Javad Zahiri

List of Publications by Year in descending order

44 papers	1,185 citations	623734 14 h-index	395702 33 g-index
50 all docs	50 docs citations	50 times ranked	1135 citing authors

#	Article	IF	Citations
1	Using ortholog information from multiple species to predict barley protein-protein interaction network. Plant Gene, 2022, , 100355.	2.3	1
2	PSSMCOOL: a comprehensive R package for generating evolutionary-based descriptors of protein sequences from PSSM profiles. Biology Methods and Protocols, 2022, 7, bpac008.	2.2	12
3	Investigation and characterization of human gut phageome in advanced liver cirrhosis of defined etiologies. Gut Pathogens, 2022, 14, 9.	3.4	1
4	Post-translational modifications in proteins: resources, tools and prediction methods. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	3.0	277
5	Proteomic profiling of the rat hippocampus from the kindling and pilocarpine models of epilepsy: potential targets in calcium regulatory network. Scientific Reports, 2021, 11, 8252.	3.3	15
6	Bioinformatic tools for DNA methylation and histone modification: A survey. Genomics, 2021, 113, 1098-1113.	2.9	11
7	Moonlighting protein prediction using physico-chemical and evolutional properties via machine learning methods. BMC Bioinformatics, 2021, 22, 261.	2.6	8
8	Drug repositioning based on gene expression data for human HER2-positive breast cancer. Archives of Biochemistry and Biophysics, 2021, 712, 109043.	3.0	4
9	Investigation of etiology-specific alterations in the gut microbiota in liver cirrhosis. Expert Review of Gastroenterology and Hepatology, 2021, 15, 1435-1441.	3.0	3
10	Reconstruction of Intercellular Signaling Network by Cytokine-Receptor Interactions. Iranian Journal of Biotechnology, 2021, 19, e2560.	0.3	0
11	Filtering of the Gene Signature as the Predictors of Cisplatin-Resistance in Ovarian Cancer. Iranian Journal of Biotechnology, 2021, 19, e2643.	0.3	0
12	Protein complex prediction: A survey. Genomics, 2020, 112, 174-183.	2.9	38
13	Gibberellin causes wide transcriptional modifications in the early stage of grape cluster development. Genomics, 2020, 112, 820-830.	2.9	15
14	RepCOOL: computational drug repositioning via integrating heterogeneous biological networks. Journal of Translational Medicine, 2020, 18, 375.	4.4	13
15	Evaluation of post-translational modifications in histone proteins: A review on histone modification defects in developmental and neurological disorders. Journal of Biosciences, 2020, 45, 1.	1.1	79
16	Evaluation of post-translational modifications in histone proteins: A review on histone modification defects in developmental and neurological disorders. Journal of Biosciences, 2020, 45, .	1.1	7
17	Novel BDNF-regulatory microRNAs in neurodegenerative disorders pathogenesis: An in silico study. Computational Biology and Chemistry, 2019, 83, 107153.	2.3	16
18	OligoCOOL: A mobile application for nucleotide sequence analysis. Biochemistry and Molecular Biology Education, 2019, 47, 201-206.	1.2	0

#	ARTICLE	IF	CITATIONS
19	Identification of the Molecular Events Involved in the Development of Prefrontal Cortex Through the Analysis of RNA-Seq Data From BrainSpan. ASN Neuro, 2019, 11, 175909141985462.	2.7	3
20	iMet: A graphical user interface software tool to merge metabolic networks. Heliyon, 2019, 5, e01766.	3.2	1
21	AntAngioCOOL: computational detection of anti-angiogenic peptides. Journal of Translational Medicine, 2019, 17, 71.	4.4	12
22	Digging deeper into volatile organic compounds associated with cancer. Biology Methods and Protocols, 2019, 4, bpz014.	2.2	75
23	Cross talk between energy cost and expression of Methyl Jasmonate-regulated genes: from DNA to protein. Journal of Plant Biochemistry and Biotechnology, 2019, 28, 230-243.	1.7	1
24	Performance evaluation measures for protein complex prediction. Genomics, 2019, 111, 1483-1492.	2.9	2
25	Identification, Prediction and Data Analysis of Noncoding RNAs: A Review. Medicinal Chemistry, 2019, 15, 216-230.	1.5	4
26	Unraveling the transcriptional complexity of compactness in sistan grape cluster. Plant Science, 2018, 270, 198-208.	3.6	10
27	afpCOOL: A tool for antifreeze protein prediction. Heliyon, 2018, 4, e00705.	3.2	16
28	Gene co-expression network reconstruction: a review on computational methods for inferring functional information from plant-based expression data. Plant Biotechnology Reports, 2017, 11, 71-86.	1.5	34
29	VIS/NIR imaging application for honey floral origin determination. Infrared Physics and Technology, 2017, 86, 218-225.	2.9	48
30	Cancer Odor Database (COD): a critical databank for cancer diagnosis research. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	3.0	16
31	A systems biology approach to reconcile metabolic network models with application to Synechocystis sp. PCC 6803 for biofuel production. Molecular BioSystems, 2016, 12, 2552-2561.	2.9	19
32	rpiCOOL: A tool for In Silico RNA–protein interaction detection using random forest. Journal of Theoretical Biology, 2016, 402, 1-8.	1.7	35
33	Computational Prediction of Proteins Sumoylation: A Review on the Methods and Databases. Journal of Nanomedicine Research, 2016, 3, .	1.8	2
34	Computational Detection of piRNA in Human Using Support Vector Machine. Avicenna Journal of Medical Biotechnology, 2016, 8, 36-41.	0.3	3
35	Prediction of Gene Co-Expression by Quantifying Heterogeneous Features. Current Bioinformatics, 2015, 10, 414-424.	1.5	2
36	LocFuse: Human protein–protein interaction prediction via classifier fusion using protein localization information. Genomics, 2014, 104, 496-503.	2.9	51

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37	Predicting protein–protein interactions between human and hepatitis C virus via an ensemble learning method. Molecular BioSystems, 2014, 10, 3147-3154.	2.9	46
38	Analysis of candidate genes has proposed the role of y chromosome in human prostate cancer. Iranian Journal of Cancer Prevention, 2014, 7, 204-11.	0.7	3
39	Multi-criteria sequencing problem in mixed-model synchronous assembly lines. International Journal of Advanced Manufacturing Technology, 2013, 67, 983-993.	3.0	10
40	PPIevo : Protein–protein interaction prediction from PSSM based evolutionary information. Genomics, 2013, 102, 237-242.	2.9	131
41	Computational Prediction of Protein–Protein Interaction Networks: Algorithms and Resources. Current Genomics, 2013, 14, 397-414.	1.6	119
42	Scatter-search with support vector machine for prediction of relative solvent accessibility. EXCLI Journal, 2013, 12, 52-63.	0.7	3
43	A novel efficient dynamic programming algorithm for haplotype block partitioning. Journal of Theoretical Biology, 2010, 267, 164-170.	1.7	10
44	Tag SNP selection via a genetic algorithm. Journal of Biomedical Informatics, 2010, 43, 800-804.	4.3	24