

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	Significance-Based Essential Protein Discovery. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 633-642.	1.9	8
2	SgRNA-RF: Identification of SgRNA On-Target Activity With Imbalanced Datasets. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 2442-2453.	1.9	5
3	CRCF: A Method of Identifying Secretory Proteins of Malaria Parasites. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 2149-2157.	1.9	1
4	RFhy-m2G: Identification of RNA N2-methylguanosine modification sites based on random forest and hybrid features. Methods, 2022, 203, 32-39.	1.9	32
5	A comparison of deep learning-based pre-processing and clustering approaches for single-cell RNA sequencing data. Briefings in Bioinformatics, 2022, 23, .	3.2	14
6	prPredâ€DRLF: Plant R protein predictor using deep representation learning features. Proteomics, 2022, 22, e2100161.	1.3	11
7	DeepM6ASeq-EL: prediction of human N6-methyladenosine (m6A) sites with LSTM and ensemble learning. Frontiers of Computer Science, 2022, 16, 1.	1.6	58
8	Characterizing viral circRNAs and their application in identifying circRNAs in viruses. Briefings in Bioinformatics, 2022, 23, .	3.2	18
9	webTWAS: a resource for disease candidate susceptibility genes identified by transcriptome-wide association study. Nucleic Acids Research, 2022, 50, D1123-D1130.	6.5	160
10	DeepCap-Kcr: accurate identification and investigation of protein lysine crotonylation sites based on capsule network. Briefings in Bioinformatics, 2022, 23, .	3.2	13
11	NmRF: identification of multispecies RNA 2â€™-O-methylation modification sites from RNA sequences. Briefings in Bioinformatics, 2022, 23, .	3.2	37
12	FTWSVM-SR: DNA-Binding Proteins Identification via Fuzzy Twin Support Vector Machines on Self-Representation. Interdisciplinary Sciences, Computational Life Sciences, 2022, 14, 372-384.	2.2	7
13	A novel fast multiple nucleotide sequence alignment method based on FM-index. Briefings in Bioinformatics, 2022, 23, .	3.2	5
14	Distant metastasis identification based on optimized graph representation of gene interaction patterns. Briefings in Bioinformatics, 2022, 23, .	3.2	6
15	Single-cell RNA analysis reveals the potential risk of organ-specific cell types vulnerable to SARS-CoV-2 infections. Computers in Biology and Medicine, 2022, 140, 105092.	3.9	73
16	Critical assessment of computational tools for prokaryotic and eukaryotic promoter prediction. Briefings in Bioinformatics, 2022, 23, .	3.2	11
17	Comparative genome analysis of plant ascomycete fungal pathogens with different lifestyles reveals distinctive virulence strategies. BMC Genomics, 2022, 23, 34.	1.2	13
18	Identification of drugâ€™target interactions via multiple kernel-based triple collaborative matrix factorization. Briefings in Bioinformatics, 2022, 23, .	3.2	38

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19	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
20	A hybrid deep learning framework for gene regulatory network inference from single-cell transcriptomic data. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	20
21	String kernels construction and fusion: a survey with bioinformatics application. <i>Frontiers of Computer Science</i> , 2022, 16, 1.	1.6	11
22	CRBPDL: Identification of circRNA-RBP interaction sites using an ensemble neural network approach. <i>PLoS Computational Biology</i> , 2022, 18, e1009798.	1.5	29
23	The Characterization of Structure and Prediction for Aquaporin in Tumour Progression by Machine Learning. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 845622.	1.8	1
24	GMNN2CD: identification of circRNA disease associations based on variational inference and graph Markov neural networks. <i>Bioinformatics</i> , 2022, 38, 2246-2253.	1.8	34
25	A road map for happiness: The psychological factors related cell types in various parts of human body from single cell RNA-seq data analysis. <i>Computers in Biology and Medicine</i> , 2022, 143, 105286.	3.9	3
26	Protein DNA/RNA interactions: Machine intelligence tools and approaches in the era of artificial intelligence and big data. <i>Proteomics</i> , 2022, 22, e2100197.	1.3	20
27	MDICC: novel method for multi-omics data integration and cancer subtype identification. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	15
28	MDADP: A Webserver Integrating Database and Prediction Tools for Microbe-Disease Associations. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2022, 26, 3427-3434.	3.9	5
29	Structured Sparse Regularized TSK Fuzzy System for predicting therapeutic peptides. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	4
30	Identifying and Classifying Enhancers by Dinucleotide-Based Auto-Cross Covariance and Attention-Based Bi-LSTM. <i>Computational and Mathematical Methods in Medicine</i> , 2022, 2022, 1-11.	0.7	2
31	scIMC: a platform for benchmarking comparison and visualization analysis of scRNA-seq data imputation methods. <i>Nucleic Acids Research</i> , 2022, 50, 4877-4899.	6.5	12
32	DeepMC-iNABP: Deep learning for multiclass identification and classification of nucleic acid-binding proteins. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 2020-2028.	1.9	14
33	Identification and classification of promoters using the attention mechanism based on long short-term memory. <i>Frontiers of Computer Science</i> , 2022, 16, .	1.6	6
34	AMPpred-EL: An effective antimicrobial peptide prediction model based on ensemble learning. <i>Computers in Biology and Medicine</i> , 2022, 146, 105577.	3.9	12
35	Machine Learning and Its Applications for Protozoal Pathogens and Protozoal Infectious Diseases. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 882995.	1.8	6
36	iLncDA-LTR: Identification of lncRNA-disease associations by learning to rank. <i>Computers in Biology and Medicine</i> , 2022, 146, 105605.	3.9	8

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37	Predicting proteinâ€“peptide binding residues via interpretable deep learning. <i>Bioinformatics</i> , 2022, 38, 3351-3360.	1.8	24
38	Prediction of Cell-Penetrating Peptides Using a Novel HSIC-Based Multiview TSK Fuzzy System. <i>Applied Sciences (Switzerland)</i> , 2022, 12, 5383.	1.3	2
39	webSCST: an interactive web application for single-cell RNA-sequencing data and spatial transcriptomic data integration. <i>Bioinformatics</i> , 2022, 38, 3488-3489.	1.8	16
40	Effector-GAN: prediction of fungal effector proteins based on pretrained deep representation learning methods and generative adversarial networks. <i>Bioinformatics</i> , 2022, 38, 3541-3548.	1.8	6
41	MLapSVM-LBS: Predicting DNA-binding proteins via a multiple Laplacian regularized support vector machine with local behavior similarity. <i>Knowledge-Based Systems</i> , 2022, 250, 109174.	4.0	13
42	Identification of plant vacuole proteins by exploiting deep representation learning features. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 2921-2927.	1.9	4
43	iKcr_CNN: A novel computational tool for imbalance classification of human nonhistone crotonylation sites based on convolutional neural networks with focal loss. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 3268-3279.	1.9	5
44	Protein-DNA Binding Residues Prediction Using a Deep Learning Model with Hierarchical Feature Extraction. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, , 1-10.	1.9	3
45	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
46	Minirmd: accurate and fast duplicate removal tool for short reads via multiple minimizers. <i>Bioinformatics</i> , 2021, 37, 1604-1606.	1.8	14
47	Revisiting genome-wide association studies from statistical modelling to machine learning. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	20
48	VPTMdb: a viral posttranslational modification database. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	9
49	Goals and approaches for each processing step for single-cell RNA sequencing data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	31
50	ITP-Pred: an interpretable method for predicting, therapeutic peptides with fused features low-dimension representation. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	53
51	Using a low correlation high orthogonality feature set and machine learning methods to identify plant pentatricopeptide repeat coding gene/protein. <i>Neurocomputing</i> , 2021, 424, 246-254.	3.5	3
52	EP3: an ensemble predictor that accurately identifies type III secreted effectors. <i>Briefings in Bioinformatics</i> , 2021, 22, 1918-1928.	3.2	26
53	iPro2L-PSTKNC: A Two-Layer Predictor for Discovering Various Types of Promoters by Position Specific of Nucleotide Composition. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2021, 25, 2329-2337.	3.9	6
54	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

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55	DeepATT: a hybrid category attention neural network for identifying functional effects of DNA sequences. Briefings in Bioinformatics, 2021, 22, .	3.2	46
56	BP4RNAseq: a babysitter package for retrospective and newly generated RNA-seq data analyses using both alignment-based and alignment-free quantification method. Bioinformatics, 2021, 37, 1319-1321.	1.8	64
57	A Convolutional Neural Network Using Dinucleotide One-hot Encoder for identifying DNA N6-Methyladenine Sites in the Rice Genome. Neurocomputing, 2021, 422, 214-221.	3.5	45
58	Prediction of bio-sequence modifications and the associations with diseases. Briefings in Functional Genomics, 2021, 20, 1-18.	1.3	64
59	Prediction of diabetic protein markers based on an ensemble method. Frontiers in Bioscience, 2021, 26, 207.	0.8	6
60	sgRNACNN: identifying sgRNA on-target activity in four crops using ensembles of convolutional neural networks. Plant Molecular Biology, 2021, 105, 483-495.	2.0	89
61	Sequence representation approaches for sequence-based protein prediction tasks that use deep learning. Briefings in Functional Genomics, 2021, 20, 61-73.	1.3	34
62	Decision Tree for Sequences. IEEE Transactions on Knowledge and Data Engineering, 2021, , 1-1.	4.0	7
63	Application of learning to rank in bioinformatics tasks. Briefings in Bioinformatics, 2021, 22, .	3.2	9
64	GutBalance: a server for the human gut microbiome-based disease prediction and biomarker discovery with compositionality addressed. Briefings in Bioinformatics, 2021, 22, .	3.2	12
65	IEEE Access Special Section Editorial: Feature Representation and Learning Methods With Applications in Large-Scale Biological Sequence Analysis. IEEE Access, 2021, 9, 33110-33119.	2.6	1
66	Instance-Based Classification Through Hypothesis Testing. IEEE Access, 2021, 9, 17485-17494.	2.6	1
67	A comprehensive overview and critical evaluation of gene regulatory network inference technologies. Briefings in Bioinformatics, 2021, 22, .	3.2	54
68	Anticancer peptides prediction with deep representation learning features. Briefings in Bioinformatics, 2021, 22, .	3.2	76
69	MRMD2.0: A Python Tool for Machine Learning with Feature Ranking and Reduction. Current Bioinformatics, 2021, 15, 1213-1221.	0.7	107
70	HSM6AP: a high-precision predictor for the Homo sapiens N6-methyladenosine (m ⁶ A) based on multiple weights and feature stitching. RNA Biology, 2021, 18, 1882-1892.	1.5	19
71	Prediction of RNA-binding protein and alternative splicing event associations during epithelial-mesenchymal transition based on inductive matrix completion. Briefings in Bioinformatics, 2021, 22, .	3.2	10
72	Machine learning for phytopathology: from the molecular scale towards the network scale. Briefings in Bioinformatics, 2021, 22, .	3.2	6

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73	Single-cell RNA Sequencing Analysis Identifies Key Genes in Brain Metastasis from Lung Adenocarcinoma. <i>Current Gene Therapy</i> , 2021, 21, 338-348.	0.9	16
74	CarSite-II: an integrated classification algorithm for identifying carbonylated sites based on K-means similarity-based undersampling and synthetic minority oversampling techniques. <i>BMC Bioinformatics</i> , 2021, 22, 216.	1.2	4
75	A comprehensive review of the imbalance classification of protein post-translational modifications. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	26
76	DisBalance: a platform to automatically build balance-based disease prediction models and discover microbial biomarkers from microbiome data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	10
77	Prediction of drug-target interactions based on multi-layer network representation learning. <i>Neurocomputing</i> , 2021, 434, 80-89.	3.5	45
78	Critical downstream analysis steps for single-cell RNA sequencing data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	33
79	Computational biology and chemistry Special section editorial: Computational analyses for miRNA. <i>Computational Biology and Chemistry</i> , 2021, 91, 107448.	1.1	3
80	Progress in the Development of Antimicrobial Peptide Prediction Tools. <i>Current Protein and Peptide Science</i> , 2021, 22, 211-216.	0.7	2
81	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
82	ORSa€Pred: An optimized reduced schemeâ€b-based identifier for antioxidant proteins. <i>Proteomics</i> , 2021, 21, e2100017.	1.3	4
83	MMFGRN: a multi-source multi-model fusion method for gene regulatory network reconstruction. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	10
84	The accurate prediction and characterization of cancerlectin by a combined machine learning and GO analysis. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	3
85	Current status and future prospects of drugâ€target interaction prediction. <i>Briefings in Functional Genomics</i> , 2021, 20, 312-322.	1.3	10
86	Briefings in functional genomics special section editorial: analysis of integrated multiple omics data. <i>Briefings in Functional Genomics</i> , 2021, 20, 196-197.	1.3	1
87	Accurate Prediction and Key Feature Recognition of Immunoglobulin. <i>Applied Sciences (Switzerland)</i> , 2021, 11, 6894.	1.3	5
88	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
89	DeepAc4C: a convolutional neural network model with hybrid features composed of physicochemical patterns and distributed representation information for identification of N4-acetylcytidine in mRNA. <i>Bioinformatics</i> , 2021, 38, 52-57.	1.8	20
90	Molecular design in drug discovery: a comprehensive review of deep generative models. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	61

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91	Matrix factorization-based data fusion for the prediction of RNA-binding proteins and alternative splicing event associations during epithelialâ€”mesenchymal transition. Briefings in Bioinformatics, 2021, 22, .	3.2	11
92	Clustering of genes from microarray data using hierarchical projective adaptive resonance theory: a case study of tuberculosis. Briefings in Functional Genomics, 2021, , .	1.3	0
93	rBPDLPredicting RNA-Binding Proteins Using Deep Learning. IEEE Journal of Biomedical and Health Informatics, 2021, 25, 3668-3676.	3.9	10
94	Identifying DNA N4-methylcytosine sites in the rosaceae genome with a deep learning model relying on distributed feature representation. Computational and Structural Biotechnology Journal, 2021, 19, 1612-1619.	1.9	21
95	Prediction of presynaptic and postsynaptic neurotoxins based on feature extraction. Mathematical Biosciences and Engineering, 2021, 18, 5943-5958.	1.0	2
96	Identify RNA-associated subcellular localizations based on multi-label learning using Chouâ€™s 5-steps rule. BMC Genomics, 2021, 22, 56.	1.2	17
97	TS-m6A-DL: Tissue-specific identification of N6-methyladenosine sites using a universal deep learning model. Computational and Structural Biotechnology Journal, 2021, 19, 4619-4625.	1.9	23
98	SubLocEP: a novel ensemble predictor of subcellular localization of eukaryotic mRNA based on machine learning. Briefings in Bioinformatics, 2021, 22, .	3.2	18
99	Identification of sub-Golgi protein localization by use of deep representation learning features. Bioinformatics, 2021, 36, 5600-5609.	1.8	50
100	Genome-Wide Analysis of LysM-Containing Gene Family in Wheat: Structural and Phylogenetic Analysis during Development and Defense. Genes, 2021, 12, 31.	1.0	13
101	Staem5: A novel computational approach for accurate prediction of m5C site. Molecular Therapy - Nucleic Acids, 2021, 26, 1027-1034.	2.3	20
102	iTTCA-RF: a random forest predictor for tumor T cell antigens. Journal of Translational Medicine, 2021, 19, 449.	1.8	28
103	DrugHybrid_BS: Using Hybrid Feature Combined With Bagging-SVM to Predict Potentially Druggable Proteins. Frontiers in Pharmacology, 2021, 12, 771808.	1.6	9
104	Laplacian Regularized Sparse Representation based Classifier for Identifying DNA N4-methylcytosine Sites via L2,1/2-matrix Norm. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	1.9	13
105	Genome-Wide Analysis of the MADS-Box Gene Family in Maize: Gene Structure, Evolution, and Relationships. Genes, 2021, 12, 1956.	1.0	14
106	Membrane Protein Identification via Multi-view Graph Regularized k-Local Hyperplane Distance Nearest Neighbor Model. , 2021, , .		2
107	Empirical comparison and analysis of web-based cell-penetrating peptide prediction tools. Briefings in Bioinformatics, 2020, 21, 408-420.	3.2	122
108	Computational methods for identifying the critical nodes in biological networks. Briefings in Bioinformatics, 2020, 21, 486-497.	3.2	69

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109	Transcription factorsâ€™DNA interactions in rice: identification and verification. <i>Briefings in Bioinformatics</i> , 2020, 21, 946-956.	3.2	19
110	Protein Complexes Identification with Family-Wise Error Rate Control. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 17, 2062-2073.	1.9	6
111	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
112	Investigating Maize Yield-Related Genes in Multiple Omics Interaction Network Data. <i>IEEE Transactions on Nanobioscience</i> , 2020, 19, 142-151.	2.2	3
113	Critical evaluation of web-based prediction tools for human protein subcellular localization. <i>Briefings in Bioinformatics</i> , 2020, 21, 1628-1640.	3.2	45
114	Machine learning and its applications in plant molecular studies. <i>Briefings in Functional Genomics</i> , 2020, 19, 40-48.	1.3	44
115	The application of machine learning to disease diagnosis and treatment. <i>Mathematical Biosciences</i> , 2020, 320, 108305.	0.9	18
116	Clustering and classification methods for single-cell RNA-sequencing data. <i>Briefings in Bioinformatics</i> , 2020, 21, 1196-1208.	3.2	125
117	Regulator Network Analysis of Rice and Maize Yield-Related Genes. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 621464.	1.8	2
118	Biocomputing and Synthetic Biology in Cells: Cells Special Issue. <i>Cells</i> , 2020, 9, 2459.	1.8	0
119	Impact of Transcatheter Aortic Valve Replacement on Risk Profiles of Surgical Aortic Valve Replacement Patients. <i>Cardiovascular Revascularization Medicine</i> , 2020, 21, 959-963.	0.3	3
120	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
121	Computational Prediction of Protein Arginine Methylation Based on Compositionâ€™Transitionâ€™Distribution Features. <i>ACS Omega</i> , 2020, 5, 27470-27479.	1.6	8
122	Reference-Based Sequence Classification. <i>IEEE Access</i> , 2020, 8, 218199-218214.	2.6	1
123	Analysis of Cyclin-Dependent Kinase 1 as an Independent Prognostic Factor for Gastric Cancer Based on Statistical Methods. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 620164.	1.8	9
124	Editorial: Computational Learning Models and Methods Driven by Omics for Precision Medicine. <i>Frontiers in Genetics</i> , 2020, 11, 620976.	1.1	0
125	Basic polar and hydrophobic properties are the main characteristics that affect the binding of transcription factors to methylation sites. <i>Bioinformatics</i> , 2020, 36, 4263-4268.	1.8	19
126	Network analysis of the hot spring microbiome sketches out possible niche differentiations among ecological guilds. <i>Ecological Modelling</i> , 2020, 431, 109147.	1.2	7

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127	CWLy-SVM: A support vector machine-based tool for identifying cell wall lytic enzymes. <i>Computational Biology and Chemistry</i> , 2020, 87, 107304.	1.1	18
128	RF-PseU: A Random Forest Predictor for RNA Pseudouridine Sites. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 134.	2.0	72
129	2 piRNAPred: a two-layered integrated algorithm for identifying piRNAs and their functions based on LFE-GM feature selection. <i>RNA Biology</i> , 2020, 17, 892-902.	1.5	18
130	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
131	Guest Editorial: Bio-Inspired Computing Models and Algorithms. <i>IEEE Transactions on Nanobioscience</i> , 2020, 19, 100-101.	2.2	1
132	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
133	mAML: an automated machine learning pipeline with a microbiome repository for human disease classification. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	20
134	StackCPPred: a stacking and pairwise energy content-based prediction of cell-penetrating peptides and their uptake efficiency. <i>Bioinformatics</i> , 2020, 36, 3028-3034.	1.8	111
135	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
136	6mA-RicePred: A Method for Identifying DNA N6-Methyladenine Sites in the Rice Genome Based on Feature Fusion. <i>Frontiers in Plant Science</i> , 2020, 11, 4.	1.7	34
137	Machine Learning Techniques for High-Throughput Structure and Function Analysis for Proteomics and Genomics. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2020, 22, 664-664.	0.6	1
138	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
139	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
140	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
141	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
142	NonClasGP-Pred: robust and efficient prediction of non-classically secreted proteins by integrating subset-specific optimal models of imbalanced data. <i>Microbial Genomics</i> , 2020, 6, .	1.0	5
143	Application and Development of Artificial Intelligence and Intelligent Disease Diagnosis. <i>Current Pharmaceutical Design</i> , 2020, 26, 3069-3075.	0.9	20
144	GRRFNet: Guided Regularized Random Forest-based Gene Regulatory Network Inference Using Data Integration. , 2020, , .		4

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145	4mCPred: machine learning methods for DNA N4-methylcytosine sites prediction. <i>Bioinformatics</i> , 2019, 35, 593-601.	1.8	146
146	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
147	Meta-Path Methods for Prioritizing Candidate Disease miRNAs. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 283-291.	1.9	126
148	Advanced Machine Learning Techniques for Bioinformatics. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1182-1183.	1.9	11
149	A novel collaborative filtering model for LncRNA-disease association prediction based on the Naïve Bayesian classifier. <i>BMC Bioinformatics</i> , 2019, 20, 396.	1.2	49
150	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
151	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
152	Molecular Computing and Bioinformatics. <i>Molecules</i> , 2019, 24, 2358.	1.7	13
153	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
154	Supervised Brain Tumor Segmentation Based on Gradient and Context-Sensitive Features. <i>Frontiers in Neuroscience</i> , 2019, 13, 144.	1.4	29
155	Selecting Essential MicroRNAs Using a Novel Voting Method. <i>Molecular Therapy - Nucleic Acids</i> , 2019, 18, 16-23.	2.3	31
156	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
157	A Random Forest Sub-Golgi Protein Classifier Optimized via Dipeptide and Amino Acid Composition Features. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 215.	2.0	100
158	ELM-MHC: An Improved MHC Identification Method with Extreme Learning Machine Algorithm. <i>Journal of Proteome Research</i> , 2019, 18, 1392-1401.	1.8	49
159	Research progress in protein posttranslational modification site prediction. <i>Briefings in Functional Genomics</i> , 2019, 18, 220-229.	1.3	39
160	Investigation and development of maize fused network analysis with multi-omics. <i>Plant Physiology and Biochemistry</i> , 2019, 141, 380-387.	2.8	14
161	Perspectives of Bioinformatics in Big Data Era. <i>Current Genomics</i> , 2019, 20, 79-80.	0.7	6
162	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

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163	Protein Function Prediction: From Traditional Classifier to Deep Learning. <i>Proteomics</i> , 2019, 19, e1900119.	1.3	110
164	TAVR in Low-Risk Patients. <i>JACC: Cardiovascular Interventions</i> , 2019, 12, 901-907.	1.1	65
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