

Ali Masoudi-Nejad

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.

129
papers

2,507
citations

28
h-index

45
g-index

143
ext. papers

3,119
ext. citations

4.4
avg, IF

5.56
L-index

#	Paper	IF	Citations
129	Predictive genomics: a cancer hallmark network framework for predicting tumor clinical phenotypes using genome sequencing data. <i>Seminars in Cancer Biology</i> , 2015 , 30, 4-12	12.7	176
128	Kavosh: a new algorithm for finding network motifs. <i>BMC Bioinformatics</i> , 2009 , 10, 318	3.6	144
127	EGassembler: online bioinformatics service for large-scale processing, clustering and assembling ESTs and genomic DNA fragments. <i>Nucleic Acids Research</i> , 2006 , 34, W459-62	20.1	126
126	PPlevo: protein-protein interaction prediction from PSSM based evolutionary information. <i>Genomics</i> , 2013 , 102, 237-42	4.3	94
125	MODA: an efficient algorithm for network motif discovery in biological networks. <i>Genes and Genetic Systems</i> , 2009 , 84, 385-95	1.4	92
124	Transfer of rye chromosome segments to wheat by a gametocidal system. <i>Chromosome Research</i> , 2002 , 10, 349-57	4.4	86
123	Computational Prediction of Protein-Protein Interaction Networks: Algorithms and Resources. <i>Current Genomics</i> , 2013 , 14, 397-414	2.6	83
122	Reconstruction of an integrated genome-scale co-expression network reveals key modules involved in lung adenocarcinoma. <i>PLoS ONE</i> , 2013 , 8, e67552	3.7	76
121	Alterations in cancer cell metabolism: the Warburg effect and metabolic adaptation. <i>Genomics</i> , 2015 , 105, 275-81	4.3	66
120	Drug-target interaction prediction via chemogenomic space: learning-based methods. <i>Expert Opinion on Drug Metabolism and Toxicology</i> , 2014 , 10, 1273-87	5.5	60
119	A hybrid gene selection algorithm for microarray cancer classification using genetic algorithm and learning automata. <i>Informatics in Medicine Unlocked</i> , 2017 , 9, 246-254	5.3	58
118	Building blocks of biological networks: a review on major network motif discovery algorithms. <i>IET Systems Biology</i> , 2012 , 6, 164-74	1.4	48
117	Drug-target interaction prediction from PSSM based evolutionary information. <i>Journal of Pharmacological and Toxicological Methods</i> , 2016 , 78, 42-51	1.7	45
116	FeatureSelect: a software for feature selection based on machine learning approaches. <i>BMC Bioinformatics</i> , 2019 , 20, 170	3.6	44
115	Controllability in cancer metabolic networks according to drug targets as driver nodes. <i>PLoS ONE</i> , 2013 , 8, e79397	3.7	44
114	LocFuse: human protein-protein interaction prediction via classifier fusion using protein localization information. <i>Genomics</i> , 2014 , 104, 496-503	4.3	40
113	QuateXelero: an accelerated exact network motif detection algorithm. <i>PLoS ONE</i> , 2013 , 8, e68073	3.7	39

112	Drug databases and their contributions to drug repurposing. <i>Genomics</i> , 2020 , 112, 1087-1095	4.3	38
111	Reconstruction of <i>Arabidopsis thaliana</i> fully integrated small RNA pathway. <i>Functional and Integrative Genomics</i> , 2009 , 9, 419-32	3.8	37
110	Emerging roles of epigenetic mechanisms in Parkinson's disease. <i>Functional and Integrative Genomics</i> , 2011 , 11, 523-37	3.8	35
109	Metabolic cancer biology: structural-based analysis of cancer as a metabolic disease, new sights and opportunities for disease treatment. <i>Seminars in Cancer Biology</i> , 2015 , 30, 21-9	12.7	31
108	Drug-target and disease networks: polypharmacology in the post-genomic era. <i>In Silico Pharmacology</i> , 2013 , 1, 17	4.3	31
107	Modeling of tumor progression in NSCLC and intrinsic resistance to TKI in loss of PTEN expression. <i>PLoS ONE</i> , 2012 , 7, e48004	3.7	31
106	EGENES: transcriptome-based plant database of genes with metabolic pathway information and expressed sequence tag indices in KEGG. <i>Plant Physiology</i> , 2007 , 144, 857-66	6.6	30
105	DeepCDA: deep cross-domain compound-protein affinity prediction through LSTM and convolutional neural networks. <i>Bioinformatics</i> , 2020 , 36, 4633-4642	7.2	29
104	Molecular epidemiology of hepatitis C virus among injection drug users in Iran: a slight change in prevalence of HCV genotypes over time. <i>Archives of Virology</i> , 2012 , 157, 1959-65	2.6	29
103	Protein Clustering and Interactome Analysis in Parkinson and Alzheimer's Diseases. <i>Archives of Iranian Medicine</i> , 2016 , 19, 101-9	2.4	29
102	Dissection of rye chromosome 1R in common wheat. <i>Genes and Genetic Systems</i> , 2008 , 83, 43-53	1.4	28
101	Trader as a new optimization algorithm predicts drug-target interactions efficiently. <i>Scientific Reports</i> , 2019 , 9, 9348	4.9	27
100	Bioinformatics study of the 3-hydroxy-3-methylglutaryl-coenzyme A reductase (HMGR) gene in Gramineae. <i>Molecular Biology Reports</i> , 2012 , 39, 8925-35	2.8	27
99	Genome scale modeling in systems biology: algorithms and resources. <i>Current Genomics</i> , 2014 , 15, 130-52.6	5.6	27
98	Cancer systems biology and modeling: microscopic scale and multiscale approaches. <i>Seminars in Cancer Biology</i> , 2015 , 30, 60-9	12.7	26
97	An alternative to radiation hybrid mapping for large-scale genome analysis in barley. <i>Molecular Genetics and Genomics</i> , 2005 , 274, 589-94	3.1	25
96	Detection of novel biomarkers for early detection of Non-Muscle-Invasive Bladder Cancer using Competing Endogenous RNA network analysis. <i>Scientific Reports</i> , 2019 , 9, 8434	4.9	24
95	Information theory in systems biology. Part II: protein-protein interaction and signaling networks. <i>Seminars in Cell and Developmental Biology</i> , 2016 , 51, 14-23	7.5	22

94	Information theory in systems biology. Part I: Gene regulatory and metabolic networks. <i>Seminars in Cell and Developmental Biology</i> , 2016 , 51, 3-13	7.5	22
93	HomoTarget: a new algorithm for prediction of microRNA targets in Homo sapiens. <i>Genomics</i> , 2013 , 101, 94-100	4.3	22
92	KEGG bioinformatics resource for plant genomics research. <i>Methods in Molecular Biology</i> , 2007 , 406, 437-58	1.4	22
91	DrugR+: A comprehensive relational database for drug repurposing, combination therapy, and replacement therapy. <i>Computers in Biology and Medicine</i> , 2019 , 109, 254-262	7	21
90	mRNA-miRNA bipartite network reconstruction to predict prognostic module biomarkers in colorectal cancer stage differentiation. <i>Molecular BioSystems</i> , 2017 , 13, 2168-2180		21
89	LncRNA and mRNA integration network reconstruction reveals novel key regulators in esophageal squamous-cell carcinoma. <i>Genomics</i> , 2019 , 111, 76-89	4.3	20
88	Molecular cloning, sequencing, and chromosome mapping of a 1A-encoded omega-type prolamin sequence from wheat. <i>Genome</i> , 2002 , 45, 661-9	2.4	19
87	Identification of biomarkers in common chronic lung diseases by co-expression networks and drug-target interactions analysis. <i>Molecular Medicine</i> , 2020 , 26, 9	6.2	17
86	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
85	Candidate novel long noncoding RNAs, MicroRNAs and putative drugs for Parkinson's disease using a robust and efficient genome-wide association study. <i>Genomics</i> , 2017 , 109, 158-164	4.3	16
84	Microarray gene expression analysis of the human airway in patients exposed to sulfur mustard. <i>Journal of Receptor and Signal Transduction Research</i> , 2014 , 34, 283-9	2.6	16
83	Network-based expression analysis reveals key genes related to glucocorticoid resistance in infant acute lymphoblastic leukemia. <i>Cellular Oncology (Dordrecht)</i> , 2017 , 40, 33-45	7.2	16
82	N4: a precise and highly sensitive promoter predictor using neural network fed by nearest neighbors. <i>Genes and Genetic Systems</i> , 2009 , 84, 425-30	1.4	14
81	Predicting brain network changes in Alzheimer's disease with link prediction algorithms. <i>Molecular BioSystems</i> , 2017 , 13, 725-735		13
80	Deep Transferable Compound Representation across Domains and Tasks for Low Data Drug Discovery. <i>Journal of Chemical Information and Modeling</i> , 2019 , 59, 4528-4539	6.1	13
79	Human RNAi pathway: crosstalk with organelles and cells. <i>Functional and Integrative Genomics</i> , 2014 , 14, 31-46	3.8	13
78	A multimodal deep learning-based drug repurposing approach for treatment of COVID-19. <i>Molecular Diversity</i> , 2021 , 25, 1717-1730	3.1	13
77	Candidate gene prioritization. <i>Molecular Genetics and Genomics</i> , 2012 , 287, 679-98	3.1	12

76	Large-scale gene co-expression network as a source of functional annotation for cattle genes. <i>BMC Genomics</i> , 2016 , 17, 846	4.5	12
75	Modeling and analysis of abnormality detection in biomolecular nano-networks. <i>Nano Communication Networks</i> , 2012 , 3, 229-241	2.9	11
74	Centrality Measures in Biological Networks. <i>Current Bioinformatics</i> , 2014 , 9, 426-441	4.7	11
73	Deep Learning in Drug Target Interaction Prediction: Current and Future Perspectives. <i>Current Medicinal Chemistry</i> , 2021 , 28, 2100-2113	4.3	11
72	mRNA and microRNA selection for breast cancer molecular subtype stratification using meta-heuristic based algorithms. <i>Genomics</i> , 2020 , 112, 3207-3217	4.3	10
71	Normalized Similarity Index: An adjusted index to prioritize article citations. <i>Journal of Informetrics</i> , 2013 , 7, 91-98	3.1	10
70	Task modulates functional connectivity networks in free viewing behavior. <i>NeuroImage</i> , 2017 , 159, 289-304	3.0	10
69	RNAi pathway integration in <i>Caenorhabditis elegans</i> development. <i>Functional and Integrative Genomics</i> , 2011 , 11, 389-405	3.8	10
68	CytoKavosh: a cytoscape plug-in for finding network motifs in large biological networks. <i>PLoS ONE</i> , 2012 , 7, e43287	3.7	10
67	Genome-scale co-expression network comparison across <i>Escherichia coli</i> and <i>Salmonella enterica</i> serovar Typhimurium reveals significant conservation at the regulon level of local regulators despite their dissimilar lifestyles. <i>PLoS ONE</i> , 2014 , 9, e102871	3.7	10
66	Expression of chalcone synthase influences flavonoid content and frequency of rhizogenesis in microshoots of <i>Juglans regia</i> L.. <i>Plant Cell, Tissue and Organ Culture</i> , 2012 , 109, 51-59	2.7	9
65	Computational analysis of reciprocal association of metabolism and epigenetics in the budding yeast: a genome-scale metabolic model (GSMM) approach. <i>PLoS ONE</i> , 2014 , 9, e111686	3.7	9
64	RPINBASE: An online toolbox to extract features for predicting RNA-protein interactions. <i>Genomics</i> , 2020 , 112, 2623-2632	4.3	8
63	Pathway reconstruction of airway remodeling in chronic lung diseases: a systems biology approach. <i>PLoS ONE</i> , 2014 , 9, e100094	3.7	8
62	Introducing a panel for early detection of lung adenocarcinoma by using data integration of genomics, epigenomics, transcriptomics and proteomics. <i>Experimental and Molecular Pathology</i> , 2020 , 112, 104360	4.4	8
61	Active repurposing of drug candidates for melanoma based on GWAS, PheWAS and a wide range of omics data. <i>Molecular Medicine</i> , 2019 , 25, 30	6.2	7
60	An efficient hybrid feature selection method to identify potential biomarkers in common chronic lung inflammatory diseases. <i>Genomics</i> , 2020 , 112, 3284-3293	4.3	7
59	Comparison of gene co-expression networks in <i>Pseudomonas aeruginosa</i> and <i>Staphylococcus aureus</i> reveals conservation in some aspects of virulence. <i>Gene</i> , 2018 , 639, 1-10	3.8	7

58	Determination of the Best Concentration of Streptozotocin to Create a Diabetic Brain Using Histological Techniques. <i>Journal of Molecular Neuroscience</i> , 2016 , 59, 24-35	3.3	7
57	Differential network analysis and protein-protein interaction study reveals active protein modules in glucocorticoid resistance for infant acute lymphoblastic leukemia. <i>Molecular Medicine</i> , 2019 , 25, 36	6.2	7
56	Improved Immune Genetic Algorithm for Clustering Protein-Protein Interaction Network 2010 ,		7
55	Nonparametric simulation of signal transduction networks with semi-synchronized update. <i>PLoS ONE</i> , 2012 , 7, e39643	3.7	7
54	Sequential and Mixed Genetic Algorithm and Learning Automata (SGALA, MGALA) for Feature Selection in QSAR. <i>Iranian Journal of Pharmaceutical Research</i> , 2017 , 16, 533-553	1.1	7
53	Genome-wide DNA methylation profiling in ectopic and eutopic of endometrial tissues. <i>Journal of Assisted Reproduction and Genetics</i> , 2019 , 36, 1743-1752	3.4	6
52	Computational structure analysis of biomacromolecule complexes by interface geometry. <i>Computational Biology and Chemistry</i> , 2013 , 47, 16-23	3.6	6
51	Molecular typing of Epidermophyton floccosum isolated from patients with dermatophytosis by RAPD-PCR. <i>Journal of Basic Microbiology</i> , 2010 , 50 Suppl 1, S68-73	2.7	6
50	Identification of common microRNA between COPD and non-small cell lung cancer through pathway enrichment analysis. <i>BMC Genomic Data</i> , 2021 , 22, 41	0	6
49	Synthetic repurposing of drugs against hypertension: a datamining method based on association rules and a novel discrete algorithm. <i>BMC Bioinformatics</i> , 2020 , 21, 313	3.6	6
48	Systematic analysis of genes and diseases using PheWAS-Associated networks. <i>Computers in Biology and Medicine</i> , 2019 , 109, 311-321	7	5
47	Expectation propagation for large scale Bayesian inference of non-linear molecular networks from perturbation data. <i>PLoS ONE</i> , 2017 , 12, e0171240	3.7	5
46	Network-based expression analyses and experimental validations revealed high co-expression between Yap1 and stem cell markers compared to differentiated cells. <i>Genomics</i> , 2019 , 111, 831-839	4.3	5
45	Disease global behavior: A systematic study of the human interactome network reveals conserved topological features among categories of diseases. <i>Informatics in Medicine Unlocked</i> , 2019 , 17, 100249	5.3	5
44	GPS: Identification of disease genes by rank aggregation of multi-genomic scoring schemes. <i>Genomics</i> , 2019 , 111, 612-618	4.3	5
43	Distinguishing drug/non-drug-like small molecules in drug discovery using deep belief network. <i>Molecular Diversity</i> , 2021 , 25, 827-838	3.1	5
42	Reconstruction of the genome-scale co-expression network for the Hippo signaling pathway in colorectal cancer. <i>Computers in Biology and Medicine</i> , 2018 , 99, 76-84	7	5
41	Identification of Key Components in Colon Adenocarcinoma Using Transcriptome to Interactome Multilayer Framework. <i>Scientific Reports</i> , 2020 , 10, 4991	4.9	4

40	Genome-scale exploration of transcriptional regulation in the nisin Z producer <i>Lactococcus lactis</i> subsp. <i>lactis</i> IO-1. <i>Scientific Reports</i> , 2020 , 10, 3787	4.9	4
39	Discovering dominant pathways and signal-response relationships in signaling networks through nonparametric approaches. <i>Genomics</i> , 2013 , 102, 195-201	4.3	4
38	Target controllability with minimal mediators in complex biological networks. <i>Genomics</i> , 2020 , 112, 4938-4944	4.9	4
37	A machine learning method based on the genetic and world competitive contests algorithms for selecting genes or features in biological applications. <i>Scientific Reports</i> , 2021 , 11, 3349	4.9	4
36	In silico design of novel aptamers utilizing a hybrid method of machine learning and genetic algorithm. <i>Molecular Diversity</i> , 2021 , 25, 1395-1407	3.1	4
35	High-throughput analysis of the interactions between viral proteins and host cell RNAs. <i>Computers in Biology and Medicine</i> , 2021 , 135, 104611	7	4
34	Systems biology study of transcriptional and post-transcriptional co-regulatory network sheds light on key regulators involved in important biological processes in. <i>Physiology and Molecular Biology of Plants</i> , 2017 , 23, 331-342	2.8	3
33	Cattle infection response network and its functional modules. <i>BMC Immunology</i> , 2018 , 19, 2	3.7	3
32	Computational analysis of RNA-protein interaction interfaces via the Voronoi diagram. <i>Journal of Theoretical Biology</i> , 2012 , 293, 55-64	2.3	3
31	Genome-scale computational analysis of DNA curvature and repeats in Arabidopsis and rice uncovers plant-specific genomic properties. <i>BMC Genomics</i> , 2011 , 12, 214	4.5	3
30	Computational Detection of piRNA in Human Using Support Vector Machine. <i>Avicenna Journal of Medical Biotechnology</i> , 2016 , 8, 36-41	1.4	3
29	Novel putative drugs and key initiating genes for neurodegenerative disease determined using network-based genetic integrative analysis. <i>Journal of Cellular Biochemistry</i> , 2019 , 120, 5459-5471	4.7	3
28	Biogeography, distribution and conservation status of maples (<i>Acer L.</i>) in Iran. <i>Trees - Structure and Function</i> , 2017 , 31, 1583-1598	2.6	2
27	Micromorphological studies of leaf epidermal features in populations of maples (<i>Acer L.</i>) from Iran. <i>Phytotaxa</i> , 2017 , 299, 36	0.7	2
26	Structure-based drug repurposing against COVID-19 and emerging infectious diseases: methods, resources and discoveries. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	2
25	DNA methylation association with stage progression of head and neck squamous cell carcinoma. <i>Computers in Biology and Medicine</i> , 2021 , 134, 104473	7	2
24	Co-expressional conservation in virulence and stress related genes of three Gammaproteobacterial species: <i>Escherichia coli</i> , <i>Salmonella enterica</i> and <i>Pseudomonas aeruginosa</i> . <i>Molecular BioSystems</i> , 2015 , 11, 3137-48		1
23	SCAN-Toolbox: Structural COBRA Add-on (SCAN) for Analysing Large Metabolic Networks. <i>Current Bioinformatics</i> , 2018 , 13, 100-107	4.7	1

22	Informative Bayesian Model Selection: a method for identifying interactions in genome-wide data. <i>Molecular BioSystems</i> , 2014 , 10, 2654-62		1
21	Extracting a cancer model by enhanced ant colony optimisation algorithm. <i>International Journal of Data Mining and Bioinformatics</i> , 2014 , 10, 83-97	0.5	1
20	Insight into gene regulatory networks involved in sesame (<i>Sesamum indicum</i> L.) drought response. <i>Biologia (Poland)</i> , 2022 , 77, 1181	1.5	1
19	The importance of ECT and Salt bridges in the Formation of Insulin and its Receptor Complex by Computational Simulation. <i>Iranian Journal of Pharmaceutical Research</i> , 2018 , 17, 63-74	1.1	1
18	CatbNet: A Multi Network Analyzer for Comparing and Analyzing the Topology of Biological Networks. <i>Current Genomics</i> , 2019 , 20, 69-75	2.6	1
17	Appropriate time to apply control input to complex dynamical systems. <i>Scientific Reports</i> , 2020 , 10, 22035	4.9	1
16	Analysis of Genome-scale Expression Network in Four Major Bacterial Residents of Cystic Fibrosis Lung. <i>Current Genomics</i> , 2014 , 15, 408-18	2.6	1
15	Nodes with the highest control power play an important role at the final level of cooperation in directed networks. <i>Scientific Reports</i> , 2021 , 11, 13668	4.9	1
14	CeFunMO: A centrality based method for discovering functional motifs with application in biological networks. <i>Computers in Biology and Medicine</i> , 2016 , 76, 154-9	7	1
13	Sequence-based 5-mers highly correlated to epigenetic modifications in genes interactions. <i>Genes and Genomics</i> , 2018 , 40, 1363-1371	2.1	1
12	Pan-cancer analysis of biological events on cell cycle instability in gastrointestinal cancers with integrative scoring method.. <i>Genomics</i> , 2021 , 114, 253-265	4.3	0
11	Re-wiring and gene expression changes of AC025034.1 and ATP2B1 play complex roles in early-to-late breast cancer progression.. <i>BMC Genomic Data</i> , 2022 , 23, 6	0	0
10	Revealing transcriptional and post-transcriptional regulatory mechanisms of Eglutamyl transferase and keratin isoforms as novel cooperative biomarkers in low-grade glioma and glioblastoma multiforme. <i>Genomics</i> , 2021 , 113, 2623-2633	4.3	0
9	A propagation-based seed-centric local community detection for multilayer environment: The case study of colon adenocarcinoma. <i>PLoS ONE</i> , 2021 , 16, e0255718	3.7	0
8	Automated Plant Species Identification Using Leaf Shape-Based Classification Techniques: A Case Study on Iranian Maples. <i>Iranian Journal of Science and Technology - Transactions of Electrical Engineering</i> , 2021 , 45, 1051-1061	1.9	0
7	mRNA-miRNA bipartite networks reconstruction in different tissues of bladder cancer based on gene co-expression network analysis.. <i>Scientific Reports</i> , 2022 , 12, 5885	4.9	0
6	Inhibitory effects of lactic acid bacteria isolated from traditional fermented foods against aflatoxigenic <i>Aspergillus</i> spp.. <i>Comparative Clinical Pathology</i> , 2017 , 26, 1083-1092	0.9	
5	Integration of Metabolic Knowledge for Genome-Scale Metabolic Reconstruction 2013 , 1023-1048		

4 Formalisms for Molecular Modeling and Simulation. *SpringerBriefs in Systems Biology*, **2015**, 1-39

3 Case Study: Modeling and Comparison of NSCLC and Normal EGFR Signaling. *SpringerBriefs in Systems Biology*, **2015**, 63-77

2 Cancer Modeling. *SpringerBriefs in Systems Biology*, **2015**, 41-61

1 C-element: a new clustering algorithm to find high quality functional modules in PPI networks. *PLoS ONE*, **2013**, 8, e72366

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