

# Quan Zou

## List of Publications by Citations

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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	Biological functions of microRNAs: a review. <i>Journal of Physiology and Biochemistry</i> , <b>2011</b> , 67, 129-39	5	481
313	The Symbiodinium kawagutii genome illuminates dinoflagellate gene expression and coral symbiosis. <i>Science</i> , <b>2015</b> , 350, 691-4	33.3	283
312	A novel features ranking metric with application to scalable visual and bioinformatics data classification. <i>Neurocomputing</i> , <b>2016</b> , 173, 346-354	5.4	280
311	Gene2vec: gene subsequence embedding for prediction of mammalian -methyladenosine sites from mRNA. <i>Rna</i> , <b>2019</b> , 25, 205-218	5.8	279
310	Integrative approaches for predicting microRNA function and prioritizing disease-related microRNA using biological interaction networks. <i>Briefings in Bioinformatics</i> , <b>2016</b> , 17, 193-203	13.4	247
309	Predicting Diabetes Mellitus With Machine Learning Techniques. <i>Frontiers in Genetics</i> , <b>2018</b> , 9, 515	4.5	241
308	A comprehensive overview and evaluation of circular RNA detection tools. <i>PLoS Computational Biology</i> , <b>2017</b> , 13, e1005420	5	225
307	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> , <b>2017</b> , 14, 905-915	3	221
306	Tumor origin detection with tissue-specific miRNA and DNA methylation markers. <i>Bioinformatics</i> , <b>2018</b> , 34, 398-406	7.2	216
305	LibD3C: Ensemble classifiers with a clustering and dynamic selection strategy. <i>Neurocomputing</i> , <b>2014</b> , 123, 424-435	5.4	199
304	Local-DPP: An improved DNA-binding protein prediction method by exploring local evolutionary information. <i>Information Sciences</i> , <b>2017</b> , 384, 135-144	7.7	172
303	Prediction of potential disease-associated microRNAs using structural perturbation method. <i>Bioinformatics</i> , <b>2018</b> , 34, 2425-2432	7.2	172
302	Improved and Promising Identification of Human MicroRNAs by Incorporating a High-Quality Negative Set. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2014</b> , 11, 192-201	3	170
301	Prediction and Validation of Disease Genes Using HeteSim Scores. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2017</b> , 14, 687-695	3	168
300	Prediction of human protein subcellular localization using deep learning. <i>Journal of Parallel and Distributed Computing</i> , <b>2018</b> , 117, 212-217	4.4	152
299	Similarity computation strategies in the microRNA-disease network: a survey. <i>Briefings in Functional Genomics</i> , <b>2016</b> , 15, 55-64	4.9	146
298	Survey of MapReduce frame operation in bioinformatics. <i>Briefings in Bioinformatics</i> , <b>2014</b> , 15, 637-47	13.4	141

297	nDNA-Prot: identification of DNA-binding proteins based on unbalanced classification. <i>BMC Bioinformatics</i> , <b>2014</b> , 15, 298	3.6	140
296	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> , <b>2019</b> , 394, 1629-1637	4.9	131
295	Pretata: predicting TATA binding proteins with novel features and dimensionality reduction strategy. <i>BMC Systems Biology</i> , <b>2016</b> , 10, 114	3.5	131
294	Transcatheter Aortic Valve Replacement in Low-Risk Patients With Symptomatic Severe Aortic Stenosis. <i>Journal of the American College of Cardiology</i> , <b>2018</b> , 72, 2095-2105	15.1	127
293	Prediction of MicroRNA-Disease Associations Based on Social Network Analysis Methods. <i>BioMed Research International</i> , <b>2015</b> , 2015, 810514	3	124
292	Fast Prediction of Protein Methylation Sites Using a Sequence-Based Feature Selection Technique. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2019</b> , 16, 1264-1273	3	123
291	CPPred-RF: A Sequence-based Predictor for Identifying Cell-Penetrating Peptides and Their Uptake Efficiency. <i>Journal of Proteome Research</i> , <b>2017</b> , 16, 2044-2053	5.6	120
290	Hierarchical classification of protein folds using a novel ensemble classifier. <i>PLoS ONE</i> , <b>2013</b> , 8, e56499	3.7	120
289	Deep-Resp-Forest: A deep forest model to predict anti-cancer drug response. <i>Methods</i> , <b>2019</b> , 166, 91-102	4.6	117
288	HAlign: Fast multiple similar DNA/RNA sequence alignment based on the centre star strategy. <i>Bioinformatics</i> , <b>2015</b> , 31, 2475-81	7.2	116
287	Integration of deep feature representations and handcrafted features to improve the prediction of N6-methyladenosine sites. <i>Neurocomputing</i> , <b>2019</b> , 324, 3-9	5.4	106
286	Exploring sequence-based features for the improved prediction of DNA N4-methylcytosine sites in multiple species. <i>Bioinformatics</i> , <b>2019</b> , 35, 1326-1333	7.2	104
285	Meta-Path Methods for Prioritizing Candidate Disease miRNAs. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2019</b> , 16, 283-291	3	99
284	PhosPred-RF: A Novel Sequence-Based Predictor for Phosphorylation Sites Using Sequential Information Only. <i>IEEE Transactions on Nanobioscience</i> , <b>2017</b> , 16, 240-247	3.4	98
283	Cancer Diagnosis Through IsomiR Expression with Machine Learning Method. <i>Current Bioinformatics</i> , <b>2018</b> , 13, 57-63	4.7	97
282	4mCPred: machine learning methods for DNA N4-methylcytosine sites prediction. <i>Bioinformatics</i> , <b>2019</b> , 35, 593-601	7.2	97
281	TiSGeD: a database for tissue-specific genes. <i>Bioinformatics</i> , <b>2010</b> , 26, 1273-5	7.2	97
280	Protein Folds Prediction with Hierarchical Structured SVM. <i>Current Proteomics</i> , <b>2016</b> , 13, 79-85	0.7	97

279	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> , <b>2018</b> , 34, 2029-2036	7.2	93
278	Protein Remote Homology Detection by Combining Chou's Pseudo Amino Acid Composition and Profile-Based Protein Representation. <i>Molecular Informatics</i> , <b>2013</b> , 32, 775-82	3.8	93
277	Finding the Best Classification Threshold in Imbalanced Classification. <i>Big Data Research</i> , <b>2016</b> , 5, 2-8	3.7	89
276	Detecting N-methyladenosine sites from RNA transcriptomes using ensemble Support Vector Machines. <i>Scientific Reports</i> , <b>2017</b> , 7, 40242	4.9	85
275	Empirical comparison and analysis of web-based cell-penetrating peptide prediction tools. <i>Briefings in Bioinformatics</i> , <b>2020</b> , 21, 408-420	13.4	83
274	Application of Machine Learning in Microbiology. <i>Frontiers in Microbiology</i> , <b>2019</b> , 10, 827	5.7	81
273	miRClassify: an advanced web server for miRNA family classification and annotation. <i>Computers in Biology and Medicine</i> , <b>2014</b> , 45, 157-60	7	81
272	MRMD2.0: A Python Tool for Machine Learning with Feature Ranking and Reduction. <i>Current Bioinformatics</i> , <b>2021</b> , 15, 1213-1221	4.7	81
271	HPSLPred: An Ensemble Multi-Label Classifier for Human Protein Subcellular Location Prediction with Imbalanced Source. <i>Proteomics</i> , <b>2017</b> , 17, 1700262	4.8	80
270	Iterative feature representations improve N4-methylcytosine site prediction. <i>Bioinformatics</i> , <b>2019</b> , 35, 4930-4937	7.2	77
269	Enhanced Protein Fold Prediction Method Through a Novel Feature Extraction Technique. <i>IEEE Transactions on Nanobioscience</i> , <b>2015</b> , 14, 649-59	3.4	77
268	Sequence clustering in bioinformatics: an empirical study. <i>Briefings in Bioinformatics</i> , <b>2018</b> ,	13.4	77
267	A Random Forest Sub-Golgi Protein Classifier Optimized via Dipeptide and Amino Acid Composition Features. <i>Frontiers in Bioengineering and Biotechnology</i> , <b>2019</b> , 7, 215	5.8	75
266	PaGenBase: a pattern gene database for the global and dynamic understanding of gene function. <i>PLoS ONE</i> , <b>2013</b> , 8, e80747	3.7	74
265	Regulatory long non-coding RNA and its functions. <i>Journal of Physiology and Biochemistry</i> , <b>2012</b> , 68, 611-8	3	73
264	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> , <b>2015</b> , 33, 1720-30	3.6	71
263	PEPred-Suite: improved and robust prediction of therapeutic peptides using adaptive feature representation learning. <i>Bioinformatics</i> , <b>2019</b> , 35, 4272-4280	7.2	68
262	Deep learning in omics: a survey and guideline. <i>Briefings in Functional Genomics</i> , <b>2019</b> , 18, 41-57	4.9	68

261	An overview of SNP interactions in genome-wide association studies. <i>Briefings in Functional Genomics</i> , <b>2015</b> , 14, 143-55	4.9	67
260	Incorporating Distance-Based Top-n-gram and Random Forest To Identify Electron Transport Proteins. <i>Journal of Proteome Research</i> , <b>2019</b> , 18, 2931-2939	5.6	66
259	An Improved Protein Structural Classes Prediction Method by Incorporating Both Sequence and Structure Information. <i>IEEE Transactions on Nanobioscience</i> , <b>2015</b> , 14, 339-349	3.4	66
258	StackCPPred: a stacking and pairwise energy content-based prediction of cell-penetrating peptides and their uptake efficiency. <i>Bioinformatics</i> , <b>2020</b> , 36, 3028-3034	7.2	63
257	Recent Progress in Machine Learning-Based Methods for Protein Fold Recognition. <i>International Journal of Molecular Sciences</i> , <b>2016</b> , 17,	6.3	63
256	SkipCPP-Pred: an improved and promising sequence-based predictor for predicting cell-penetrating peptides. <i>BMC Genomics</i> , <b>2017</b> , 18, 742	4.5	62
255	An approach for identifying cytokines based on a novel ensemble classifier. <i>BioMed Research International</i> , <b>2013</b> , 2013, 686090	3	61
254	Predicting disease-associated circular RNAs using deep forests combined with positive-unlabeled learning methods. <i>Briefings in Bioinformatics</i> , <b>2020</b> , 21, 1425-1436	13.4	60
253	Protein Function Prediction: From Traditional Classifier to Deep Learning. <i>Proteomics</i> , <b>2019</b> , 19, e19001108	10.8	59
252	sgRNACNN: identifying sgRNA on-target activity in four crops using ensembles of convolutional neural networks. <i>Plant Molecular Biology</i> , <b>2021</b> , 105, 483-495	4.6	58
251	BinMemPredict: a Web Server and Software for Predicting Membrane Protein Types. <i>Current Proteomics</i> , <b>2013</b> , 10, 2-9	0.7	57
250	Probability-based collaborative filtering model for predicting gene-disease associations. <i>BMC Medical Genomics</i> , <b>2017</b> , 10, 76	3.7	56
249	A Review of DNA-binding Proteins Prediction Methods. <i>Current Bioinformatics</i> , <b>2019</b> , 14, 246-254	4.7	56
248	Asynchronous spiking neural P systems with rules on synapses. <i>Neurocomputing</i> , <b>2015</b> , 151, 1439-1445	5.4	55
247	70ProPred: a predictor for discovering sigma70 promoters based on combining multiple features. <i>BMC Systems Biology</i> , <b>2018</b> , 12, 44	3.5	52
246	Comparative analysis and prediction of quorum-sensing peptides using feature representation learning and machine learning algorithms. <i>Briefings in Bioinformatics</i> , <b>2018</b> ,	13.4	51
245	Improving tRNAscan-SE Annotation Results via Ensemble Classifiers. <i>Molecular Informatics</i> , <b>2015</b> , 34, 761-70	3.8	50
244	Clustering and classification methods for single-cell RNA-sequencing data. <i>Briefings in Bioinformatics</i> , <b>2020</b> , 21, 1196-1208	13.4	50

243	An in silico approach to identification, categorization and prediction of nucleic acid binding proteins. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,	13.4	50
242	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> , <b>2021</b> , 37, 1319-1321	7.2	50
241	A study of miRNAs targets prediction and experimental validation. <i>Protein and Cell</i> , <b>2010</b> , 1, 979-86	7.2	49
240	RF-PseU: A Random Forest Predictor for RNA Pseudouridine Sites. <i>Frontiers in Bioengineering and Biotechnology</i> , <b>2020</b> , 8, 134	5.8	48
239	Briefing in family characteristics of microRNAs and their applications in cancer research. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , <b>2014</b> , 1844, 191-7	4	46
238	A global characterization and identification of multifunctional enzymes. <i>PLoS ONE</i> , <b>2012</b> , 7, e38979	3.7	46
237	Sequencing and de novo analysis of <i>Crassostrea angulata</i> (Fujian oyster) from 8 different developing phases using 454 GSFlx. <i>PLoS ONE</i> , <b>2012</b> , 7, e43653	3.7	46
236	Computational identification and characteristics of novel microRNAs from the silkworm ( <i>Bombyx mori</i> L.). <i>Molecular Biology Reports</i> , <b>2010</b> , 37, 3171-6	2.8	45
235	AOPs-SVM: A Sequence-Based Classifier of Antioxidant Proteins Using a Support Vector Machine. <i>Frontiers in Bioengineering and Biotechnology</i> , <b>2019</b> , 7, 224	5.8	44
234	Biophysical and phenomenological models of multiple spike interactions in spike-timing dependent plasticity. <i>International Journal of Neural Systems</i> , <b>2006</b> , 16, 79-97	6.2	44
233	An Empirical Study of Features Fusion Techniques for Protein-Protein Interaction Prediction. <i>Current Bioinformatics</i> , <b>2016</b> , 11, 4-12	4.7	44
232	Computational methods for identifying the critical nodes in biological networks. <i>Briefings in Bioinformatics</i> , <b>2020</b> , 21, 486-497	13.4	44
231	HITS-PR-HHblits: protein remote homology detection by combining PageRank and Hyperlink-Induced Topic Search. <i>Briefings in Bioinformatics</i> , <b>2018</b> ,	13.4	44
230	Using distances between Top-n-gram and residue pairs for protein remote homology detection. <i>BMC Bioinformatics</i> , <b>2014</b> , 15 Suppl 2, S3	3.6	43
229	Prediction of Potential Disease-Associated MicroRNAs by Using Neural Networks. <i>Molecular Therapy - Nucleic Acids</i> , <b>2019</b> , 16, 566-575	10.7	41
228	The discovery approaches and detection methods of microRNAs. <i>Molecular Biology Reports</i> , <b>2011</b> , 38, 4125-35	2.8	41
227	PaGeFinder: quantitative identification of spatiotemporal pattern genes. <i>Bioinformatics</i> , <b>2012</b> , 28, 1544-5.2	5.2	41
226	Exploratory Predicting Protein Folding Model with Random Forest and Hybrid Features. <i>Current Proteomics</i> , <b>2015</b> , 11, 289-299	0.7	40

225	miR-isomiRExp: a web-server for the analysis of expression of miRNA at the miRNA/isomiR levels. <i>Scientific Reports</i> , <b>2016</b> , 6, 23700	4.9	40
224	ELM-MHC: An Improved MHC Identification Method with Extreme Learning Machine Algorithm. <i>Journal of Proteome Research</i> , <b>2019</b> , 18, 1392-1401	5.6	39
223	TAVR in Low-Risk Patients: 1-Year Results From the LRT Trial. <i>JACC: Cardiovascular Interventions</i> , <b>2019</b> , 12, 901-907	5	39
222	A novel machine learning method for cytokine-receptor interaction prediction. <i>Combinatorial Chemistry and High Throughput Screening</i> , <b>2016</b> , 19, 144-52	1.3	39
221	Identifying Multi-Functional Enzyme by Hierarchical Multi-Label Classifier. <i>Journal of Computational and Theoretical Nanoscience</i> , <b>2013</b> , 10, 1038-1043	0.3	38
220	DeepAVP: A Dual-Channel Deep Neural Network for Identifying Variable-Length Antiviral Peptides. <i>IEEE Journal of Biomedical and Health Informatics</i> , <b>2020</b> , 24, 3012-3019	7.2	36
219	Approaches for recognizing disease genes based on network. <i>BioMed Research International</i> , <b>2014</b> , 2014, 416323	3	36
218	Bioinformatics applications on Apache Spark. <i>GigaScience</i> , <b>2018</b> , 7,	7.6	35
217	Which statistical significance test best detects oncomiRNAs in cancer tissues? An exploratory analysis. <i>Oncotarget</i> , <b>2016</b> , 7, 85613-85623	3.3	34
216	SecProMTB: Support Vector Machine-Based Classifier for Secretory Proteins Using Imbalanced Data Sets Applied to Mycobacterium tuberculosis. <i>Proteomics</i> , <b>2019</b> , 19, e1900007	4.8	33
215	Representation of fluctuation features in pathological knee joint vibroarthrographic signals using kernel density modeling method. <i>Medical Engineering and Physics</i> , <b>2014</b> , 36, 1305-11	2.4	33
214	Critical evaluation of web-based prediction tools for human protein subcellular localization. <i>Briefings in Bioinformatics</i> , <b>2020</b> , 21, 1628-1640	13.4	33
213	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> , <b>2021</b> , 140, 105092	7	32
212	Computational approaches in detecting non- coding RNA. <i>Current Genomics</i> , <b>2013</b> , 14, 371-7	2.6	32
211	imDC: an ensemble learning method for imbalanced classification with miRNA data. <i>Genetics and Molecular Research</i> , <b>2015</b> , 14, 123-33	1.2	31
210	PPTPP: a novel therapeutic peptide prediction method using physicochemical property encoding and adaptive feature representation learning. <i>Bioinformatics</i> , <b>2020</b> , 36, 3982-3987	7.2	30
209	Biological functions of microRNAs. <i>Russian Journal of Bioorganic Chemistry</i> , <b>2010</b> , 36, 747-52	1	30
208	Prediction of G Protein-Coupled Receptors with SVM-Prot Features and Random Forest. <i>Scientifica</i> , <b>2016</b> , 2016, 8309253	2.6	30

207	A Comprehensive Analysis of miRNA/isomiR Expression with Gender Difference. <i>PLoS ONE</i> , <b>2016</b> , 11, e0154955	3.7	29
206	BP Neural Network Could Help Improve Pre-miRNA Identification in Various Species. <i>BioMed Research International</i> , <b>2016</b> , 2016, 9565689	3	29
205	A novel collaborative filtering model for LncRNA-disease association prediction based on the Naïve Bayesian classifier. <i>BMC Bioinformatics</i> , <b>2019</b> , 20, 396	3.6	28
204	DeepM6ASeq-EL: prediction of human N6-methyladenosine (m6A) sites with LSTM and ensemble learning. <i>Frontiers of Computer Science</i> , <b>2022</b> , 16, 1	2.2	28
203	NucPosPred: Predicting species-specific genomic nucleosome positioning via four different modes of general PseKNC. <i>Journal of Theoretical Biology</i> , <b>2018</b> , 450, 15-21	2.3	26
202	enDNA-Prot: identification of DNA-binding proteins by applying ensemble learning. <i>BioMed Research International</i> , <b>2014</b> , 2014, 294279	3	26
201	Classification of Small GTPases with Hybrid Protein Features and Advanced Machine Learning Techniques. <i>Current Bioinformatics</i> , <b>2018</b> , 13, 492-500	4.7	26
200	ITP-Pred: an interpretable method for predicting, therapeutic peptides with fused features low-dimension representation. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,	13.4	25
199	Review of Protein Subcellular Localization Prediction. <i>Current Bioinformatics</i> , <b>2014</b> , 9, 331-342	4.7	25
198	Research progress in protein posttranslational modification site prediction. <i>Briefings in Functional Genomics</i> , <b>2018</b> , 18, 220-229	4.9	24
197	Identification of cytokine via an improved genetic algorithm. <i>Frontiers of Computer Science</i> , <b>2015</b> , 9, 643-651	6.1	23
196	Prediction of bio-sequence modifications and the associations with diseases. <i>Briefings in Functional Genomics</i> , <b>2021</b> , 20, 1-18	4.9	23
195	Anticancer peptides prediction with deep representation learning features. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,	13.4	23
194	Exploiting Discriminative Regions of Brain Slices Based on 2D CNNs for Alzheimer's Disease Classification. <i>IEEE Access</i> , <b>2019</b> , 7, 181423-181433	3.5	22
193	Selecting Essential MicroRNAs Using a Novel Voting Method. <i>Molecular Therapy - Nucleic Acids</i> , <b>2019</b> , 18, 16-23	10.7	21
192	Kinetic models of spike-timing dependent plasticity and their functional consequences in detecting correlations. <i>Biological Cybernetics</i> , <b>2007</b> , 97, 81-97	2.8	21
191	HAlign-II: efficient ultra-large multiple sequence alignment and phylogenetic tree reconstruction with distributed and parallel computing. <i>Algorithms for Molecular Biology</i> , <b>2017</b> , 12, 25	1.8	20
190	Identification of Sub-Golgi protein localization by use of deep representation learning features. <i>Bioinformatics</i> , <b>2020</b> ,	7.2	20



189	Prediction of drug-target interactions based on multi-layer network representation learning. <i>Neurocomputing</i> , <b>2021</b> , 434, 80-89	5.4	20
188	Analysis of gene expression profiles of lung cancer subtypes with machine learning algorithms. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , <b>2020</b> , 1866, 165822	6.9	19
187	Specifying architecture of knowledge graph with data graph, information graph, knowledge graph and wisdom graph <b>2017</b> ,		19
186	A Discussion of MicroRNAs in Cancers. <i>Current Bioinformatics</i> , <b>2014</b> , 9, 453-462	4.7	19
185	Machine learning and its applications in plant molecular studies. <i>Briefings in Functional Genomics</i> , <b>2020</b> , 19, 40-48	4.9	19
184	CirRNAPL: A web server for the identification of circRNA based on extreme learning machine. <i>Computational and Structural Biotechnology Journal</i> , <b>2020</b> , 18, 834-842	6.8	19
183	DeepATT: a hybrid category attention neural network for identifying functional effects of DNA sequences. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,	13.4	19
182	A Convolutional Neural Network Using Dinucleotide One-hot Encoder for identifying DNA N6-Methyladenine Sites in the Rice Genome. <i>Neurocomputing</i> , <b>2021</b> , 422, 214-221	5.4	19
181	6mA-RicePred: A Method for Identifying DNA -Methyladenine Sites in the Rice Genome Based on Feature Fusion. <i>Frontiers in Plant Science</i> , <b>2020</b> , 11, 4	6.2	18
180	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> , <b>2018</b> , 1864, 2376-2383	6.9	18
179	Improved method for predicting protein fold patterns with ensemble classifiers. <i>Genetics and Molecular Research</i> , <b>2012</b> , 11, 174-81	1.2	18
178	Virtual Neurorobotics (VNR) to Accelerate Development of Plausible Neuromorphic Brain Architectures. <i>Frontiers in Neurorobotics</i> , <b>2007</b> , 1, 1	3.4	18
177	Accurate Identification of Cancerlectins through Hybrid Machine Learning Technology. <i>International Journal of Genomics</i> , <b>2016</b> , 2016, 7604641	2.5	18
176	RicyerDB: A Database For Collecting Rice Yield-related Genes with Biological Analysis. <i>International Journal of Biological Sciences</i> , <b>2018</b> , 14, 965-970	11.2	17
175	CMSA: a heterogeneous CPU/GPU computing system for multiple similar RNA/DNA sequence alignment. <i>BMC Bioinformatics</i> , <b>2017</b> , 18, 315	3.6	17
174	Predicting RNA secondary structure based on the class information and Hopfield network. <i>Computers in Biology and Medicine</i> , <b>2009</b> , 39, 206-14	7	17
173	Computational Analysis of miRNA Target Identification. <i>Current Bioinformatics</i> , <b>2012</b> , 7, 512-525	4.7	17
172	A network-based method for the identification of putative genes related to infertility. <i>Biochimica Et Biophysica Acta - General Subjects</i> , <b>2016</b> , 1860, 2716-24	4	17

171	Sc-ncDNAPred: A Sequence-Based Predictor for Identifying Non-coding DNA in. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 2174	5.7	17
170	Exploration of the correlation between GPCRs and drugs based on a learning to rank algorithm. <i>Computers in Biology and Medicine</i> , <b>2020</b> , 119, 103660	7	16
169	Research on Cloud Databases. <i>Ruan Jian Xue Bao/Journal of Software</i> , <b>2012</b> , 23, 1148-1166		16
168	Exploring Drug Treatment Patterns Based on the Action of Drug and Multilayer Network Model. <i>International Journal of Molecular Sciences</i> , <b>2020</b> , 21,	6.3	16
167	Latest Machine Learning Techniques for Biomedicine and Bioinformatics. <i>Current Bioinformatics</i> , <b>2019</b> , 14, 176-177	4.7	15
166	Review and comparative analysis of machine learning-based phage virion protein identification methods. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , <b>2020</b> , 1868, 140406	4	15
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164	EP3: an ensemble predictor that accurately identifies type III secreted effectors. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22, 1918-1928	13.4	15
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8	iLncDA-LTR: Identification of lncRNA-disease associations by learning to rank. <i>Computers in Biology and Medicine</i> , <b>2022</b> , 105605	7	0
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6	BDSCyto: An Automated Approach for Identifying Cytokines Based on Best Dimension Searching. <i>Lecture Notes in Computer Science</i> , <b>2016</b> , 713-725	0.9	
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