

# Quan Zou

## List of Publications by Year in descending order

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351  
papers

17,003  
citations

13854

67  
h-index

20943

115  
g-index

360  
all docs

360  
docs citations

360  
times ranked

11435  
citing authors

#	ARTICLE	IF	CITATIONS
1	Biological functions of microRNAs: a review. <i>Journal of Physiology and Biochemistry</i> , 2011, 67, 129-139.	1.3	568
2	Predicting Diabetes Mellitus With Machine Learning Techniques. <i>Frontiers in Genetics</i> , 2018, 9, 515.	1.1	497
3	The <i>Symbiodinium kawagutii</i> genome illuminates dinoflagellate gene expression and coral symbiosis. <i>Science</i> , 2015, 350, 691-694.	6.0	430
4	Gene2vec: gene subsequence embedding for prediction of mammalian <i>N<sup>6</sup></i> -methyladenosine sites from mRNA. <i>Rna</i> , 2019, 25, 205-218.	1.6	421
5	A novel features ranking metric with application to scalable visual and bioinformatics data classification. <i>Neurocomputing</i> , 2016, 173, 346-354.	3.5	353
6	A comprehensive overview and evaluation of circular RNA detection tools. <i>PLoS Computational Biology</i> , 2017, 13, e1005420.	1.5	313
7	Tumor origin detection with tissue-specific miRNA and DNA methylation markers. <i>Bioinformatics</i> , 2018, 34, 398-406.	1.8	308
8	Integrative approaches for predicting microRNA function and prioritizing disease-related microRNA using biological interaction networks. <i>Briefings in Bioinformatics</i> , 2016, 17, 193-203.	3.2	307
9	Inferring MicroRNA-Disease Associations by Random Walk on a Heterogeneous Network with Multiple Data Sources. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 905-915.	1.9	265
10	Identification of patients and plaques vulnerable to future coronary events with near-infrared spectroscopy intravascular ultrasound imaging: a prospective, cohort study. <i>Lancet, The</i> , 2019, 394, 1629-1637.	6.3	263
11	Prediction of potential disease-associated microRNAs using structural perturbation method. <i>Bioinformatics</i> , 2018, 34, 2425-2432.	1.8	229
12	LibD3C: Ensemble classifiers with a clustering and dynamic selection strategy. <i>Neurocomputing</i> , 2014, 123, 424-435.	3.5	227
13	Local-DPP: An improved DNA-binding protein prediction method by exploring local evolutionary information. <i>Information Sciences</i> , 2017, 384, 135-144.	4.0	226
14	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.	1.9	207
15	Prediction and Validation of Disease Genes Using HeteSim Scores. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 687-695.	1.9	199
16	Prediction of human protein subcellular localization using deep learning. <i>Journal of Parallel and Distributed Computing</i> , 2018, 117, 212-217.	2.7	184
17	Deep-Resp-Forest: A deep forest model to predict anti-cancer drug response. <i>Methods</i> , 2019, 166, 91-102.	1.9	182
18	Transcatheter Aortic Valve Replacement in Low-Risk Patients With Symptomatic Severe Aortic Stenosis. <i>Journal of the American College of Cardiology</i> , 2018, 72, 2095-2105.	1.2	175

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19	Similarity computation strategies in the microRNA-disease network: a survey. <i>Briefings in Functional Genomics</i> , 2016, 15, e1v024.	1.3	172
20	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.	1.8	168
21	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.	1.9	163
22	Survey of MapReduce frame operation in bioinformatics. <i>Briefings in Bioinformatics</i> , 2014, 15, 637-647.	3.2	160
23	webTWAS: a resource for disease candidate susceptibility genes identified by transcriptome-wide association study. <i>Nucleic Acids Research</i> , 2022, 50, D1123-D1130.	6.5	160
24	nDNA-prot: identification of DNA-binding proteins based on unbalanced classification. <i>BMC Bioinformatics</i> , 2014, 15, 298.	1.2	158
25	Exploring sequence-based features for the improved prediction of DNA N4-methylcytosine sites in multiple species. <i>Bioinformatics</i> , 2019, 35, 1326-1333.	1.8	156
26	Finding the Best Classification Threshold in Imbalanced Classification. <i>Big Data Research</i> , 2016, 5, 2-8.	2.6	148
27	4mCPred: machine learning methods for DNA N4-methylcytosine sites prediction. <i>Bioinformatics</i> , 2019, 35, 593-601.	1.8	146
28	Hierarchical Classification of Protein Folds Using a Novel Ensemble Classifier. <i>PLoS ONE</i> , 2013, 8, e56499.	1.1	144
29	Pretata: predicting TATA binding proteins with novel features and dimensionality reduction strategy. <i>BMC Systems Biology</i> , 2016, 10, 114.	3.0	143
30	Prediction of MicroRNA-Disease Associations Based on Social Network Analysis Methods. <i>BioMed Research International</i> , 2015, 2015, 1-9.	0.9	140
31	Cancer Diagnosis Through IsomiR Expression with Machine Learning Method. <i>Current Bioinformatics</i> , 2018, 13, 57-63.	0.7	138
32	HAlign: Fast multiple similar DNA/RNA sequence alignment based on the centre star strategy. <i>Bioinformatics</i> , 2015, 31, 2475-2481.	1.8	136
33	TiSGeD: a database for tissue-specific genes. <i>Bioinformatics</i> , 2010, 26, 1273-1275.	1.8	132
34	Integration of deep feature representations and handcrafted features to improve the prediction of N6-methyladenosine sites. <i>Neurocomputing</i> , 2019, 324, 3-9.	3.5	130
35	Application of Machine Learning in Microbiology. <i>Frontiers in Microbiology</i> , 2019, 10, 827.	1.5	130
36	O-GlcNAcPRED-II: an integrated classification algorithm for identifying O-GlcNAcylation sites based on fuzzy undersampling and a $k$ -means PCA oversampling technique. <i>Bioinformatics</i> , 2018, 34, 2029-2036.	1.8	128

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37	Meta-Path Methods for Prioritizing Candidate Disease miRNAs. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 283-291.	1.9	126
38	Clustering and classification methods for single-cell RNA-sequencing data. Briefings in Bioinformatics, 2020, 21, 1196-1208.	3.2	125
39	Detecting N6-methyladenosine sites from RNA transcriptomes using ensemble Support Vector Machines. Scientific Reports, 2017, 7, 40242.	1.6	123
40	Empirical comparison and analysis of web-based cell-penetrating peptide prediction tools. Briefings in Bioinformatics, 2020, 21, 408-420.	3.2	122
41	Deep learning in omics: a survey and guideline. Briefings in Functional Genomics, 2019, 18, 41-57.	1.3	119
42	PEPred-Suite: improved and robust prediction of therapeutic peptides using adaptive feature representation learning. Bioinformatics, 2019, 35, 4272-4280.	1.8	116
43	HPSLPred: An Ensemble Multi-label Classifier for Human Protein Subcellular Location Prediction with Imbalanced Source. Proteomics, 2017, 17, 1700262.	1.3	114
44	Iterative feature representations improve N4-methylcytosine site prediction. Bioinformatics, 2019, 35, 4930-4937.	1.8	113
45	PhosPred-RF: A Novel Sequence-Based Predictor for Phosphorylation Sites Using Sequential Information Only. IEEE Transactions on Nanobioscience, 2017, 16, 240-247.	2.2	112
46	Protein Folds Prediction with Hierarchical Structured SVM. Current Proteomics, 2016, 13, 79-85.	0.1	112
47	StackCPPred: a stacking and pairwise energy content-based prediction of cell-penetrating peptides and their uptake efficiency. Bioinformatics, 2020, 36, 3028-3034.	1.8	111
48	Protein Function Prediction: From Traditional Classifier to Deep Learning. Proteomics, 2019, 19, e1900119.	1.3	110
49	PaGenBase: A Pattern Gene Database for the Global and Dynamic Understanding of Gene Function. PLoS ONE, 2013, 8, e80747.	1.1	108
50	MRMD2.0: A Python Tool for Machine Learning with Feature Ranking and Reduction. Current Bioinformatics, 2021, 15, 1213-1221.	0.7	107
51	Sequence clustering in bioinformatics: an empirical study. Briefings in Bioinformatics, 2018, , .	3.2	104
52	Protein Remote Homology Detection by Combining Chou's Pseudo Amino Acid Composition and Profile-Based Protein Representation. Molecular Informatics, 2013, 32, 775-782.	1.4	103
53	miRClassify: An advanced web server for miRNA family classification and annotation. Computers in Biology and Medicine, 2014, 45, 157-160.	3.9	101
54	A Random Forest Sub-Golgi Protein Classifier Optimized via Dipeptide and Amino Acid Composition Features. Frontiers in Bioengineering and Biotechnology, 2019, 7, 215.	2.0	100

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55	Predicting disease-associated circular RNAs using deep forests combined with positive-unlabeled learning methods. <i>Briefings in Bioinformatics</i> , 2020, 21, 1425-1436.	3.2	96
56	Regulatory long non-coding RNA and its functions. <i>Journal of Physiology and Biochemistry</i> , 2012, 68, 611-618.	1.3	93
57	An overview of SNP interactions in genome-wide association studies. <i>Briefings in Functional Genomics</i> , 2015, 14, 143-155.	1.3	91
58	sgRNACNN: identifying sgRNA on-target activity in four crops using ensembles of convolutional neural networks. <i>Plant Molecular Biology</i> , 2021, 105, 483-495.	2.0	89
59	Enhanced Protein Fold Prediction Method Through a Novel Feature Extraction Technique. <i>IEEE Transactions on Nanobioscience</i> , 2015, 14, 649-659.	2.2	87
60	Incorporating Distance-Based Top-n-gram and Random Forest To Identify Electron Transport Proteins. <i>Journal of Proteome Research</i> , 2019, 18, 2931-2939.	1.8	87
61	SkipCPP-Pred: an improved and promising sequence-based predictor for predicting cell-penetrating peptides. <i>BMC Genomics</i> , 2017, 18, 742.	1.2	85
62	An Improved Protein Structural Classes Prediction Method by Incorporating Both Sequence and Structure Information. <i>IEEE Transactions on Nanobioscience</i> , 2015, 14, 339-349.	2.2	80
63	Identification of DNA-binding proteins by incorporating evolutionary information into pseudo amino acid composition via the top-n-gram approach. <i>Journal of Biomolecular Structure and Dynamics</i> , 2015, 33, 1720-1730.	2.0	80
64	A Review of DNA-binding Proteins Prediction Methods. <i>Current Bioinformatics</i> , 2019, 14, 246-254.	0.7	79
65	An Approach for Identifying Cytokines Based on a Novel Ensemble Classifier. <i>BioMed Research International</i> , 2013, 2013, 1-11.	0.9	76
66	Anticancer peptides prediction with deep representation learning features. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	76
67	Recent Progress in Machine Learning-Based Methods for Protein Fold Recognition. <i>International Journal of Molecular Sciences</i> , 2016, 17, 2118.	1.8	73
68	Probability-based collaborative filtering model for predicting gene-disease associations. <i>BMC Medical Genomics</i> , 2017, 10, 76.	0.7	73
69	Single-cell RNA analysis reveals the potential risk of organ-specific cell types vulnerable to SARS-CoV-2 infections. <i>Computers in Biology and Medicine</i> , 2022, 140, 105092.	3.9	73
70	70ProPred: a predictor for discovering sigma70 promoters based on combining multiple features. <i>BMC Systems Biology</i> , 2018, 12, 44.	3.0	72
71	RF-PseU: A Random Forest Predictor for RNA Pseudouridine Sites. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 134.	2.0	72
72	Prediction of Potential Disease-Associated MicroRNAs by Using Neural Networks. <i>Molecular Therapy - Nucleic Acids</i> , 2019, 16, 566-575.	2.3	70

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73	Computational methods for identifying the critical nodes in biological networks. <i>Briefings in Bioinformatics</i> , 2020, 21, 486-497.	3.2	69
74	DeepAVP: A Dual-Channel Deep Neural Network for Identifying Variable-Length Antiviral Peptides. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2020, 24, 3012-3019.	3.9	69
75	An <i>in silico</i> approach to identification, categorization and prediction of nucleic acid binding proteins. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	69
76	Improving tRNAscan-ES Annotation Results via Ensemble Classifiers. <i>Molecular Informatics</i> , 2015, 34, 761-770.	1.4	66
77	PPTPP: a novel therapeutic peptide prediction method using physicochemical property encoding and adaptive feature representation learning. <i>Bioinformatics</i> , 2020, 36, 3982-3987.	1.8	66
78	Asynchronous spiking neural P systems with rules on synapses. <i>Neurocomputing</i> , 2015, 151, 1439-1445.	3.5	65
79	TAVR in Low-Risk Patients. <i>JACC: Cardiovascular Interventions</i> , 2019, 12, 901-907.	1.1	65
80	BP4RNAseq: a babysitter package for retrospective and newly generated RNA-seq data analyses using both alignment-based and alignment-free quantification method. <i>Bioinformatics</i> , 2021, 37, 1319-1321.	1.8	64
81	Prediction of bio-sequence modifications and the associations with diseases. <i>Briefings in Functional Genomics</i> , 2021, 20, 1-18.	1.3	64
82	Sequencing and de novo Analysis of <i>Crassostrea angulata</i> (Fujian Oyster) from 8 Different Developing Phases Using 454 GSFlx. <i>PLoS ONE</i> , 2012, 7, e43653.	1.1	63
83	AOPs-SVM: A Sequence-Based Classifier of Antioxidant Proteins Using a Support Vector Machine. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 224.	2.0	63
84	Molecular design in drug discovery: a comprehensive review of deep generative models. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	61
85	Comparative analysis and prediction of quorum-sensing peptides using feature representation learning and machine learning algorithms. <i>Briefings in Bioinformatics</i> , 2018, , .	3.2	60
86	BinMemPredict: a Web Server and Software for Predicting Membrane Protein Types. <i>Current Proteomics</i> , 2013, 10, 2-9.	0.1	59
87	DeepM6ASeq-EL: prediction of human N6-methyladenosine (m6A) sites with LSTM and ensemble learning. <i>Frontiers of Computer Science</i> , 2022, 16, 1.	1.6	58
88	BIOPHYSICAL AND PHENOMENOLOGICAL MODELS OF MULTIPLE SPIKE INTERACTIONS IN SPIKE-TIMING DEPENDENT PLASTICITY. <i>International Journal of Neural Systems</i> , 2006, 16, 79-97.	3.2	56
89	Bioinformatics applications on Apache Spark. <i>GigaScience</i> , 2018, 7, .	3.3	55
90	Using distances between Top-n-gram and residue pairs for protein remote homology detection. <i>BMC Bioinformatics</i> , 2014, 15, S3.	1.2	54

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91	A comprehensive overview and critical evaluation of gene regulatory network inference technologies. Briefings in Bioinformatics, 2021, 22, .	3.2	54
92	The discovery approaches and detection methods of microRNAs. Molecular Biology Reports, 2011, 38, 4125-4135.	1.0	53
93	A Global Characterization and Identification of Multifunctional Enzymes. PLoS ONE, 2012, 7, e38979.	1.1	53
94	HITS-PR-HHblits: protein remote homology detection by combining PageRank and Hyperlink-Induced Topic Search. Briefings in Bioinformatics, 2018, , .	3.2	53
95	ITP-Pred: an interpretable method for predicting, therapeutic peptides with fused features low-dimension representation. Briefings in Bioinformatics, 2021, 22, .	3.2	53
96	An Empirical Study of Features Fusion Techniques for Protein-Protein Interaction Prediction. Current Bioinformatics, 2016, 11, 4-12.	0.7	52
97	A study of miRNAs targets prediction and experimental validation. Protein and Cell, 2010, 1, 979-986.	4.8	51
98	Briefing in family characteristics of microRNAs and their applications in cancer research. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 191-197.	1.1	51
99	Identification of sub-Golgi protein localization by use of deep representation learning features. Bioinformatics, 2021, 36, 5600-5609.	1.8	50
100	Exploratory Predicting Protein Folding Model with Random Forest and Hybrid Features. Current Proteomics, 2015, 11, 289-299.	0.1	50
101	A novel collaborative filtering model for LncRNA-disease association prediction based on the Naïve Bayesian classifier. BMC Bioinformatics, 2019, 20, 396.	1.2	49
102	ELM-MHC: An Improved MHC Identification Method with Extreme Learning Machine Algorithm. Journal of Proteome Research, 2019, 18, 1392-1401.	1.8	49
103	PaGeFinder: quantitative identification of spatiotemporal pattern genes. Bioinformatics, 2012, 28, 1544-1545.	1.8	48
104	Computational identification and characteristics of novel microRNAs from the silkworm (Bombyx Tj ETQq0 0 0 rgBT /Overlock_10 Tf 50	1.0	47
105	Approaches for Recognizing Disease Genes Based on Network. BioMed Research International, 2014, 2014, 1-10.	0.9	46
106	DeepATT: a hybrid category attention neural network for identifying functional effects of DNA sequences. Briefings in Bioinformatics, 2021, 22, .	3.2	46
107	Identifying Multi-Functional Enzyme by Hierarchical Multi-Label Classifier. Journal of Computational and Theoretical Nanoscience, 2013, 10, 1038-1043.	0.4	45
108	Critical evaluation of web-based prediction tools for human protein subcellular localization. Briefings in Bioinformatics, 2020, 21, 1628-1640.	3.2	45

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109	A Convolutional Neural Network Using Dinucleotide One-hot Encoder for identifying DNA N6-Methyladenine Sites in the Rice Genome. <i>Neurocomputing</i> , 2021, 422, 214-221.	3.5	45
110	Prediction of drug-target interactions based on multi-layer network representation learning. <i>Neurocomputing</i> , 2021, 434, 80-89.	3.5	45
111	miR-isomiRExp: a web-server for the analysis of expression of miRNA at the miRNA/isomiR levels. <i>Scientific Reports</i> , 2016, 6, 23700.	1.6	44
112	Machine learning and its applications in plant molecular studies. <i>Briefings in Functional Genomics</i> , 2020, 19, 40-48.	1.3	44
113	SecProMTB: Support Vector Machine-Based Classifier for Secretory Proteins Using Imbalanced Data Sets Applied to <i>Mycobacterium tuberculosis</i> . <i>Proteomics</i> , 2019, 19, 1900007.	1.3	43
114	Analysis of gene expression profiles of lung cancer subtypes with machine learning algorithms. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2020, 1866, 165822.	1.8	43
115	A novel machine learning method for cytokine-receptor interaction prediction. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2016, 19, 144-152.	0.6	43
116	Classification of Small GTPases with Hybrid Protein Features and Advanced Machine Learning Techniques. <i>Current Bioinformatics</i> , 2018, 13, 492-500.	0.7	43
117	Computational Approaches in Detecting Non-Coding RNA. <i>Current Genomics</i> , 2013, 14, 371-377.	0.7	41
118	Representation of fluctuation features in pathological knee joint vibroarthrographic signals using kernel density modeling method. <i>Medical Engineering and Physics</i> , 2014, 36, 1305-1311.	0.8	40
119	Research progress in protein posttranslational modification site prediction. <i>Briefings in Functional Genomics</i> , 2019, 18, 220-229.	1.3	39
120	imDC: an ensemble learning method for imbalanced classification with miRNA data. <i>Genetics and Molecular Research</i> , 2015, 14, 123-133.	0.3	39
121	Prediction of G Protein-Coupled Receptors with SVM-Prot Features and Random Forest. <i>Scientifica</i> , 2016, 2016, 1-10.	0.6	38
122	Exploiting Discriminative Regions of Brain Slices Based on 2D CNNs for Alzheimer's Disease Classification. <i>IEEE Access</i> , 2019, 7, 181423-181433.	2.6	38
123	Identification of drug-target interactions via multiple kernel-based triple collaborative matrix factorization. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	38
124	Specifying architecture of knowledge graph with data graph, information graph, knowledge graph and wisdom graph. , 2017, , .		37
125	CirRNAPL: A web server for the identification of circRNA based on extreme learning machine. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 834-842.	1.9	37
126	Which statistical significance test best detects oncomiRNAs in cancer tissues? An exploratory analysis. <i>Oncotarget</i> , 2016, 7, 85613-85623.	0.8	37



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127	NmRF: identification of multispecies RNA 2â€™-O-methylation modification sites from RNA sequences. Briefings in Bioinformatics, 2022, 23, .	3.2	37
128	NucPosPred: Predicting species-specific genomic nucleosome positioning via four different modes of general PseKNC. Journal of Theoretical Biology, 2018, 450, 15-21.	0.8	35
129	6mA-RicePred: A Method for Identifying DNA N6-Methyladenine Sites in the Rice Genome Based on Feature Fusion. Frontiers in Plant Science, 2020, 11, 4.	1.7	34
130	Sequence representation approaches for sequence-based protein prediction tasks that use deep learning. Briefings in Functional Genomics, 2021, 20, 61-73.	1.3	34
131	A Comprehensive Analysis of miRNA/isomiR Expression with Gender Difference. PLoS ONE, 2016, 11, e0154955.	1.1	34
132	GMNN2CD: identification of circRNAâ€™disease associations based on variational inference and graph Markov neural networks. Bioinformatics, 2022, 38, 2246-2253.	1.8	34
133	Biological functions of MicroRNAs. Russian Journal of Bioorganic Chemistry, 2010, 36, 684-689.	0.3	33
134	BP Neural Network Could Help Improve Pre-miRNA Identification in Various Species. BioMed Research International, 2016, 2016, 1-11.	0.9	33
135	Critical downstream analysis steps for single-cell RNA sequencing data. Briefings in Bioinformatics, 2021, 22, .	3.2	33
136	Virtual neurorobotics (VNR) to accelerate development of plausible neuromorphic brain architectures. Frontiers in Neurorobotics, 2007, 1, 1.	1.6	32
137	enDNA-Prot: Identification of DNA-Binding Proteins by Applying Ensemble Learning. BioMed Research International, 2014, 2014, 1-10.	0.9	32
138	RFhy-m2G: Identification of RNA N2-methylguanosine modification sites based on random forest and hybrid features. Methods, 2022, 203, 32-39.	1.9	32
139	Review of Protein Subcellular Localization Prediction. Current Bioinformatics, 2014, 9, 331-342.	0.7	32
140	Network-based method for mining novel HPV infection related genes using random walk with restart algorithm. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2018, 1864, 2376-2383.	1.8	31
141	Selecting Essential MicroRNAs Using a Novel Voting Method. Molecular Therapy - Nucleic Acids, 2019, 18, 16-23.	2.3	31
142	Goals and approaches for each processing step for single-cell RNA sequencing data. Briefings in Bioinformatics, 2021, 22, .	3.2	31
143	HAlign-II: efficient ultra-large multiple sequence alignment and phylogenetic tree reconstruction with distributed and parallel computing. Algorithms for Molecular Biology, 2017, 12, 25.	0.3	30
144	Supervised Brain Tumor Segmentation Based on Gradient and Context-Sensitive Features. Frontiers in Neuroscience, 2019, 13, 144.	1.4	29

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145	Exploration of the correlation between GPCRs and drugs based on a learning to rank algorithm. <i>Computers in Biology and Medicine</i> , 2020, 119, 103660.	3.9	29
146	NerLTR-DTA: drug-target binding affinity prediction based on neighbor relationship and learning to rank. <i>Bioinformatics</i> , 2022, 38, 1964-1971.	1.8	29
147	CRBPD: Identification of circRNA-RBP interaction sites using an ensemble neural network approach. <i>PLoS Computational Biology</i> , 2022, 18, e1009798.	1.5	29
148	Identifying cell types to interpret scRNA-seq data: how, why and more possibilities. <i>Briefings in Functional Genomics</i> , 2020, 19, 286-291.	1.3	28
149	iTTCA-RF: a random forest predictor for tumor T cell antigens. <i>Journal of Translational Medicine</i> , 2021, 19, 449.	1.8	28
150	Identification of cytokine via an improved genetic algorithm. <i>Frontiers of Computer Science</i> , 2015, 9, 643-651.	1.6	26
151	Machine learning and graph analytics in computational biomedicine. <i>Artificial Intelligence in Medicine</i> , 2017, 83, 1.	3.8	26
152	EP3: an ensemble predictor that accurately identifies type III secreted effectors. <i>Briefings in Bioinformatics</i> , 2021, 22, 1918-1928.	3.2	26
153	A comprehensive review of the imbalance classification of protein post-translational modifications. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	26
154	CMSA: a heterogeneous CPU/GPU computing system for multiple similar RNA/DNA sequence alignment. <i>BMC Bioinformatics</i> , 2017, 18, 315.	1.2	25
155	A spectral clustering with self-weighted multiple kernel learning method for single-cell RNA-seq data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	25
156	Review and comparative analysis of machine learning-based phage virion protein identification methods. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2020, 1868, 140406.	1.1	25
157	Kinetic models of spike-timing dependent plasticity and their functional consequences in detecting correlations. <i>Biological Cybernetics</i> , 2007, 97, 81-97.	0.6	24
158	Ecological and network analyses identify four microbial species with potential significance for the diagnosis/treatment of ulcerative colitis (UC). <i>BMC Microbiology</i> , 2021, 21, 138.	1.3	24
159	High-resolution transcription factor binding sites prediction improved performance and interpretability by deep learning method. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	24
160	A Discussion of MicroRNAs in Cancers. <i>Current Bioinformatics</i> , 2014, 9, 453-462.	0.7	24
161	Predicting protein-peptide binding residues via interpretable deep learning. <i>Bioinformatics</i> , 2022, 38, 3351-3360.	1.8	24
162	Accurate Identification of Cancerlectins through Hybrid Machine Learning Technology. <i>International Journal of Genomics</i> , 2016, 2016, 1-11.	0.8	23

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163	Processing Optimization of Typed Resources with Synchronized Storage and Computation Adaptation in Fog Computing. <i>Wireless Communications and Mobile Computing</i> , 2018, 2018, 1-13.	0.8	23
164	Taxonomy dimension reduction for colorectal cancer prediction. <i>Computational Biology and Chemistry</i> , 2019, 83, 107160.	1.1	23
165	TS-m6A-DL: Tissue-specific identification of N6-methyladenosine sites using a universal deep learning model. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 4619-4625.	1.9	23
166	Exploring Drug Treatment Patterns Based on the Action of Drug and Multilayer Network Model. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5014.	1.8	22
167	Predicting RNA secondary structure based on the class information and Hopfield network. <i>Computers in Biology and Medicine</i> , 2009, 39, 206-214.	3.9	21
168	Improved method for predicting protein fold patterns with ensemble classifiers. <i>Genetics and Molecular Research</i> , 2012, 11, 174-181.	0.3	21
169	Identifying DNA N4-methylcytosine sites in the rosaceae genome with a deep learning model relying on distributed feature representation. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 1612-1619.	1.9	21
170	Computational Analysis of miRNA Target Identification. <i>Current Bioinformatics</i> , 2012, 7, 512-525.	0.7	20
171	A network-based method for the identification of putative genes related to infertility. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2016, 1860, 2716-2724.	1.1	20
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