

Javad Zahiri

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.

44
papers

564
citations

13
h-index

23
g-index

50
ext. papers

857
ext. citations

3.7
avg, IF

4.57
L-index

#	Paper	IF	Citations
44	PPIevo: protein-protein interaction prediction from PSSM based evolutionary information. <i>Genomics</i> , 2013 , 102, 237-42	4.3	94
43	Computational Prediction of Protein-Protein Interaction Networks: Algorithms and Resources. <i>Current Genomics</i> , 2013 , 14, 397-414	2.6	83
42	Posttranslational modifications in proteins: resources, tools and prediction methods. <i>Database: the Journal of Biological Databases and Curation</i> , 2021 , 2021,	5	48
41	LocFuse: human protein-protein interaction prediction via classifier fusion using protein localization information. <i>Genomics</i> , 2014 , 104, 496-503	4.3	40
40	Predicting protein-protein interactions between human and hepatitis C virus via an ensemble learning method. <i>Molecular BioSystems</i> , 2014 , 10, 3147-54		35
39	VIS/NIR imaging application for honey floral origin determination. <i>Infrared Physics and Technology</i> , 2017 , 86, 218-225	2.7	31
38	Digging deeper into volatile organic compounds associated with cancer. <i>Biology Methods and Protocols</i> , 2019 , 4, bpz014	2.4	25
37	rpiCOOL: A tool for In Silico RNA-protein interaction detection using random forest. <i>Journal of Theoretical Biology</i> , 2016 , 402, 1-8	2.3	24
36	Gene co-expression network reconstruction: a review on computational methods for inferring functional information from plant-based expression data. <i>Plant Biotechnology Reports</i> , 2017 , 11, 71-86	2.5	18
35	Tag SNP selection via a genetic algorithm. <i>Journal of Biomedical Informatics</i> , 2010 , 43, 800-4	10.2	18
34	A systems biology approach to reconcile metabolic network models with application to <i>Synechocystis</i> sp. PCC 6803 for biofuel production. <i>Molecular BioSystems</i> , 2016 , 12, 2552-61		17
33	Evaluation of post-translational modifications in histone proteins: A review on histone modification defects in developmental and neurological disorders. <i>Journal of Biosciences</i> , 2020 , 45, 1	2.3	16
32	Protein complex prediction: A survey. <i>Genomics</i> , 2020 , 112, 174-183	4.3	14
31	Novel BDNF-regulatory microRNAs in neurodegenerative disorders pathogenesis: An in silico study. <i>Computational Biology and Chemistry</i> , 2019 , 83, 107153	3.6	10
30	Multi-criteria sequencing problem in mixed-model synchronous assembly lines. <i>International Journal of Advanced Manufacturing Technology</i> , 2013 , 67, 983-993	3.2	10
29	A novel efficient dynamic programming algorithm for haplotype block partitioning. <i>Journal of Theoretical Biology</i> , 2010 , 267, 164-70	2.3	9
28	AntAngioCOOL: computational detection of anti-angiogenic peptides. <i>Journal of Translational Medicine</i> , 2019 , 17, 71	8.5	8

27	Cancer Odor Database (COD): a critical databank for cancer diagnosis research. <i>Database: the Journal of Biological Databases and Curation</i> , 2017 , 2017,	5	8
26	afpCOOL: A tool for antifreeze protein prediction. <i>Heliyon</i> , 2018 , 4, e00705	3.6	8
25	Bioinformatic tools for DNA methylation and histone modification: A survey. <i>Genomics</i> , 2021 , 113, 1098-1113	4.13	6
24	Unraveling the transcriptional complexity of compactness in sistan grape cluster. <i>Plant Science</i> , 2018 , 270, 198-208	5.3	4
23	RepCOOL: computational drug repositioning via integrating heterogeneous biological networks. <i>Journal of Translational Medicine</i> , 2020 , 18, 375	8.5	4
22	Gibberellin causes wide transcriptional modifications in the early stage of grape cluster development. <i>Genomics</i> , 2020 , 112, 820-830	4.3	4
21	Scatter-search with support vector machine for prediction of relative solvent accessibility. <i>EXCLI Journal</i> , 2013 , 12, 52-63	2.4	3
20	Computational Detection of piRNA in Human Using Support Vector Machine. <i>Avicenna Journal of Medical Biotechnology</i> , 2016 , 8, 36-41	1.4	3
19	Identification, Prediction and Data Analysis of Noncoding RNAs: A Review. <i>Medicinal Chemistry</i> , 2019 , 15, 216-230	1.8	3
18	Moonlighting protein prediction using physico-chemical and evolutionary properties via machine learning methods. <i>BMC Bioinformatics</i> , 2021 , 22, 261	3.6	3
17	Evaluation of post-translational modifications in histone proteins: A review on histone modification defects in developmental and neurological disorders. <i>Journal of Biosciences</i> , 2020 , 45,	2.3	3
16	Identification of the Molecular Events Involved in the Development of Prefrontal Cortex Through the Analysis of RNA-Seq Data From BrainSpan. <i>ASN Neuro</i> , 2019 , 11, 1759091419854627	5.3	2
15	Computational Prediction of Proteins Sumoylation: A Review on the Methods and Databases. <i>Journal of Nanomedicine Research</i> , 2016 , 3,	9	2
14	Analysis of candidate genes has proposed the role of y chromosome in human prostate cancer. <i>Iranian Journal of Cancer Prevention</i> , 2014 , 7, 204-11		2
13	Prediction of Gene Co-Expression by Quantifying Heterogeneous Features. <i>Current Bioinformatics</i> , 2015 , 10, 414-424	4.7	2
12	Proteomic profiling of the rat hippocampus from the kindling and pilocarpine models of epilepsy: potential targets in calcium regulatory network. <i>Scientific Reports</i> , 2021 , 11, 8252	4.9	2
11	Performance evaluation measures for protein complex prediction. <i>Genomics</i> , 2019 , 111, 1483-1492	4.3	2
10	Cross talk between energy cost and expression of Methyl Jasmonate-regulated genes: from DNA to protein. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2019 , 28, 230-243	1.6	1

9	PSSMCOOL: a comprehensive R package for generating evolutionary-based descriptors of protein sequences from PSSM profiles.. <i>Biology Methods and Protocols</i> , 2022 , 7, bpac008	2.4	1
8	Investigation of etiology-specific alterations in the gut microbiota in liver cirrhosis. <i>Expert Review of Gastroenterology and Hepatology</i> , 2021 , 1-7	4.2	0
7	Drug repositioning based on gene expression data for human HER2-positive breast cancer. <i>Archives of Biochemistry and Biophysics</i> , 2021 , 712, 109043	4.1	0
6	OligoCOOL: A mobile application for nucleotide sequence analysis. <i>Biochemistry and Molecular Biology Education</i> , 2019 , 47, 201-206	1.3	
5	iMet: A graphical user interface software tool to merge metabolic networks. <i>Heliyon</i> , 2019 , 5, e01766	3.6	
4	Using ortholog information from multiple species to predict barley protein-protein interaction network. <i>Plant Gene</i> , 2022 , 100355	3.1	
3	Reconstruction of Intercellular Signaling Network by Cytokine-Receptor Interactions. <i>Iranian Journal of Biotechnology</i> , 2021 , 19, e2560	1	
2	Investigation and characterization of human gut phageome in advanced liver cirrhosis of defined etiologies.. <i>Gut Pathogens</i> , 2022 , 14, 9	5.4	
1	Filtering of the Gene Signature as the Predictors of Cisplatin-Resistance in Ovarian Cancer. <i>Iranian Journal of Biotechnology</i> , 2021 , 19, e2643	1	