

Quan Zou

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

314
papers

11,495
citations

60
h-index

97
g-index

360
ext. papers

14,675
ext. citations

5.6
avg, IF

7.49
L-index

#	Paper	IF	Citations
314	Comparative genome analysis of plant ascomycete fungal pathogens with different lifestyles reveals distinctive virulence strategies.. <i>BMC Genomics</i> , 2022 , 23, 34	4.5	1
313	Identification of drug-target interactions via multiple kernel-based triple collaborative matrix factorization.. <i>Briefings in Bioinformatics</i> , 2022 ,	13.4	5
312	String kernels construction and fusion: a survey with bioinformatics application. <i>Frontiers of Computer Science</i> , 2022 , 16, 1	2.2	3
311	CRBPDFL: Identification of circRNA-RBP interaction sites using an ensemble neural network approach.. <i>PLoS Computational Biology</i> , 2022 , 18, e1009798	5	1
310	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	5.7	
309	GMNN2CD: Identification of circRNA-disease associations based on variational inference and graph markov neural networks.. <i>Bioinformatics</i> , 2022 ,	7.2	4
308	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	7	1
307	Protein-DNA/RNA interactions: Machine intelligence tools and approaches in the era of artificial intelligence and big data.. <i>Proteomics</i> , 2022 , e2100197	4.8	1
306	Critical assessment of computational tools for prokaryotic and eukaryotic promoter prediction.. <i>Briefings in Bioinformatics</i> , 2022 ,	13.4	1
305	DeepM6ASeq-EL: prediction of human N6-methyladenosine (m6A) sites with LSTM and ensemble learning. <i>Frontiers of Computer Science</i> , 2022 , 16, 1	2.2	28
304	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, 7518779	2.8	1
303	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	6.8	2
302	AMPpred-EL: An effective antimicrobial peptide prediction model based on ensemble learning.. <i>Computers in Biology and Medicine</i> , 2022 , 146, 105577	7	0
301	Machine Learning and Its Applications for Protozoal Pathogens and Protozoal Infectious Diseases.. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022 , 12, 882995	5.9	1
300	iLncDA-LTR: Identification of lncRNA-disease associations by learning to rank. <i>Computers in Biology and Medicine</i> , 2022 , 105605	7	0
299	Prediction of Cell-Penetrating Peptides Using a Novel HSIC-Based Multiview TSK Fuzzy System. <i>Applied Sciences (Switzerland)</i> , 2022 , 12, 5383	2.6	
298	MLapSVM-LBS: Predicting DNA-binding proteins via a multiple Laplacian regularized support vector machine with local behavior similarity. <i>Knowledge-Based Systems</i> , 2022 , 109174	7.3	0

297	Goals and approaches for each processing step for single-cell RNA sequencing data. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	8
296	ITP-Pred: an interpretable method for predicting, therapeutic peptides with fused features low-dimension representation. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	25
295	FTWSVM-SR: DNA-Binding Proteins Identification via Fuzzy Twin Support Vector Machines on Self-Representation. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2021 , 1	3.5	3
294	A novel fast multiple nucleotide sequence alignment method based on FM-index. <i>Briefings in Bioinformatics</i> , 2021 ,	13.4	1
293	Distant metastasis identification based on optimized graph representation of gene interaction patterns. <i>Briefings in Bioinformatics</i> , 2021 ,	13.4	1
292	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> , 2021 , 140, 105092	7	32
291	DrugHybrid_BS: Using Hybrid Feature Combined With Bagging-SVM to Predict Potentially Druggable Proteins.. <i>Frontiers in Pharmacology</i> , 2021 , 12, 771808	5.6	0
290	Laplacian Regularized Sparse Representation based Classifier for Identifying DNA N4-methylcytosine Sites via L2,1/2-matrix Norm. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021 , PP,	3	4
289	webTWAS: a resource for disease candidate susceptibility genes identified by transcriptome-wide association study. <i>Nucleic Acids Research</i> , 2021 ,	20.1	9
288	NmRF: identification of multispecies RNA 2'-O-methylation modification sites from RNA sequences. <i>Briefings in Bioinformatics</i> , 2021 ,	13.4	4
287	Staem5: A novel computational approach for accurate prediction of m5C site. <i>Molecular Therapy - Nucleic Acids</i> , 2021 , 26, 1027-1034	10.7	3
286	iTTCA-RF: a random forest predictor for tumor T cell antigens. <i>Journal of Translational Medicine</i> , 2021 , 19, 449	8.5	9
285	A spectral clustering with self-weighted multiple kernel learning method for single-cell RNA-seq data. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	6
284	Minirmd: accurate and fast duplicate removal tool for short reads via multiple minimizers. <i>Bioinformatics</i> , 2021 , 37, 1604-1606	7.2	6
283	Revisiting genome-wide association studies from statistical modelling to machine learning. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	6
282	VPTMdb: a viral posttranslational modification database. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	4
281	Machine learning for phytopathology: from the molecular scale towards the network scale. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	4
280	Single-cell RNA Sequencing Analysis Identifies Key Genes in Brain Metastasis from Lung Adenocarcinoma. <i>Current Gene Therapy</i> , 2021 , 21, 338-348	4.3	1

279	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	3.6	0
278	A comprehensive review of the imbalance classification of protein post-translational modifications. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	9
277	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,	13.4	2
276	Prediction of drug-target interactions based on multi-layer network representation learning. <i>Neurocomputing</i> , 2021 , 434, 80-89	5.4	20
275	Critical downstream analysis steps for single-cell RNA sequencing data. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	6
274	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	4.5	8
273	RFhy-m2G: Identification of RNA N2-methylguanosine modification sites based on random forest and hybrid features. <i>Methods</i> , 2021 ,	4.6	10
272	ORS-Pred: An optimized reduced scheme-based identifier for antioxidant proteins. <i>Proteomics</i> , 2021 , 21, e2100017	4.8	2
271	Current status and future prospects of drug-target interaction prediction. <i>Briefings in Functional Genomics</i> , 2021 , 20, 312-322	4.9	2
270	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	5.4	3
269	EP3: an ensemble predictor that accurately identifies type III secreted effectors. <i>Briefings in Bioinformatics</i> , 2021 , 22, 1918-1928	13.4	15
268	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	7.7	4
267	An in silico approach to identification, categorization and prediction of nucleic acid binding proteins. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	50
266	DeepATT: a hybrid category attention neural network for identifying functional effects of DNA sequences. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	19
265	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	7.2	50
264	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	5.4	19
263	Prediction of bio-sequence modifications and the associations with diseases. <i>Briefings in Functional Genomics</i> , 2021 , 20, 1-18	4.9	23
262	Prediction of diabetic protein markers based on an ensemble method. <i>Frontiers in Bioscience</i> , 2021 , 26, 207-221		1

261	sgRNACNN: identifying sgRNA on-target activity in four crops using ensembles of convolutional neural networks. <i>Plant Molecular Biology</i> , 2021 , 105, 483-495	4.6	58
260	SgRNA-RF: identification of SgRNA on-target activity with imbalanced datasets. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021 , PP,	3	4
259	Sequence representation approaches for sequence-based protein prediction tasks that use deep learning. <i>Briefings in Functional Genomics</i> , 2021 , 20, 61-73	4.9	7
258	Decision Tree for Sequences. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2021 , 1-1	4.2	1
257	Application of learning to rank in bioinformatics tasks. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	2
256	GutBalance: a server for the human gut microbiome-based disease prediction and biomarker discovery with compositionality addressed. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	5
255	IEEE Access Special Section Editorial: Feature Representation and Learning Methods With Applications in Large-Scale Biological Sequence Analysis. <i>IEEE Access</i> , 2021 , 9, 33110-33119	3.5	1
254	Instance-Based Classification Through Hypothesis Testing. <i>IEEE Access</i> , 2021 , 9, 17485-17494	3.5	1
253	CRCF: A Method of Identifying Secretory Proteins of Malaria Parasites. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021 , PP,	3	1
252	A comprehensive overview and critical evaluation of gene regulatory network inference technologies. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	8
251	Anticancer peptides prediction with deep representation learning features. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	23
250	MRMD2.0: A Python Tool for Machine Learning with Feature Ranking and Reduction. <i>Current Bioinformatics</i> , 2021 , 15, 1213-1221	4.7	81
249	HSM6AP: a high-precision predictor for the Homo N6-methyladenosine (m ⁶ A) based on multiple weights and feature stitching. <i>RNA Biology</i> , 2021 , 18, 1882-1892	4.8	8
248	Prediction of RNA-binding protein and alternative splicing event associations during epithelial-mesenchymal transition based on inductive matrix completion. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	5
247	Accurate Prediction and Key Feature Recognition of Immunoglobulin. <i>Applied Sciences (Switzerland)</i> , 2021 , 11, 6894	2.6	3
246	High-resolution transcription factor binding sites prediction improved performance and interpretability by deep learning method. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	5
245	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 ,	7.2	2
244	Molecular design in drug discovery: a comprehensive review of deep generative models. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	13

243	Matrix factorization-based data fusion for the prediction of RNA-binding proteins and alternative splicing event associations during epithelial-mesenchymal transition. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	4
242	A comparison of deep learning-based pre-processing and clustering approaches for single-cell RNA sequencing data. <i>Briefings in Bioinformatics</i> , 2021 ,	13.4	1
241	prPred-DRLF: Plant R protein predictor using deep representation learning features. <i>Proteomics</i> , 2021 , e2100161	4.8	2
240	Characterizing viral circRNAs and their application in identifying circRNAs in viruses. <i>Briefings in Bioinformatics</i> , 2021 ,	13.4	3
239	rBPDL:Predicting RNA-Binding Proteins Using Deep Learning. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2021 , 25, 3668-3676	7.2	5
238	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	6.8	8
237	Prediction of presynaptic and postsynaptic neurotoxins based on feature extraction. <i>Mathematical Biosciences and Engineering</i> , 2021 , 18, 5943-5958	2.1	0
236	Identify RNA-associated subcellular localizations based on multi-label learning using Chou's 5-steps rule. <i>BMC Genomics</i> , 2021 , 22, 56	4.5	9
235	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	6.8	3
234	SubLocEP: a novel ensemble predictor of subcellular localization of eukaryotic mRNA based on machine learning. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	3
233	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	7.2	13
232	Network analysis of the hot spring microbiome sketches out possible niche differentiations among ecological guilds. <i>Ecological Modelling</i> , 2020 , 431, 109147	3	3
231	CWLy-SVM: A support vector machine-based tool for identifying cell wall lytic enzymes. <i>Computational Biology and Chemistry</i> , 2020 , 87, 107304	3.6	12
230	RF-PseU: A Random Forest Predictor for RNA Pseudouridine Sites. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020 , 8, 134	5.8	48
229	2lpiRNApred: 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	4.8	8
228	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	7.2	36
227	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	4	15
226	Significance-Based Essential Protein Discovery. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020 , PP,	3	3

225	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,	5	10
224	StackCPPred: a stacking and pairwise energy content-based prediction of cell-penetrating peptides and their uptake efficiency. <i>Bioinformatics</i> , 2020 , 36, 3028-3034	7.2	63
223	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	7	16
222	6mA-RicePred: A Method for Identifying DNA -Methyladenine Sites in the Rice Genome Based on Feature Fusion. <i>Frontiers in Plant Science</i> , 2020 , 11, 4	6.2	18
221	PPTPP: a novel therapeutic peptide prediction method using physicochemical property encoding and adaptive feature representation learning. <i>Bioinformatics</i> , 2020 , 36, 3982-3987	7.2	30
220	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	6.9	19
219	Identifying cell types to interpret scRNA-seq data: how, why and more possibilities. <i>Briefings in Functional Genomics</i> , 2020 , 19, 286-291	4.9	9
218	Application and Development of Artificial Intelligence and Intelligent Disease Diagnosis. <i>Current Pharmaceutical Design</i> , 2020 , 26, 3069-3075	3.3	10
217	Genome-Wide Analysis of LysM-Containing Gene Family in Wheat: Structural and Phylogenetic Analysis during Development and Defense. <i>Genes</i> , 2020 , 12,	4.2	2
216	Identification of Sub-Golgi protein localization by use of deep representation learning features. <i>Bioinformatics</i> , 2020 ,	7.2	20
215	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,	4.4	2
214	Critical evaluation of web-based prediction tools for human protein subcellular localization. <i>Briefings in Bioinformatics</i> , 2020 , 21, 1628-1640	13.4	33
213	Machine learning and its applications in plant molecular studies. <i>Briefings in Functional Genomics</i> , 2020 , 19, 40-48	4.9	19
212	Clustering and classification methods for single-cell RNA-sequencing data. <i>Briefings in Bioinformatics</i> , 2020 , 21, 1196-1208	13.4	50
211	Regulator Network Analysis of Rice and Maize Yield-Related Genes. <i>Frontiers in Cell and Developmental Biology</i> , 2020 , 8, 621464	5.7	1
210	Impact of Transcatheter Aortic Valve Replacement on Risk Profiles of Surgical Aortic Valve Replacement Patients. <i>Cardiovascular Revascularization Medicine</i> , 2020 , 21, 959-963	1.6	2
209	Exploring Drug Treatment Patterns Based on the Action of Drug and Multilayer Network Model. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	16
208	Computational Prediction of Protein Arginine Methylation Based on Composition-Transition-Distribution Features. <i>ACS Omega</i> , 2020 , 5, 27470-27479	3.9	1

207	Reference-Based Sequence Classification. <i>IEEE Access</i> , 2020 , 8, 218199-218214	3.5	1
206	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	5.7	4
205	Progress in the development of antimicrobial peptide prediction tools. <i>Current Protein and Peptide Science</i> , 2020 ,	2.8	1
204	Empirical comparison and analysis of web-based cell-penetrating peptide prediction tools. <i>Briefings in Bioinformatics</i> , 2020 , 21, 408-420	13.4	83
203	Computational methods for identifying the critical nodes in biological networks. <i>Briefings in Bioinformatics</i> , 2020 , 21, 486-497	13.4	44
202	Transcription factors-DNA interactions in rice: identification and verification. <i>Briefings in Bioinformatics</i> , 2020 , 21, 946-956	13.4	10
201	Protein Complexes Identification with Family-Wise Error Rate Control. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020 , 17, 2062-2073	3	5
200	Predicting disease-associated circular RNAs using deep forests combined with positive-unlabeled learning methods. <i>Briefings in Bioinformatics</i> , 2020 , 21, 1425-1436	13.4	60
199	Investigating Maize Yield-Related Genes in Multiple Omics Interaction Network Data. <i>IEEE Transactions on Nanobioscience</i> , 2020 , 19, 142-151	3.4	1
198	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	6.8	19
197	Selecting Essential MicroRNAs Using a Novel Voting Method. <i>Molecular Therapy - Nucleic Acids</i> , 2019 , 18, 16-23	10.7	21
196	AOPs-SVM: A Sequence-Based Classifier of Antioxidant Proteins Using a Support Vector Machine. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019 , 7, 224	5.8	44
195	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	5.8	75
194	ELM-MHC: An Improved MHC Identification Method with Extreme Learning Machine Algorithm. <i>Journal of Proteome Research</i> , 2019 , 18, 1392-1401	5.6	39
193	Investigation and development of maize fused network analysis with multi-omics. <i>Plant Physiology and Biochemistry</i> , 2019 , 141, 380-387	5.4	11
192	Perspectives of Bioinformatics in Big Data Era. <i>Current Genomics</i> , 2019 , 20, 79-80	2.6	5
191	Incorporating Distance-Based Top-n-gram and Random Forest To Identify Electron Transport Proteins. <i>Journal of Proteome Research</i> , 2019 , 18, 2931-2939	5.6	66
190	Protein Function Prediction: From Traditional Classifier to Deep Learning. <i>Proteomics</i> , 2019 , 19, e19001198	10.8	59

189	TAVR in Low-Risk Patients: 1-Year Results From the LRT Trial. <i>JACC: Cardiovascular Interventions</i> , 2019 , 12, 901-907	5	39
188	Prediction of Potential Disease-Associated MicroRNAs by Using Neural Networks. <i>Molecular Therapy - Nucleic Acids</i> , 2019 , 16, 566-575	10.7	41
187	Iterative feature representations improve N4-methylcytosine site prediction. <i>Bioinformatics</i> , 2019 , 35, 4930-4937	7.2	77
186	Combining Sparse Group Lasso and Linear Mixed Model Improves Power to Detect Genetic Variants Underlying Quantitative Traits. <i>Frontiers in Genetics</i> , 2019 , 10, 271	4.5	4
185	Prediction of Thermophilic Proteins Using Voting Algorithm. <i>Lecture Notes in Computer Science</i> , 2019 , 195-203	0.9	2
184	PEPred-Suite: improved and robust prediction of therapeutic peptides using adaptive feature representation learning. <i>Bioinformatics</i> , 2019 , 35, 4272-4280	7.2	68
183	Details in the evaluation of circular RNA detection tools: Reply to Chen and Chuang. <i>PLoS Computational Biology</i> , 2019 , 15, e1006916	5	6
182	Latest Machine Learning Techniques for Biomedicine and Bioinformatics. <i>Current Bioinformatics</i> , 2019 , 14, 176-177	4.7	15
181	Diagnosis of Brain Diseases via Multi-Scale Time-Series Model. <i>Frontiers in Neuroscience</i> , 2019 , 13, 197	5.1	2
180	Application of Machine Learning in Microbiology. <i>Frontiers in Microbiology</i> , 2019 , 10, 827	5.7	81
179	4mCPred: machine learning methods for DNA N4-methylcytosine sites prediction. <i>Bioinformatics</i> , 2019 , 35, 593-601	7.2	97
178	Integration of deep feature representations and handcrafted features to improve the prediction of N6-methyladenosine sites. <i>Neurocomputing</i> , 2019 , 324, 3-9	5.4	106
177	Meta-Path Methods for Prioritizing Candidate Disease miRNAs. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019 , 16, 283-291	3	99
176	Advanced Machine Learning Techniques for Bioinformatics. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019 , 16, 1182-1183	3	7
175	A novel collaborative filtering model for LncRNA-disease association prediction based on the Naïve Bayesian classifier. <i>BMC Bioinformatics</i> , 2019 , 20, 396	3.6	28
174	Exploiting Discriminative Regions of Brain Slices Based on 2D CNNs for Alzheimer's Disease Classification. <i>IEEE Access</i> , 2019 , 7, 181423-181433	3.5	22
173	SecProMTB: Support Vector Machine-Based Classifier for Secretory Proteins Using Imbalanced Data Sets Applied to Mycobacterium tuberculosis. <i>Proteomics</i> , 2019 , 19, e1900007	4.8	33
172	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	10.7	131

171	Supervised Brain Tumor Segmentation Based on Gradient and Context-Sensitive Features. <i>Frontiers in Neuroscience</i> , 2019 , 13, 144	5.1	14
170	Perspectives of Bioinformatics in Big Data Era. <i>Current Genomics</i> , 2019 , 20, 79-80	2.6	1
169	Review of Progress in Predicting Protein Methylation Sites. <i>Current Organic Chemistry</i> , 2019 , 23, 1663-1670	7	7
168	A Review of DNA-binding Proteins Prediction Methods. <i>Current Bioinformatics</i> , 2019 , 14, 246-254	4.7	56
167	Deep-Resp-Forest: A deep forest model to predict anti-cancer drug response. <i>Methods</i> , 2019 , 166, 91-102	4.6	117
166	Current Bioinformatics's New and Improved Impact Factor. <i>Current Bioinformatics</i> , 2019 , 14, 686-687	1.189	7
165	Taxonomy dimension reduction for colorectal cancer prediction. <i>Computational Biology and Chemistry</i> , 2019 , 83, 107160	3.6	13
164	Prediction of tumor metastasis from sequencing data in the era of genome sequencing. <i>Briefings in Functional Genomics</i> , 2019 , 18, 412-418	4.9	11
163	Identifying protein-protein interface via a novel multi-scale local sequence and structural representation. <i>BMC Bioinformatics</i> , 2019 , 20, 483	3.6	4
162	Exploring sequence-based features for the improved prediction of DNA N4-methylcytosine sites in multiple species. <i>Bioinformatics</i> , 2019 , 35, 1326-1333	7.2	104
161	Gene2vec: gene subsequence embedding for prediction of mammalian -methyladenosine sites from mRNA. <i>Rna</i> , 2019 , 25, 205-218	5.8	279
160	Deep learning in omics: a survey and guideline. <i>Briefings in Functional Genomics</i> , 2019 , 18, 41-57	4.9	68
159	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	3	123
158	Research progress in protein posttranslational modification site prediction. <i>Briefings in Functional Genomics</i> , 2018 , 18, 220-229	4.9	24
157	A Novel Approach Based on a Weighted Interactive Network to Predict Associations of MiRNAs and Diseases. <i>International Journal of Molecular Sciences</i> , 2018 , 20,	6.3	11
156	Prediction of potential disease-associated microRNAs using structural perturbation method. <i>Bioinformatics</i> , 2018 , 34, 2425-2432	7.2	172
155	NucPosPred: Predicting species-specific genomic nucleosome positioning via four different modes of general PseKNC. <i>Journal of Theoretical Biology</i> , 2018 , 450, 15-21	2.3	26
154	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	7.2	93

153	Network-based method for mining novel HPV infection related genes using random walk with restart algorithm. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2018 , 1864, 2376-2383	6.9	18
152	Tumor origin detection with tissue-specific miRNA and DNA methylation markers. <i>Bioinformatics</i> , 2018 , 34, 398-406	7.2	216
151	Prediction of human protein subcellular localization using deep learning. <i>Journal of Parallel and Distributed Computing</i> , 2018 , 117, 212-217	4.4	152
150	VCSRA: A fast and accurate multiple sequence alignment algorithm with a high degree of parallelism. <i>Journal of Genetics and Genomics</i> , 2018 , 45, 407-410	4	5
149	Cancer Diagnosis Through IsomiR Expression with Machine Learning Method. <i>Current Bioinformatics</i> , 2018 , 13, 57-63	4.7	97
148	RicyerDB: A Database For Collecting Rice Yield-related Genes with Biological Analysis. <i>International Journal of Biological Sciences</i> , 2018 , 14, 965-970	11.2	17
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1	Studying the drug treatment pattern based on the action of drug and multi-layer network model		2