

# Javad Zahiri

## List of Publications by Year in descending order

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Version: 2024-02-01

44  
papers

1,185  
citations

623188

14  
h-index

395343

33  
g-index

50  
all docs

50  
docs citations

50  
times ranked

1135  
citing authors

#	ARTICLE	IF	CITATIONS
1	Post-translational modifications in proteins: resources, tools and prediction methods. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	1.4	277
2	PPlevo : Proteinâ€“protein interaction prediction from PSSM based evolutionary information. Genomics, 2013, 102, 237-242.	1.3	131
3	Computational Prediction of Proteinâ€“Protein Interaction Networks: Algorithms and Resources. Current Genomics, 2013, 14, 397-414.	0.7	119
4	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.	0.5	79
5	Digging deeper into volatile organic compounds associated with cancer. Biology Methods and Protocols, 2019, 4, bpz014.	1.0	75
6	LocFuse: Human proteinâ€“protein interaction prediction via classifier fusion using protein localization information. Genomics, 2014, 104, 496-503.	1.3	51
7	VIS/NIR imaging application for honey floral origin determination. Infrared Physics and Technology, 2017, 86, 218-225.	1.3	48
8	Predicting proteinâ€“protein interactions between human and hepatitis C virus via an ensemble learning method. Molecular BioSystems, 2014, 10, 3147-3154.	2.9	46
9	Protein complex prediction: A survey. Genomics, 2020, 112, 174-183.	1.3	38
10	rpiCOOL: A tool for In Silico RNAâ€“protein interaction detection using random forest. Journal of Theoretical Biology, 2016, 402, 1-8.	0.8	35
11	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.	0.9	34
12	Tag SNP selection via a genetic algorithm. Journal of Biomedical Informatics, 2010, 43, 800-804.	2.5	24
13	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
14	Cancer Odor Database (COD): a critical databank for cancer diagnosis research. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	1.4	16
15	afpCOOL: A tool for antifreeze protein prediction. Heliyon, 2018, 4, e00705.	1.4	16
16	Novel BDNF-regulatory microRNAs in neurodegenerative disorders pathogenesis: An in silico study. Computational Biology and Chemistry, 2019, 83, 107153.	1.1	16
17	Gibberellin causes wide transcriptional modifications in the early stage of grape cluster development. Genomics, 2020, 112, 820-830.	1.3	15
18	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.	1.6	15

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19	RepCOOL: computational drug repositioning via integrating heterogeneous biological networks. <i>Journal of Translational Medicine</i> , 2020, 18, 375.	1.8	13
20	AntAngioCOOL: computational detection of anti-angiogenic peptides. <i>Journal of Translational Medicine</i> , 2019, 17, 71.	1.8	12
21	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.	1.0	12
22	Bioinformatic tools for DNA methylation and histone modification: A survey. <i>Genomics</i> , 2021, 113, 1098-1113.	1.3	11
23	A novel efficient dynamic programming algorithm for haplotype block partitioning. <i>Journal of Theoretical Biology</i> , 2010, 267, 164-170.	0.8	10
24	Multi-criteria sequencing problem in mixed-model synchronous assembly lines. <i>International Journal of Advanced Manufacturing Technology</i> , 2013, 67, 983-993.	1.5	10
25	Unraveling the transcriptional complexity of compactness in sistan grape cluster. <i>Plant Science</i> , 2018, 270, 198-208.	1.7	10
26	Moonlighting protein prediction using physico-chemical and evolutionary properties via machine learning methods. <i>BMC Bioinformatics</i> , 2021, 22, 261.	1.2	8
27	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, .	0.5	7
28	Drug repositioning based on gene expression data for human HER2-positive breast cancer. <i>Archives of Biochemistry and Biophysics</i> , 2021, 712, 109043.	1.4	4
29	Identification, Prediction and Data Analysis of Noncoding RNAs: A Review. <i>Medicinal Chemistry</i> , 2019, 15, 216-230.	0.7	4
30	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, 175909141985462.	1.5	3
31	Investigation of etiology-specific alterations in the gut microbiota in liver cirrhosis. <i>Expert Review of Gastroenterology and Hepatology</i> , 2021, 15, 1435-1441.	1.4	3
32	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.	0.7	3
33	Scatter-search with support vector machine for prediction of relative solvent accessibility. <i>EXCLI Journal</i> , 2013, 12, 52-63.	0.5	3
34	Computational Detection of piRNA in Human Using Support Vector Machine. <i>Avicenna Journal of Medical Biotechnology</i> , 2016, 8, 36-41.	0.2	3
35	Performance evaluation measures for protein complex prediction. <i>Genomics</i> , 2019, 111, 1483-1492.	1.3	2
36	Computational Prediction of Proteins Sumoylation: A Review on the Methods and Databases. <i>Journal of Nanomedicine Research</i> , 2016, 3, .	1.8	2

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37	Prediction of Gene Co-Expression by Quantifying Heterogeneous Features. <i>Current Bioinformatics</i> , 2015, 10, 414-424.	0.7	2
38	iMet: A graphical user interface software tool to merge metabolic networks. <i>Heliyon</i> , 2019, 5, e01766.	1.4	1
39	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.	0.9	1
40	Using ortholog information from multiple species to predict barley protein-protein interaction network. <i>Plant Gene</i> , 2022, , 100355.	1.4	1
41	Investigation and characterization of human gut phageome in advanced liver cirrhosis of defined etiologies. <i>Gut Pathogens</i> , 2022, 14, 9.	1.6	1
42	OligoCOOL: A mobile application for nucleotide sequence analysis. <i>Biochemistry and Molecular Biology Education</i> , 2019, 47, 201-206.	0.5	0
43	Reconstruction of Intercellular Signaling Network by Cytokine-Receptor Interactions. <i>Iranian Journal of Biotechnology</i> , 2021, 19, e2560.	0.3	0
44	Filtering of the Gene Signature as the Predictors of Cisplatin-Resistance in Ovarian Cancer. <i>Iranian Journal of Biotechnology</i> , 2021, 19, e2643.	0.3	0