## List of Publications by Year in descending order

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Bolino

π	Article	IF	CITATIONS
1	The Advances and Challenges of Deep Learning Application in Biological Big Data Processing. Current Bioinformatics, 2018, 13, 352-359.	1.5	91
2	Network Consistency Projection for Human miRNA-Disease Associations Inference. Scientific Reports, 2016, 6, 36054.	3.3	89
3	Global network random walk for predicting potential human lncRNA-disease associations. Scientific Reports, 2017, 7, 12442.	3.3	89
4	Seeksv: an accurate tool for somatic structural variation and virus integration detection. Bioinformatics, 2017, 33, 184-191.	4.1	64
5	BPLLDA: Predicting IncRNA-Disease Associations Based on Simple Paths With Limited Lengths in a Heterogeneous Network. Frontiers in Genetics, 2018, 9, 411.	2.3	52
6	Gene Selection Using Locality Sensitive Laplacian Score. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 1146-1156.	3.0	47
7	Coronavirus phylogeny based on 2D graphical representation of DNA sequence. Journal of Computational Chemistry, 2006, 27, 1196-1202.	3.3	45
8	A Novel method for similarity analysis and protein sub-cellular localization prediction. Bioinformatics, 2010, 26, 2678-2683.	4.1	43
9	Graphical approach to analyzing DNA sequences. Journal of Computational Chemistry, 2005, 26, 1519-1523.	3.3	42
10	Predicting influenza antigenicity from Hemagglutintin sequence data based on a joint random forest method. Scientific Reports, 2017, 7, 1545.	3.3	40
11	On the Similarity of DNA Primary Sequences Based on 5-D Representation. Journal of Mathematical Chemistry, 2007, 42, 47-57.	1.5	39
12	Incorporating Secondary Features into the General form of Chou's PseAAC for Predicting Protein Structural Class. Protein and Peptide Letters, 2012, 19, 1133-1138.	0.9	36
13	Screening drug-target interactions with positive-unlabeled learning. Scientific Reports, 2017, 7, 8087.	3.3	35
14	A group of 3D graphical representation of DNA sequences based on dual nucleotides. International Journal of Quantum Chemistry, 2008, 108, 1485-1490.	2.0	34
15	Matrix completion with side information and its applications in predicting the antigenicity of influenza viruses. Bioinformatics, 2017, 33, 3195-3201.	4.1	33
16	Scalable One-Pass Self-Representation Learning for Hyperspectral Band Selection. IEEE Transactions on Geoscience and Remote Sensing, 2019, 57, 4360-4374.	6.3	32
17	Global Similarity Method Based on a Two-tier Random Walk for the Prediction of microRNA–Disease Association. Scientific Reports, 2018, 8, 6481	3.3	31
18	Predicting Apoptosis Protein Subcellular Location with PseAAC by Incorporating Tripeptide Composition. Protein and Peptide Letters, 2011, 18, 1086-1092.	0.9	30

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19	A new graphical coding of DNA sequence and its similarity calculation. Physica A: Statistical Mechanics and Its Applications, 2013, 392, 4663-4667.	2.6	30
20	Subcellular localization prediction of apoptosis proteins based on evolutionary information and support vector machine. Artificial Intelligence in Medicine, 2017, 78, 41-46.	6.5	29
21	Improved Pre-miRNAs Identification Through Mutual Information of Pre-miRNA Sequences and Structures. Frontiers in Genetics, 2019, 10, 119.	2.3	28
22	A 2D graphical representation of DNA sequence based on dual nucleotides and its application. International Journal of Quantum Chemistry, 2009, 109, 948-958.	2.0	26
23	A novel graphical representation of protein sequences and its application. Journal of Computational Chemistry, 2011, 32, 2539-2544.	3.3	25
24	Coronavirus phylogeny based on triplets of nucleic acids bases. Chemical Physics Letters, 2006, 421, 313-318.	2.6	24
25	RNA secondary structure 2D graphical representation without degeneracy. International Journal of Quantum Chemistry, 2006, 106, 1749-1755.	2.0	21
26	Improved low-rank matrix recovery method for predicting miRNA-disease association. Scientific Reports, 2017, 7, 6007.	3.3	21
27	Prediction of Protein Subcellular Localization Based on Fusion of Multi-view Features. Molecules, 2019, 24, 919.	3.8	21
28	A novel feature selection method based on CFS in cancer recognition. , 2012, , .		20
29	Predicting Influenza Antigenicity by Matrix Completion With Antigen and Antiserum Similarity. Frontiers in Microbiology, 2018, 9, 2500.	3.5	16
30	Uncover miRNA-Disease Association by Exploiting Global Network Similarity. PLoS ONE, 2016, 11, e0166509.	2.5	16
31	Local-View-Assisted Discriminative Band Selection With Hypergraph Autolearning for Hyperspectral Image Classification. IEEE Transactions on Geoscience and Remote Sensing, 2020, 58, 2042-2055.	6.3	15
32	Multiple ant colony algorithm method for selecting tag SNPs. Journal of Biomedical Informatics, 2012, 45, 931-937.	4.3	14
33	A novel information diffusion method based on network consistency for identifying disease related microRNAs. RSC Advances, 2018, 8, 36675-36690.	3.6	14
34	A co-expression modules based gene selection for cancer recognition. Journal of Theoretical Biology, 2014, 362, 75-82.	1.7	13
35	Learning a Weighted Meta-Sample Based Parameter Free Sparse Representation Classification for Microarray Data. PLoS ONE, 2014, 9, e104314.	2.5	13
36	Informative SNPs Selection Based on Two-Locus and Multilocus Linkage Disequilibrium: Criteria of Max-Correlation and Min-Redundancy. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 688-695.	3.0	12

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37	Improving gene regulatory network structure using redundancy reduction in the MRNET algorithm. RSC Advances, 2017, 7, 23222-23233.	3.6	11
38	A graphical method to construct a phylogenetic tree. International Journal of Quantum Chemistry, 2006, 106, 1998-2005.	2.0	10
39	RNA Secondary Structure 3D Graphical Representation Without Degeneracy. Journal of Mathematical Chemistry, 2006, 39, 629-636.	1.5	10
40	On a four-dimensional representation of RNA secondary structures. Journal of Mathematical Chemistry, 2007, 42, 1015-1022.	1.5	10
41	A Hierarchical Clustering Method of Selecting Kernel SNP to Unify Informative SNP and Tag SNP. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 113-122.	3.0	10
42	A novel information fusion strategy based on a regularized framework for identifying disease-related microRNAs. RSC Advances, 2017, 7, 44447-44455.	3.6	10
43	Network-based collaborative filtering recommendation model for inferring novel disease-related miRNAs. RSC Advances, 2017, 7, 44961-44971.	3.6	10
44	Semi-Supervised Maximum Discriminative Local Margin for Gene Selection. Scientific Reports, 2018, 8, 8619.	3.3	10
45	A Novel Method to Select Informative SNPs and Their Application in Genetic Association Studies. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1529-1534.	3.0	9
46	Maxdenominator Reweighted Sparse Representation for Tumor Classification. Scientific Reports, 2017, 7, 46030.	3.3	9
47	Matrix-Based Margin-Maximization Band Selection With Data-Driven Diversity for Hyperspectral Image Classification. IEEE Transactions on Geoscience and Remote Sensing, 2018, 56, 7294-7309.	6.3	9
48	Novel method for analyzing proteome. International Journal of Quantum Chemistry, 2007, 107, 1295-1300.	2.0	8
49	A binary coding method of RNA secondary structure and its application. Journal of Computational Chemistry, 2009, 30, 2205-2212.	3.3	7
50	Gene Regulatory Network Inferences Using a Maximum-Relevance and Maximum-Significance Strategy. PLoS ONE, 2016, 11, e0166115.	2.5	7
51	New multilocus linkage disequilibrium measure for tag SNP selection. Journal of Bioinformatics and Computational Biology, 2017, 15, 1750001.	0.8	6
52	New 3D graphical representation for RNA structure analysis and its application in the pre-miRNA identification of plants. RSC Advances, 2018, 8, 30833-30841.	3.6	6
53	Using Multi-Instance Hierarchical Clustering Learning System to Predict Yeast Gene Function. PLoS ONE, 2014, 9, e90962.	2.5	6
54	A new technique for generating pathogenic barcodes in breast cancer susceptibility analysis. Journal of Theoretical Biology, 2015, 366, 84-90.	1.7	5

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55	Gene function prediction based on combining gene ontology hierarchy with multi-instance multi-label learning. RSC Advances, 2018, 8, 28503-28509.	3.6	5
56	An Improved Binary Differential Evolution Algorithm to Infer Tumor Phylogenetic Trees. BioMed Research International, 2017, 2017, 1-13.	1.9	4
57	Predicting Drug-Target Interactions with Neighbor Interaction Information and Discriminative Low-rank Representation. Current Protein and Peptide Science, 2018, 19, 455-467.	1.4	3
58	Fisher Discrimination Regularized Robust Coding Based on a Local Center for Tumor Classification. Scientific Reports, 2018, 8, 9152.	3.3	2
59	Incorporating Secondary Structural Features into Sequence Information for Predicting Protein Structural Class. Protein and Peptide Letters, 2013, 20, 1079-1087.	0.9	2
60	RNA secondary structure alignment based on an extended binary coding method. International Journal of Quantum Chemistry, 2011, 111, 978-982.	2.0	1
61	Subcellular localization prediction of apoptosis proteins based on the data mining for amino acid index database. , 2013, , .		1
62	Accelerating processing speed in pathway research based on GPU. , 2013, , .		0
63	Computational Tools for Investigating Pathogen, Pathogen-Host Interaction, and Infectious Disease. Canadian Journal of Infectious Diseases and Medical Microbiology, 2018, 2018, 1-2.	1.9	0