Induction Model Empowered by Fuzzy-Rough Particle Swarm Optimization Algorithm for Classification of Microarray Dataset. Smart Innovation, Systems and Technologies, 2015, , 291-303. | 0.5 | 4 |
| 397 | Improving Classification Accuracy based on Random Forest Model through Weighted Sampling for Noisy Data with Linear Decision Boundary. Indian Journal of Science and Technology, 2015, 8, 614. | 0.5 | 8 |
| 398 | Avaliação de Desempenho em Bioinformática: Estudo de caso de sistemas computacionais para a investigação de microRNAs. , 0, , . | | 0 |
| 399 | SVM-Based Pre-microRNA Classifier Using Sequence, Structural, and Thermodynamic Parameters. Advances in Intelligent Systems and Computing, 2016, , 57-67. | 0.5 | 0 |
| 400 | Identification of MicroRNA-Like Molecules Derived from the Antigenome RNA of Hepatitis C Virus: A Bioinformatics Approach. Natural Science, 2016, 08, 180-191. | 0.2 | 0 |
| 403 | A Mixed Convolutional Neural Network for Pre-miRNA Classification. , 2019, , . | | 0 |
| 404 | MicroRNA Prediction in the FVIII Gene Locus: A Step Towards Hemophilia A Control. Gene, Cell and Tissue, 2020, 7, . | 0.2 | 0 |
| 405 | MirCure: a tool for quality control, filter and curation of microRNAs of animals and plants. Bioinformatics, 2020, 36, i618-i624. | 1.8 | 4 |
| 406 | Supervised Deep Learning Methods for Human pre-miRNA Identification. , 2020, , . | | 0 |

| # | ARTICLE | IF | CITATIONS |
|---|---------|----|-----------| 
| 407 | A Brief Survey for MicroRNA Precursor Identification Using Machine Learning Methods. Current Genomics, 2020, 21, 11-25. | 0.7 | 3 |
| 408 | MicroRNA Precursor Prediction Using SVM with RNA Pairing Continuity Feature. Advances in Bioinformatics and Biomedical Engineering Book Series, 0, , 73-82. | 0.2 | 0 |
| 409 | Variable importance-weighted Random Forests. Quantitative Biology, 2017, 5, 338-351. | 0.3 | 5 |
| 410 | Price forecasting for real estate using machine learning: A case study on Riyadh city. Concurrency Computation Practice and Experience, 2022, 34, e6748. | 1.4 | 17 |
| 411 | Meteorological and social conditions contribute to infectious diarrhea in China. Scientific Reports, 2021, 11, 23374. | 1.6 | 9 |
| 412 | Construction of a Diagnostic Model for Lymph Node Metastasis of the Papillary Thyroid Carcinoma Using Preoperative Ultrasound Features and Imaging Omics. Journal of Healthcare Engineering, 2022, 2022, 1-10. | 1.1 | 1 |
| 413 | Viral Derived Mirnas in OrNV- &lt;i&gt;Oryctes Rhinoceros&lt;/i&gt; Interaction. SSRN Electronic Journal, 0, , . | 0.4 | 1 |
| 414 | LANDMark: an ensemble approach to the supervised selection of biomarkers in high-throughput sequencing data. BMC Bioinformatics, 2022, 23, 110. | 1.2 | 5 |
| 416 | miRNAFinder: A comprehensive web resource for plant Pre-microRNA classification. BioSystems, 2022, 215-216, 104662. | 0.9 | 1 |
| 419 | Forest yield prediction under different climate change scenarios using data intelligent models in Pakistan. Brazilian Journal of Biology, 2021, 84, e253106. | 0.4 | 4 |
| 420 | Provable Boolean interaction recovery from tree ensemble obtained via random forests. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, . | 3.3 | 2 |
| 421 | A Novel miRNA Located in the HER2 Gene Shows an Inhibitory Effect on Wnt Signaling and Cell Cycle Progression. BioMed Research International, 2022, 2022, 1-9. | 0.9 | 1 |
| 422 | Prediction of factor of safety of modified expansive soil slope modeled with non-associated flow rule considering dilatancy effect. Arabian Journal of Geosciences, 2022, 15, . | 0.6 | 1 |
| 423 | Statistical analysis and prediction of spatial resilient modulus of coarse-grained soils for pavement subbase and base layers using MLR, ANN and Ensemble techniques. Innovative Infrastructure Solutions, 2022, 7, . | 1.1 | 2 |
| 424 | Real-Time Safety Decision-Making Method for Multirotor Flight Strategies Based on TOPSIS Model. Applied Sciences (Switzerland), 2022, 12, 6696. | 1.3 | 1 |
| 425 | microRNAs as critical regulators in heart development and diseases. , 2022, , 187-203. | | 0 |
| 426 | Covid-19'un YayÄ±lÄ±m Tahminine YÃ¶nelik Makine Ã–ÄŸrenmesi ve Derin Ã–ÄŸrenme TabanlÄ± KarÅŸÄ±laÅŸtÄ±rmalÄ± Bir Analiz: TÃ¼rkiye Ä°Ã§in Ã–rnek Bir Ã‡alÄ±ÅŸma. FÄ±rat Ãœniversitesi MÃ¼hendislik Bilimleri Dergisi, 0, , . | 0.2 | 0 |
| 427 | Updated review of advances in microRNAs and complex diseases: experimental results, databases, webservers and data fusion. Briefings in Bioinformatics, 2022, 23, . | 3.2 | 27 |

| # | Article | IF | Citations |
|---|---------|----|-----------| 
| 428 | Diagnosis of hepatocellular carcinoma based on salivary protein glycopatterns and machine learning algorithms. Clinical Chemistry and Laboratory Medicine, 2022, 60, 1963-1973. | 1.4 | 6 |
| 429 | Prediction models based on miRNA-disease relationship: Diagnostic relevance to multiple diseases including COVID-19. Current Pharmaceutical Biotechnology, 2022, 24, . | 0.9 | 2 |
| 430 | Machine Learning Based Methods and Best Practices of microRNA-Target Prediction and Validation. Advances in Experimental Medicine and Biology, 2022, , 109-131. | 0.8 | 1 |
| 431 | MicroRNA Bioinformatics. , 2023, , 791-815. | | 0 |