Ali Masoudi-Nejad

List of Publications by Year in Descending Order

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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	Re-wiring and gene expression changes of AC025034.1 and ATP2B1 play complex roles in early-to-late breast cancer progression.. *BMC Genomic Data*, **2022**, 23, 6	0	0
128	Insight into gene regulatory networks involved in sesame (Sesamum indicum L.) drought response. *Biologia (Poland)*, **2022**, 77, 1181	1.5	1
127	mRNA-miRNA bipartite networks reconstruction in different tissues of bladder cancer based on gene co-expression network analysis.. *Scientific Reports*, **2022**, 12, 5885	4.9	0
126	Pan-cancer analysis of biological events on cell cycle instability in gastrointestinal cancers with integrative scoring method.. *Genomics*, **2021**, 114, 253-265	4.3	0
125	Identification of common microRNA between COPD and non-small cell lung cancer through pathway enrichment analysis. *BMC Genomic Data*, **2021**, 22, 41	0	6
124	A multimodal deep learning-based drug repurposing approach for treatment of COVID-19. *Molecular Diversity*, **2021**, 25, 1717-1730	3.1	13
123	Deep Learning in Drug Target Interaction Prediction: Current and Future Perspectives. *Current Medicinal Chemistry*, **2021**, 28, 2100-2113	4.3	11
122	Structure-based drug repurposing against COVID-19 and emerging infectious diseases: methods, resources and discoveries. *Briefings in Bioinformatics*, **2021**, 22,	13.4	2
121	DNA methylation association with stage progression of head and neck squamous cell carcinoma. *Computers in Biology and Medicine*, **2021**, 134, 104473	7	2
120	Nodes with the highest control power play an important role at the final level of cooperation in directed networks. *Scientific Reports*, **2021**, 11, 13668	4.9	1
119	Revealing transcriptional and post-transcriptional regulatory mechanisms of □glutamyl transferase and keratin isoforms as novel cooperative biomarkers in low-grade glioma and glioblastoma multiforme. *Genomics*, **2021**, 113, 2623-2633	4.3	0
118	Distinguishing drug/non-drug-like small molecules in drug discovery using deep belief network. *Molecular Diversity*, **2021**, 25, 827-838	3.1	5
117	A machine learning method based on the genetic and world competitive contests algorithms for selecting genes or features in biological applications. *Scientific Reports*, **2021**, 11, 3349	4.9	4
116	In silico design of novel aptamers utilizing a hybrid method of machine learning and genetic algorithm. *Molecular Diversity*, **2021**, 25, 1395-1407	3.1	4
115	High-throughput analysis of the interactions between viral proteins and host cell RNAs. *Computers in Biology and Medicine*, **2021**, 135, 104611	7	4
114	A propagation-based seed-centric local community detection for multilayer environment: The case study of colon adenocarcinoma. *PLoS ONE*, **2021**, 16, e0255718	3.7	0
113	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	1.9	0

112	DeepCDA: deep cross-domain compound-protein affinity prediction through LSTM and convolutional neural networks. *Bioinformatics*, **2020**, 36, 4633-4642	7.2	29
111	mRNA and microRNA selection for breast cancer molecular subtype stratification using meta-heuristic based algorithms. *Genomics*, **2020**, 112, 3207-3217	4.3	10
110	Identification of Key Components in Colon Adenocarcinoma Using Transcriptome to Interactome Multilayer Framework. *Scientific Reports*, **2020**, 10, 4991	4.9	4
109	Genome-scale exploration of transcriptional regulation in the nisin Z producer Lactococcus lactis subsp. lactis IO-1. *Scientific Reports*, **2020**, 10, 3787	4.9	4
108	An efficient hybrid feature selection method to identify potential biomarkers in common chronic lung inflammatory diseases. *Genomics*, **2020**, 112, 3284-3293	4.3	7
107	RPINBASE: An online toolbox to extract features for predicting RNA-protein interactions. *Genomics*, **2020**, 112, 2623-2632	4.3	8
106	Identification of biomarkers in common chronic lung diseases by co-expression networks and drug-target interactions analysis. *Molecular Medicine*, **2020**, 26, 9	6.2	17
105	Target controllability with minimal mediators in complex biological networks. *Genomics*, **2020**, 112, 4938-4944	4.3	4
104	Appropriate time to apply control input to complex dynamical systems. *Scientific Reports*, **2020**, 10, 22035	4.9	1
103	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	4.4	8
102	Synthetic repurposing of drugs against hypertension: a datamining method based on association rules and a novel discrete algorithm. *BMC Bioinformatics*, **2020**, 21, 313	3.6	6
101	Drug databases and their contributions to drug repurposing. *Genomics*, **2020**, 112, 1087-1095	4.3	38
100	Active repurposing of drug candidates for melanoma based on GWAS, PheWAS and a wide range of omics data. *Molecular Medicine*, **2019**, 25, 30	6.2	7
99	Detection of novel biomarkers for early detection of Non-Muscle-Invasive Bladder Cancer using Competing Endogenous RNA network analysis. *Scientific Reports*, **2019**, 9, 8434	4.9	24
98	Systematic analysis of genes and diseases using PheWAS-Associated networks. *Computers in Biology and Medicine*, **2019**, 109, 311-321	7	5
97	DrugR+: A comprehensive relational database for drug repurposing, combination therapy, and replacement therapy. *Computers in Biology and Medicine*, **2019**, 109, 254-262	7	21
96	FeatureSelect: a software for feature selection based on machine learning approaches. *BMC Bioinformatics*, **2019**, 20, 170	3.6	44
95	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	4.3	5

94	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	6.2	7
93	Genome-wide DNA methylation profiling in ectopic and eutopic of endometrial tissues. *Journal of Assisted Reproduction and Genetics*, **2019**, 36, 1743-1752	3.4	6
92	Trader as a new optimization algorithm predicts drug-target interactions efficiently. *Scientific Reports*, **2019**, 9, 9348	4.9	27
91	Disease global behavior: A systematic study of the human interactome network reveals conserved topological features among categories of diseases. *Informatics in Medicine Unlocked*, **2019**, 17, 100249	5.3	5
90	Deep Transferable Compound Representation across Domains and Tasks for Low Data Drug Discovery. *Journal of Chemical Information and Modeling*, **2019**, 59, 4528-4539	6.1	13
89	CatbNet: A Multi Network Analyzer for Comparing and Analyzing the Topology of Biological Networks. *Current Genomics*, **2019**, 20, 69-75	2.6	1
88	Novel putative drugs and key initiating genes for neurodegenerative disease determined using network-based genetic integrative analysis. *Journal of Cellular Biochemistry*, **2019**, 120, 5459-5471	4.7	3
87	GPS: Identification of disease genes by rank aggregation of multi-genomic scoring schemes. *Genomics*, **2019**, 111, 612-618	4.3	5
86	LncRNA and mRNA integration network reconstruction reveals novel key regulators in esophageal squamous-cell carcinoma. *Genomics*, **2019**, 111, 76-89	4.3	20
85	Comparison of gene co-expression networks in Pseudomonas aeruginosa and Staphylococcus aureus reveals conservation in some aspects of virulence. *Gene*, **2018**, 639, 1-10	3.8	7
84	Cattle infection response network and its functional modules. *BMC Immunology*, **2018**, 19, 2	3.7	3
83	SCAN-Toolbox: Structural COBRA Add-oN (SCAN) for Analysing Large Metabolic Networks. *Current Bioinformatics*, **2018**, 13, 100-107	4.7	1
82	The importance of □CT and Salt bridges in the Formation of Insulin and its Receptor Complex by Computational Simulation. *Iranian Journal of Pharmaceutical Research*, **2018**, 17, 63-74	1.1	1
81	Sequence-based 5-mers highly correlated to epigenetic modifications in genes interactions. *Genes and Genomics*, **2018**, 40, 1363-1371	2.1	1
80	Reconstruction of the genome-scale co-expression network for the Hippo signaling pathway in colorectal cancer. *Computers in Biology and Medicine*, **2018**, 99, 76-84	7	5
79	Systems biology study of transcriptional and post-transcriptional co-regulatory network sheds light on key regulators involved in important biological processes in. *Physiology and Molecular Biology of Plants*, **2017**, 23, 331-342	2.8	3
78	Candidate novel long noncoding RNAs, MicroRNAs and putative drugs for Parkinson's disease using a robust and efficient genome-wide association study. *Genomics*, **2017**, 109, 158-164	4.3	16
77	Predicting brain network changes in Alzheimer's disease with link prediction algorithms. *Molecular BioSystems*, **2017**, 13, 725-735		13

76	Inhibitory effects of lactic acid bacteria isolated from traditional fermented foods against aflatoxigenic Aspergillus spp.. *Comparative Clinical Pathology*, **2017**, 26, 1083-1092	0.9	
75	Biogeography, distribution and conservation status of maples (Acer L.) in Iran. *Trees - Structure and Function*, **2017**, 31, 1583-1598	2.6	2
74	Micromorphological studies of leaf epidermal features in populations of maples (Acer L.) from Iran. *Phytotaxa*, **2017**, 299, 36	0.7	2
73	A hybrid gene selection algorithm for microarray cancer classification using genetic algorithm and learning automata. *Informatics in Medicine Unlocked*, **2017**, 9, 246-254	5.3	58
72	Expectation propagation for large scale Bayesian inference of non-linear molecular networks from perturbation data. *PLoS ONE*, **2017**, 12, e0171240	3.7	5
71	mRNA-miRNA bipartite network reconstruction to predict prognostic module biomarkers in colorectal cancer stage differentiation. *Molecular BioSystems*, **2017**, 13, 2168-2180		21
70	Task modulates functional connectivity networks in free viewing behavior. *NeuroImage*, **2017**, 159, 289-301	7.9	10
69	Network-based expression analysis reveals key genes related to glucocorticoid resistance in infant acute lymphoblastic leukemia. *Cellular Oncology (Dordrecht)*, **2017**, 40, 33-45	7.2	16
68	Sequential and Mixed Genetic Algorithm and Learning Automata (SGALA, MGALA) for Feature Selection in QSAR. *Iranian Journal of Pharmaceutical Research*, **2017**, 16, 533-553	1.1	7
67	Determination of the Best Concentration of Streptozotocin to Create a Diabetic Brain Using Histological Techniques. *Journal of Molecular Neuroscience*, **2016**, 59, 24-35	3.3	7
66	Information theory in systems biology. Part II: protein-protein interaction and signaling networks. *Seminars in Cell and Developmental Biology*, **2016**, 51, 14-23	7.5	22
65	Drug-target interaction prediction from PSSM based evolutionary information. *Journal of Pharmacological and Toxicological Methods*, **2016**, 78, 42-51	1.7	45
64	Information theory in systems biology. Part I: Gene regulatory and metabolic networks. *Seminars in Cell and Developmental Biology*, **2016**, 51, 3-13	7.5	22
63	Computational Detection of piRNA in Human Using Support Vector Machine. *Avicenna Journal of Medical Biotechnology*, **2016**, 8, 36-41	1.4	3
62	Large-scale gene co-expression network as a source of functional annotation for cattle genes. *BMC Genomics*, **2016**, 17, 846	4.5	12
61	A systems biology approach to reconcile metabolic network models with application to Synechocystis sp. PCC 6803 for biofuel production. *Molecular BioSystems*, **2016**, 12, 2552-61		17
60	CeFunMO: A centrality based method for discovering functional motifs with application in biological networks. *Computers in Biology and Medicine*, **2016**, 76, 154-9	7	1
59	Protein Clustering and Interactome Analysis in Parkinson and Alzheimer's Diseases. *Archives of Iranian Medicine*, **2016**, 19, 101-9	2.4	29

58	Alterations in cancer cell metabolism: the Warburg effect and metabolic adaptation. *Genomics*, **2015**, 105, 275-81	4.3	66
57	Co-expressional conservation in virulence and stress related genes of three Gammaproteobacterial species: Escherichia coli, Salmonella enterica and Pseudomonas aeruginosa. *Molecular BioSystems*, **2015**, 11, 3137-48		1
56	Cancer systems biology and modeling: microscopic scale and multiscale approaches. *Seminars in Cancer Biology*, **2015**, 30, 60-9	12.7	26
55	Predictive genomics: a cancer hallmark network framework for predicting tumor clinical phenotypes using genome sequencing data. *Seminars in Cancer Biology*, **2015**, 30, 4-12	12.7	176
54	Metabolic cancer biology: structural-based analysis of cancer as a metabolic disease, new sights and opportunities for disease treatment. *Seminars in Cancer Biology*, **2015**, 30, 21-9	12.7	31
53	Formalisms for Molecular Modeling and Simulation. *SpringerBriefs in Systems Biology*, **2015**, 1-39		
52	Case Study: Modeling and Comparison of NSCLC and Normal EGFR Signaling. *SpringerBriefs in Systems Biology*, **2015**, 63-77		
51	Cancer Modeling. *SpringerBriefs in Systems Biology*, **2015**, 41-61		
50	Informative Bayesian Model Selection: a method for identifying interactions in genome-wide data. *Molecular BioSystems*, **2014**, 10, 2654-62		1
49	LocFuse: human protein-protein interaction prediction via classifier fusion using protein localization information. *Genomics*, **2014**, 104, 496-503	4.3	40
48	Drug-target interaction prediction via chemogenomic space: learning-based methods. *Expert Opinion on Drug Metabolism and Toxicology*, **2014**, 10, 1273-87	5.5	60
47	Microarray gene expression analysis of the human airway in patients exposed to sulfur mustard. *Journal of Receptor and Signal Transduction Research*, **2014**, 34, 283-9	2.6	16
46	Pathway reconstruction of airway remodeling in chronic lung diseases: a systems biology approach. *PLoS ONE*, **2014**, 9, e100094	3.7	8
45	Extracting a cancer model by enhanced ant colony optimisation algorithm. *International Journal of Data Mining and Bioinformatics*, **2014**, 10, 83-97	0.5	1
44	Human RNAi pathway: crosstalk with organelles and cells. *Functional and Integrative Genomics*, **2014**, 14, 31-46	3.8	13
43	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	3.7	10
42	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	3.7	9
41	Genome scale modeling in systems biology: algorithms and resources. *Current Genomics*, **2014**, 15, 130-59	2.6	27

40	Centrality Measures in Biological Networks. *Current Bioinformatics*, **2014**, 9, 426-441	4.7	11
39	Analysis of Genome-scale Expression Network in Four Major Bacterial Residents of Cystic Fibrosis Lung. *Current Genomics*, **2014**, 15, 408-18	2.6	1
38	Computational structure analysis of biomacromolecule complexes by interface geometry. *Computational Biology and Chemistry*, **2013**, 47, 16-23	3.6	6
37	HomoTarget: a new algorithm for prediction of microRNA targets in Homo sapiens. *Genomics*, **2013**, 101, 94-100	4.3	22
36	Drug-target and disease networks: polypharmacology in the post-genomic era. *In Silico Pharmacology*, **2013**, 1, 17	4.3	31
35	Normalized Similarity Index: An adjusted index to prioritize article citations. *Journal of Informetrics*, **2013**, 7, 91-98	3.1	10
34	Discovering dominant pathways and signal-response relationships in signaling networks through nonparametric approaches. *Genomics*, **2013**, 102, 195-201	4.3	4
33	PPIevo: protein-protein interaction prediction from PSSM based evolutionary information. *Genomics*, **2013**, 102, 237-42	4.3	94
32	Controllability in cancer metabolic networks according to drug targets as driver nodes. *PLoS ONE*, **2013**, 8, e79397	3.7	44
31	Integration of Metabolic Knowledge for Genome-Scale Metabolic Reconstruction **2013**, 1023-1048		
30	Reconstruction of an integrated genome-scale co-expression network reveals key modules involved in lung adenocarcinoma. *PLoS ONE*, **2013**, 8, e67552	3.7	76
29	QuateXelero: an accelerated exact network motif detection algorithm. *PLoS ONE*, **2013**, 8, e68073	3.7	39
28	Computational Prediction of Protein-Protein Interaction Networks: Algo-rithms and Resources. *Current Genomics*, **2013**, 14, 397-414	2.6	83
27	C-element: a new clustering algorithm to find high quality functional modules in PPI networks. *PLoS ONE*, **2013**, 8, e72366	3.7	
26	Computational analysis of RNA-protein interaction interfaces via the Voronoi diagram. *Journal of Theoretical Biology*, **2012**, 293, 55-64	2.3	3
25	Molecular epidemiology of hepatitis C virus among injection drug users in Iran: a slight change in prevalence of HCV genotypes over time. *Archives of Virology*, **2012**, 157, 1959-65	2.6	29
24	Building blocks of biological networks: a review on major network motif discovery algorithms. *IET Systems Biology*, **2012**, 6, 164-74	1.4	48
23	Modeling and analysis of abnormality detection in biomolecular nano-networks. *Nano Communication Networks*, **2012**, 3, 229-241	2.9	11

22	Candidate gene prioritization. *Molecular Genetics and Genomics*, **2012**, 287, 679-98	3.1	12
21	Bioinformatics study of the 3-hydroxy-3-methylglotaryl-coenzyme A reductase (HMGR) gene in Gramineae. *Molecular Biology Reports*, **2012**, 39, 8925-35	2.8	27
20	Expression of chalcone synthase influences flavonoid content and frequency of rhizogenesis in microshoots of Juglans regia L.. *Plant Cell, Tissue and Organ Culture*, **2012**, 109, 51-59	2.7	9
19	Nonparametric simulation of signal transduction networks with semi-synchronized update. *PLoS ONE*, **2012**, 7, e39643	3.7	7
18	CytoKavosh: a cytoscape plug-in for finding network motifs in large biological networks. *PLoS ONE*, **2012**, 7, e43287	3.7	10
17	Modeling of tumor progression in NSCLC and intrinsic resistance to TKI in loss of PTEN expression. *PLoS ONE*, **2012**, 7, e48004	3.7	31
16	RNAi pathway integration in Caenorhabditis elegans development. *Functional and Integrative Genomics*, **2011**, 11, 389-405	3.8	10
15	Emerging roles of epigenetic mechanisms in Parkinson's disease. *Functional and Integrative Genomics*, **2011**, 11, 523-37	3.8	35
14	Genome-scale computational analysis of DNA curvature and repeats in Arabidopsis and rice uncovers plant-specific genomic properties. *BMC Genomics*, **2011**, 12, 214	4.5	3
13	Improved Immune Genetic Algorithm for Clustering Protein-Protein Interaction Network **2010**,		7
12	Molecular typing of Epidermophyton floccosum isolated from patients with dermatophytosis by RAPD-PCR. *Journal of Basic Microbiology*, **2010**, 50 Suppl 1, S68-73	2.7	6
11	Kavosh: a new algorithm for finding network motifs. *BMC Bioinformatics*, **2009**, 10, 318	3.6	144
10	Reconstruction of Arabidopsis thaliana fully integrated small RNA pathway. *Functional and Integrative Genomics*, **2009**, 9, 419-32	3.8	37
9	MODA: an efficient algorithm for network motif discovery in biological networks. *Genes and Genetic Systems*, **2009**, 84, 385-95	1.4	92
8	N4: a precise and highly sensitive promoter predictor using neural network fed by nearest neighbors. *Genes and Genetic Systems*, **2009**, 84, 425-30	1.4	14
7	Dissection of rye chromosome 1R in common wheat. *Genes and Genetic Systems*, **2008**, 83, 43-53	1.4	28
6	KEGG bioinformatics resource for plant genomics research. *Methods in Molecular Biology*, **2007**, 406, 437-58	1.4	22
5	EGENES: transcriptome-based plant database of genes with metabolic pathway information and expressed sequence tag indices in KEGG. *Plant Physiology*, **2007**, 144, 857-66	6.6	30

4	EGassembler: online bioinformatics service for large-scale processing, clustering and assembling ESTs and genomic DNA fragments. *Nucleic Acids Research*, **2006**, 34, W459-62	20.1	126
3	An alternative to radiation hybrid mapping for large-scale genome analysis in barley. *Molecular Genetics and Genomics*, **2005**, 274, 589-94	3.1	25
2	Transfer of rye chromosome segments to wheat by a gametocidal system. *Chromosome Research*, **2002**, 10, 349-57	4.4	86
1	Molecular cloning, sequencing, and chromosome mapping of a 1A-encoded omega-type prolamin sequence from wheat. *Genome*, **2002**, 45, 661-9	2.4	19