

# Ali Masoudi-Nejad

## List of Publications by Year in descending order

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Version: 2024-02-01

134  
papers

3,615  
citations

136950

32  
h-index

161849

54  
g-index

143  
all docs

143  
docs citations

143  
times ranked

4719  
citing authors

#	ARTICLE	IF	CITATIONS
1	A fuzzy logic-based computational method for the repurposing of drugs against COVID-19. <i>BioImpacts</i> , 2022, 12, 315-324.	1.5	6
2	Pan-cancer analysis of biological events on cell cycle instability in gastrointestinal cancers with integrative scoring method. <i>Genomics</i> , 2022, 114, 253-265.	2.9	5
3	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.	1.7	6
4	Insight into gene regulatory networks involved in sesame ( <i>Sesamum indicum</i> L.) drought response. <i>Biologia (Poland)</i> , 2022, 77, 1181-1196.	1.5	6
5	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.	3.3	6
6	Drug repositioning in non-small cell lung cancer (NSCLC) using gene co-expression and drug-gene interaction networks analysis. <i>Scientific Reports</i> , 2022, 12, .	3.3	10
7	Impact of 5HydroxyMethylCytosine (5hmC) on reverse/direct association of cell-cycle, apoptosis, and extracellular matrix pathways in gastrointestinal cancers. <i>BMC Genomic Data</i> , 2022, 23, .	1.7	4
8	A multimodal deep learning-based drug repurposing approach for treatment of COVID-19. <i>Molecular Diversity</i> , 2021, 25, 1717-1730.	3.9	44
9	Distinguishing drug/non-drug-like small molecules in drug discovery using deep belief network. <i>Molecular Diversity</i> , 2021, 25, 827-838.	3.9	13
10	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.	3.3	13
11	In silico design of novel aptamers utilizing a hybrid method of machine learning and genetic algorithm. <i>Molecular Diversity</i> , 2021, 25, 1395-1407.	3.9	12
12	Deep Learning in Drug Target Interaction Prediction: Current and Future Perspectives. <i>Current Medicinal Chemistry</i> , 2021, 28, 2100-2113.	2.4	43
13	Structure-based drug repurposing against COVID-19 and emerging infectious diseases: methods, resources and discoveries. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	12
14	DNA methylation association with stage progression of head and neck squamous cell carcinoma. <i>Computers in Biology and Medicine</i> , 2021, 134, 104473.	7.0	6
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.	3.3	3
16	Revealing transcriptional and post-transcriptional regulatory mechanisms of $\beta$ -glutamyl transferase and keratin isoforms as novel cooperative biomarkers in low-grade glioma and glioblastoma multiforme. <i>Genomics</i> , 2021, 113, 2623-2633.	2.9	3
17	High-throughput analysis of the interactions between viral proteins and host cell RNAs. <i>Computers in Biology and Medicine</i> , 2021, 135, 104611.	7.0	9
18	A propagation-based seed-centric local community detection for multilayer environment: The case study of colon adenocarcinoma. <i>PLoS ONE</i> , 2021, 16, e0255718.	2.5	1

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19	Automated Plant Species Identification Using Leaf Shape-Based Classification Techniques: A Case Study on Iranian Maples. Iranian Journal of Science and Technology - Transactions of Electrical Engineering, 2021, 45, 1051-1061.	2.3	3
20	Identification of common microRNA between COPD and non-small cell lung cancer through pathway enrichment analysis. BMC Genomic Data, 2021, 22, 41.	1.7	13
21	Drug databases and their contributions to drug repurposing. Genomics, 2020, 112, 1087-1095.	2.9	68
22	Introducing a panel for early detection of lung adenocarcinoma by using data integration of genomics, epigenomics, transcriptomics and proteomics. Experimental and Molecular Pathology, 2020, 112, 104360.	2.1	17
23	Synthetic repurposing of drugs against hypertension: a datamining method based on association rules and a novel discrete algorithm. BMC Bioinformatics, 2020, 21, 313.	2.6	16
24	DeepCDA: deep cross-domain compound-protein affinity prediction through LSTM and convolutional neural networks. Bioinformatics, 2020, 36, 4633-4642.	4.1	110
25	mRNA and microRNA selection for breast cancer molecular subtype stratification using meta-heuristic based algorithms. Genomics, 2020, 112, 3207-3217.	2.9	18
26	Identification of Key Components in Colon Adenocarcinoma Using Transcriptome to Interactome Multilayer Framework. Scientific Reports, 2020, 10, 4991.	3.3	8
27	Genome-scale exploration of transcriptional regulation in the nisin Z producer Lactococcus lactis subsp. lactis IO-1. Scientific Reports, 2020, 10, 3787.	3.3	7
28	An efficient hybrid feature selection method to identify potential biomarkers in common chronic lung inflammatory diseases. Genomics, 2020, 112, 3284-3293.	2.9	17
29	RPINBASE: An online toolbox to extract features for predicting RNA-protein interactions. Genomics, 2020, 112, 2623-2632.	2.9	11
30	Identification of biomarkers in common chronic lung diseases by co-expression networks and drug-target interactions analysis. Molecular Medicine, 2020, 26, 9.	4.4	34
31	Target controllability with minimal mediators in complex biological networks. Genomics, 2020, 112, 4938-4944.	2.9	6
32	Appropriate time to apply control input to complex dynamical systems. Scientific Reports, 2020, 10, 22035.	3.3	2
33	ParaKavosh: A Parallel Algorithm for Finding Biological Network Motifs. , 2020, , .		0
34	Network-based expression analyses and experimental validations revealed high co-expression between Yap1 and stem cell markers compared to differentiated cells. Genomics, 2019, 111, 831-839.	2.9	10
35	Differential network analysis and protein-protein interaction study reveals active protein modules in glucocorticoid resistance for infant acute lymphoblastic leukemia. Molecular Medicine, 2019, 25, 36.	4.4	7
36	Genome-wide DNA methylation profiling in ectopic and eutopic of endometrial tissues. Journal of Assisted Reproduction and Genetics, 2019, 36, 1743-1752.	2.5	14

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37	Trader as a new optimization algorithm predicts drug-target interactions efficiently. <i>Scientific Reports</i> , 2019, 9, 9348.	3.3	41
38	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.	3.4	5
39	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.	5.4	31
40	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.	4.4	21
41	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.	3.3	34
42	Systematic analysis of genes and diseases using PheWAS-Associated networks. <i>Computers in Biology and Medicine</i> , 2019, 109, 311-321.	7.0	7
43	DrugR+: A comprehensive relational database for drug repurposing, combination therapy, and replacement therapy. <i>Computers in Biology and Medicine</i> , 2019, 109, 254-262.	7.0	37
44	FeatureSelect: a software for feature selection based on machine learning approaches. <i>BMC Bioinformatics</i> , 2019, 20, 170.	2.6	83
45	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.	2.6	4
46	GPS: Identification of disease genes by rank aggregation of multi-genomic scoring schemes. <i>Genomics</i> , 2019, 111, 612-618.	2.9	5
47	LncRNA and mRNA integration network reconstruction reveals novel key regulators in esophageal squamous-cell carcinoma. <i>Genomics</i> , 2019, 111, 76-89.	2.9	26
48	CatbNet: A Multi Network Analyzer for Comparing and Analyzing the Topology of Biological Networks. <i>Current Genomics</i> , 2019, 20, 69-75.	1.6	2
49	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.	2.2	17
50	Sequence-based 5-mers highly correlated to epigenetic modifications in genes interactions. <i>Genes and Genomics</i> , 2018, 40, 1363-1371.	1.4	1
51	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.	7.0	8
52	Cattle infection response network and its functional modules. <i>BMC Immunology</i> , 2018, 19, 2.	2.2	7
53	SCAN-Toolbox: Structural COBRA Add-on (SCAN) for Analysing Large Metabolic Networks. <i>Current Bioinformatics</i> , 2018, 13, 100-107.	1.5	2
54	The importance of $\hat{\pm}$ -CT 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.	0.5	1

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55	Systems biology study of transcriptional and post-transcriptional co-regulatory network sheds light on key regulators involved in important biological processes in <i>Citrus sinensis</i> . <i>Physiology and Molecular Biology of Plants</i> , 2017, 23, 331-342.	3.1	5
56	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.	2.9	22
57	Predicting brain network changes in Alzheimer's disease with link prediction algorithms. <i>Molecular BioSystems</i> , 2017, 13, 725-735.	2.9	20
58	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.	0.7	1
59	Biogeography, distribution and conservation status of maples ( <i>Acer L.</i> ) in Iran. <i>Trees - Structure and Function</i> , 2017, 31, 1583-1598.	1.9	8
60	Micromorphological studies of leaf epidermal features in populations of maples ( <i>Acer L.</i> ) from Iran. <i>Phytotaxa</i> , 2017, 299, 36.	0.3	5
61	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.	3.4	86
62	mRNA-miRNA bipartite network reconstruction to predict prognostic module biomarkers in colorectal cancer stage differentiation. <i>Molecular BioSystems</i> , 2017, 13, 2168-2180.	2.9	33
63	Task modulates functional connectivity networks in free viewing behavior. <i>NeuroImage</i> , 2017, 159, 289-301.	4.2	14
64	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.	4.4	21
65	Expectation propagation for large scale Bayesian inference of non-linear molecular networks from perturbation data. <i>PLoS ONE</i> , 2017, 12, e0171240.	2.5	5
66	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.	0.5	7
67	Large-scale gene co-expression network as a source of functional annotation for cattle genes. <i>BMC Genomics</i> , 2016, 17, 846.	2.8	18
68	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, 2552-2561.	2.9	19
69	CeFunMO: A centrality based method for discovering functional motifs with application in biological networks. <i>Computers in Biology and Medicine</i> , 2016, 76, 154-159.	7.0	4
70	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.	2.3	9
71	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.	5.0	34
72	Drug-target interaction prediction from PSSM based evolutionary information. <i>Journal of Pharmacological and Toxicological Methods</i> , 2016, 78, 42-51.	0.7	68

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73	Information theory in systems biology. Part I: Gene regulatory and metabolic networks. <i>Seminars in Cell and Developmental Biology</i> , 2016, 51, 3-13.	5.0	31
74	Flow of Information in Biological Systems. <i>Seminars in Cell and Developmental Biology</i> , 2016, 51, 1-2.	5.0	0
75	Computational Detection of piRNA in Human Using Support Vector Machine. <i>Avicenna Journal of Medical Biotechnology</i> , 2016, 8, 36-41.	0.3	3
76	Protein Clustering and Interactome Analysis in Parkinson and Alzheimer's Diseases. <i>Archives of Iranian Medicine</i> , 2016, 19, 101-9.	0.6	31
77	Alterations in cancer cell metabolism: The Warburg effect and metabolic adaptation. <i>Genomics</i> , 2015, 105, 275-281.	2.9	90
78	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, 3137-3148.	2.9	1
79	Cancer systems biology and modeling: Microscopic scale and multiscale approaches. <i>Seminars in Cancer Biology</i> , 2015, 30, 60-69.	9.6	31
80	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.	9.6	231
81	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, 21-29.	9.6	38
82	Cancer modeling and network biology: Accelerating toward personalized medicine. <i>Seminars in Cancer Biology</i> , 2015, 30, 1-3.	9.6	21
83	Formalisms for Molecular Modeling and Simulation. <i>SpringerBriefs in Systems Biology</i> , 2015, , 1-39.	0.3	0
84	Case Study: Modeling and Comparison of NSCLC and Normal EGFR Signaling. <i>SpringerBriefs in Systems Biology</i> , 2015, , 63-77.	0.3	0
85	Cancer Modeling. <i>SpringerBriefs in Systems Biology</i> , 2015, , 41-61.	0.3	0
86	Human RNAi pathway: crosstalk with organelles and cells. <i>Functional and Integrative Genomics</i> , 2014, 14, 31-46.	3.5	16
87	Informative Bayesian Model Selection: a method for identifying interactions in genome-wide data. <i>Molecular BioSystems</i> , 2014, 10, 2654-2662.	2.9	1
88	LocFuse: Human protein-protein interaction prediction via classifier fusion using protein localization information. <i>Genomics</i> , 2014, 104, 496-503.	2.9	51
89	Drug-target interaction prediction via chemogenomic space: learning-based methods. <i>Expert Opinion on Drug Metabolism and Toxicology</i> , 2014, 10, 1273-1287.	3.3	83
90	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, 283-289.	2.5	19

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91	Pathway Reconstruction of Airway Remodeling in Chronic Lung Diseases: A Systems Biology Approach. PLoS ONE, 2014, 9, e100094.	2.5	9
92	Extracting a cancer model by enhanced ant colony optimisation algorithm. International Journal of Data Mining and Bioinformatics, 2014, 10, 83.	0.1	1
93	Genome-Scale Co-Expression Network Comparison across Escherichia coli and Salmonella enterica Serovar Typhimurium Reveals Significant Conservation at the Regulon Level of Local Regulators Despite Their Dissimilar Lifestyles. PLoS ONE, 2014, 9, e102871.	2.5	16
94	Computational Analysis of Reciprocal Association of Metabolism and Epigenetics in the Budding Yeast: A Genome-Scale Metabolic Model (GSMM) Approach. PLoS ONE, 2014, 9, e111686.	2.5	12
95	Genome Scale Modeling in Systems Biology: Algorithms and Resources. Current Genomics, 2014, 15, 130-159.	1.6	37
96	Centrality Measures in Biological Networks. Current Bioinformatics, 2014, 9, 426-441.	1.5	20
97	Analysis of Genome-scale Expression Network in Four Major Bacterial Residents of Cystic Fibrosis Lung. Current Genomics, 2014, 15, 408-418.	1.6	1
98	Computational structure analysis of biomacromolecule complexes by interface geometry. Computational Biology and Chemistry, 2013, 47, 16-23.	2.3	6
99	HomoTarget: A new algorithm for prediction of microRNA targets in Homo sapiens. Genomics, 2013, 101, 94-100.	2.9	30
100	Drug-target and disease networks: polypharmacology in the post-genomic era. In Silico Pharmacology, 2013, 1, 17.	3.3	47
101	Normalized Similarity Index: An adjusted index to prioritize article citations. Journal of Informetrics, 2013, 7, 91-98.	2.9	12
102	Discovering dominant pathways and signalâ€“response relationships in signaling networks through nonparametric approaches. Genomics, 2013, 102, 195-201.	2.9	6
103	PPlevo : Proteinâ€“protein interaction prediction from PSSM based evolutionary information. Genomics, 2013, 102, 237-242.	2.9	131
104	Controllability in Cancer Metabolic Networks According to Drug Targets as Driver Nodes. PLoS ONE, 2013, 8, e79397.	2.5	57
105	Reconstruction of an Integrated Genome-Scale Co-Expression Network Reveals Key Modules Involved in Lung Adenocarcinoma. PLoS ONE, 2013, 8, e67552.	2.5	99
106	QuateXelero: An Accelerated Exact Network Motif Detection Algorithm. PLoS ONE, 2013, 8, e68073.	2.5	44
107	Computational Prediction of Proteinâ€“Protein Interaction Networks: Algorithms and Resources. Current Genomics, 2013, 14, 397-414.	1.6	119
108	C-element: A New Clustering Algorithm to Find High Quality Functional Modules in PPI Networks. PLoS ONE, 2013, 8, e72366.	2.5	1

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109	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, 1959-1965.	2.1	32
110	Hubs and Non-hubs in Protein-Protein Interaction Networks: A Biophysical Interpretation. , 2012, , .		0
111	Building blocks of biological networks: a review on major network motif discovery algorithms. <i>IET Systems Biology</i> , 2012, 6, 164-174.	1.5	56
112	Modeling and analysis of abnormality detection in biomolecular nano-networks. <i>Nano Communication Networks</i> , 2012, 3, 229-241.	2.9	16
113	Bioinformatics study of the 3-hydroxy-3-methylglutaryl-coenzyme A reductase (HMGR) gene in Gramineae. <i>Molecular Biology Reports</i> , 2012, 39, 8925-8935.	2.3	30
114	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.	2.3	16
115	Computational analysis of RNA-protein interaction interfaces via the Voronoi diagram. <i>Journal of Theoretical Biology</i> , 2012, 293, 55-64.	1.7	4
116	Nonparametric Simulation of Signal Transduction Networks with Semi-Synchronized Update. <i>PLoS ONE</i> , 2012, 7, e39643.	2.5	7
117	CytoKavosh: A Cytoscape Plug-In for Finding Network Motifs in Large Biological Networks. <i>PLoS ONE</i> , 2012, 7, e43287.	2.5	11
118	Modeling of Tumor Progression in NSCLC and Intrinsic Resistance to TKI in Loss of PTEN Expression. <i>PLoS ONE</i> , 2012, 7, e48004.	2.5	42
119	RNAi pathway integration in <i>Caenorhabditis elegans</i> development. <i>Functional and Integrative Genomics</i> , 2011, 11, 389-405.	3.5	11
120	Emerging roles of epigenetic mechanisms in Parkinson's disease. <i>Functional and Integrative Genomics</i> , 2011, 11, 523-537.	3.5	42
121	Genome-scale computational analysis of DNA curvature and repeats in <i>Arabidopsis</i> and rice uncovers plant-specific genomic properties. <i>BMC Genomics</i> , 2011, 12, 214.	2.8	3
122	Molecular typing of <i>Epidermophyton floccosum</i> isolated from patients with dermatophytosis by RAPD-PCR. <i>Journal of Basic Microbiology</i> , 2010, 50, S68-73.	3.3	8
123	Improved Immune Genetic Algorithm for Clustering Protein-Protein Interaction Network. , 2010, , .		9
124	Kavosh: a new algorithm for finding network motifs. <i>BMC Bioinformatics</i> , 2009, 10, 318.	2.6	176
125	Reconstruction of <i>Arabidopsis thaliana</i> fully integrated small RNA pathway. <i>Functional and Integrative Genomics</i> , 2009, 9, 419-432.	3.5	42
126	MODA: An efficient algorithm for network motif discovery in biological networks. <i>Genes and Genetic Systems</i> , 2009, 84, 385-395.	0.7	109



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127	N4: A precise and highly sensitive promoter predictor using neural network fed by nearest neighbors. <i>Genes and Genetic Systems</i> , 2009, 84, 425-430.	0.7	14
128	Dissection of rye chromosome 1R in common wheat. <i>Genes and Genetic Systems</i> , 2008, 83, 43-53.	0.7	36
129	EGENES: Transcriptome-Based Plant Database of Genes with Metabolic Pathway Information and Expressed Sequence Tag Indices in KEGG. <i>Plant Physiology</i> , 2007, 144, 857-866.	4.8	35
130	KEGG Bioinformatics Resource for Plant Genomics Research. , 2007, 406, 437-458.		27
131	EGassembler: online bioinformatics service for large-scale processing, clustering and assembling ESTs and genomic DNA fragments. <i>Nucleic Acids Research</i> , 2006, 34, W459-W462.	14.5	139
132	An alternative to radiation hybrid mapping for large-scale genome analysis in barley. <i>Molecular Genetics and Genomics</i> , 2005, 274, 589-594.	2.1	29
133	Molecular cloning, sequencing, and chromosome mapping of a 1A-encoded $\gamma$ -type prolamin sequence from wheat. <i>Genome</i> , 2002, 45, 661-669.	2.0	22
134	Transfer of rye chromosome segments to wheat by a gametocidal system. <i>Chromosome Research</i> , 2002, 10, 349-357.	2.2	109