

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	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
2	Kavosh: a new algorithm for finding network motifs. <i>BMC Bioinformatics</i> , 2009, 10, 318.	2.6	176
3	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
4	PPlevo : Proteinâ€“protein interaction prediction from PSSM based evolutionary information. <i>Genomics</i> , 2013, 102, 237-242.	2.9	131
5	Computational Prediction of Proteinâ€“Protein Interaction Networks: Algorithms and Resources. <i>Current Genomics</i> , 2013, 14, 397-414.	1.6	119
6	DeepCDA: deep cross-domain compoundâ€“protein affinity prediction through LSTM and convolutional neural networks. <i>Bioinformatics</i> , 2020, 36, 4633-4642.	4.1	110
7	Transfer of rye chromosome segments to wheat by a gametocidal system. <i>Chromosome Research</i> , 2002, 10, 349-357.	2.2	109
8	MODA: An efficient algorithm for network motif discovery in biological networks. <i>Genes and Genetic Systems</i> , 2009, 84, 385-395.	0.7	109
9	Reconstruction of an Integrated Genome-Scale Co-Expression Network Reveals Key Modules Involved in Lung Adenocarcinoma. <i>PLoS ONE</i> , 2013, 8, e67552.	2.5	99
10	Alterations in cancer cell metabolism: The Warburg effect and metabolic adaptation. <i>Genomics</i> , 2015, 105, 275-281.	2.9	90
11	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
12	Drugâ€“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
13	FeatureSelect: a software for feature selection based on machine learning approaches. <i>BMC Bioinformatics</i> , 2019, 20, 170.	2.6	83
14	Drugâ€“target interaction prediction from PSSM based evolutionary information. <i>Journal of Pharmacological and Toxicological Methods</i> , 2016, 78, 42-51.	0.7	68
15	Drug databases and their contributions to drug repurposing. <i>Genomics</i> , 2020, 112, 1087-1095.	2.9	68
16	Controllability in Cancer Metabolic Networks According to Drug Targets as Driver Nodes. <i>PLoS ONE</i> , 2013, 8, e79397.	2.5	57
17	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
18	LocFuse: Human proteinâ€“protein interaction prediction via classifier fusion using protein localization information. <i>Genomics</i> , 2014, 104, 496-503.	2.9	51

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19	Drug-target and disease networks: polypharmacology in the post-genomic era. <i>In Silico Pharmacology</i> , 2013, 1, 17.	3.3	47
20	QuateXelero: An Accelerated Exact Network Motif Detection Algorithm. <i>PLoS ONE</i> , 2013, 8, e68073.	2.5	44
21	A multimodal deep learning-based drug repurposing approach for treatment of COVID-19. <i>Molecular Diversity</i> , 2021, 25, 1717-1730.	3.9	44
22	Deep Learning in Drug Target Interaction Prediction: Current and Future Perspectives. <i>Current Medicinal Chemistry</i> , 2021, 28, 2100-2113.	2.4	43
23	Reconstruction of Arabidopsis thaliana fully integrated small RNA pathway. <i>Functional and Integrative Genomics</i> , 2009, 9, 419-432.	3.5	42
24	Emerging roles of epigenetic mechanisms in Parkinson's disease. <i>Functional and Integrative Genomics</i> , 2011, 11, 523-537.	3.5	42
25	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
26	Trader as a new optimization algorithm predicts drug-target interactions efficiently. <i>Scientific Reports</i> , 2019, 9, 9348.	3.3	41
27	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
28	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
29	Genome Scale Modeling in Systems Biology: Algorithms and Resources. <i>Current Genomics</i> , 2014, 15, 130-159.	1.6	37
30	Dissection of rye chromosome 1R in common wheat. <i>Genes and Genetic Systems</i> , 2008, 83, 43-53.	0.7	36
31	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
32	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
33	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
34	Identification of biomarkers in common chronic lung diseases by co-expression networks and drug-target interactions analysis. <i>Molecular Medicine</i> , 2020, 26, 9.	4.4	34
35	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
36	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

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37	Cancer systems biology and modeling: Microscopic scale and multiscale approaches. <i>Seminars in Cancer Biology</i> , 2015, 30, 60-69.	9.6	31
38	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
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	Protein Clustering and Interactome Analysis in Parkinson and Alzheimer's Diseases. <i>Archives of Iranian Medicine</i> , 2016, 19, 101-9.	0.6	31
41	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
42	HomoTarget: A new algorithm for prediction of microRNA targets in Homo sapiens. <i>Genomics</i> , 2013, 101, 94-100.	2.9	30
43	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
44	KEGG Bioinformatics Resource for Plant Genomics Research. , 2007, 406, 437-458.		27
45	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
46	Molecular cloning, sequencing, and chromosome mapping of a 1A-encoded I%-type prolamin sequence from wheat. <i>Genome</i> , 2002, 45, 661-669.	2.0	22
47	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
48	Cancer modeling and network biology: Accelerating toward personalized medicine. <i>Seminars in Cancer Biology</i> , 2015, 30, 1-3.	9.6	21
49	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
50	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
51	Predicting brain network changes in Alzheimer's disease with link prediction algorithms. <i>Molecular BioSystems</i> , 2017, 13, 725-735.	2.9	20
52	Centrality Measures in Biological Networks. <i>Current Bioinformatics</i> , 2014, 9, 426-441.	1.5	20
53	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
54	A systems biology approach to reconcile metabolic network models with application to Synechocystis sp. PCC 6803 for biofuel production. <i>Molecular BioSystems</i> , 2016, 12, 2552-2561.	2.9	19

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55	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
56	mRNA and microRNA selection for breast cancer molecular subtype stratification using meta-heuristic based algorithms. <i>Genomics</i> , 2020, 112, 3207-3217.	2.9	18
57	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
58	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.	2.1	17
59	An efficient hybrid feature selection method to identify potential biomarkers in common chronic lung inflammatory diseases. <i>Genomics</i> , 2020, 112, 3284-3293.	2.9	17
60	Modeling and analysis of abnormality detection in biomolecular nano-networks. <i>Nano Communication Networks</i> , 2012, 3, 229-241.	2.9	16
61	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
62	Human RNAi pathway: crosstalk with organelles and cells. <i>Functional and Integrative Genomics</i> , 2014, 14, 31-46.	3.5	16
63	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.	2.6	16
64	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.	2.5	16
65	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
66	Task modulates functional connectivity networks in free viewing behavior. <i>NeuroImage</i> , 2017, 159, 289-301.	4.2	14
67	Genome-wide DNA methylation profiling in ectopic and eutopic of endometrial tissues. <i>Journal of Assisted Reproduction and Genetics</i> , 2019, 36, 1743-1752.	2.5	14
68	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
69	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
70	Identification of common microRNA between COPD and non-small cell lung cancer through pathway enrichment analysis. <i>BMC Genomic Data</i> , 2021, 22, 41.	1.7	13
71	Normalized Similarity Index: An adjusted index to prioritize article citations. <i>Journal of Informetrics</i> , 2013, 7, 91-98.	2.9	12
72	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

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73	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
74	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.	2.5	12
75	RNAi pathway integration in <i>Caenorhabditis elegans</i> development. <i>Functional and Integrative Genomics</i> , 2011, 11, 389-405.	3.5	11
76	RPINBASE: An online toolbox to extract features for predicting RNA-protein interactions. <i>Genomics</i> , 2020, 112, 2623-2632.	2.9	11
77	CytoKavosh: A Cytoscape Plug-In for Finding Network Motifs in Large Biological Networks. <i>PLoS ONE</i> , 2012, 7, e43287.	2.5	11
78	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.	2.9	10
79	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
80	Improved Immune Genetic Algorithm for Clustering Protein-Protein Interaction Network. , 2010, , .		9
81	Pathway Reconstruction of Airway Remodeling in Chronic Lung Diseases: A Systems Biology Approach. <i>PLoS ONE</i> , 2014, 9, e100094.	2.5	9
82	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
83	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
84	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
85	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
86	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
87	Identification of Key Components in Colon Adenocarcinoma Using Transcriptome to Interactome Multilayer Framework. <i>Scientific Reports</i> , 2020, 10, 4991.	3.3	8
88	Cattle infection response network and its functional modules. <i>BMC Immunology</i> , 2018, 19, 2.	2.2	7
89	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.	4.4	7
90	Systematic analysis of genes and diseases using PheWAS-Associated networks. <i>Computers in Biology and Medicine</i> , 2019, 109, 311-321.	7.0	7

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91	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.	3.3	7
92	Nonparametric Simulation of Signal Transduction Networks with Semi-Synchronized Update. <i>PLoS ONE</i> , 2012, 7, e39643.	2.5	7
93	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
94	Computational structure analysis of biomacromolecule complexes by interface geometry. <i>Computational Biology and Chemistry</i> , 2013, 47, 16-23.	2.3	6
95	Discovering dominant pathways and signalâ€“response relationships in signaling networks through nonparametric approaches. <i>Genomics</i> , 2013, 102, 195-201.	2.9	6
96	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
97	A fuzzy logic-based computational method for the repurposing of drugs against COVID-19. <i>BioImpacts</i> , 2022, 12, 315-324.	1.5	6
98	Target controllability with minimal mediators in complex biological networks. <i>Genomics</i> , 2020, 112, 4938-4944.	2.9	6
99	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
100	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
101	mRNAâ€“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
102	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
103	Micromorphological studies of leaf epidermal features in populations of maples (<i>Acer</i> L.) from Iran. <i>Phytotaxa</i> , 2017, 299, 36.	0.3	5
104	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
105	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
106	GPS: Identification of disease genes by rank aggregation of multi-genomic scoring schemes. <i>Genomics</i> , 2019, 111, 612-618.	2.9	5
107	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
108	Computational analysis of RNAâ€“protein interaction interfaces via the Voronoi diagram. <i>Journal of Theoretical Biology</i> , 2012, 293, 55-64.	1.7	4

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109	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
110	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
111	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
112	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.	2.8	3
113	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
114	Revealing transcriptional and post-transcriptional regulatory mechanisms of \hat{I}^3 -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
115	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.	2.3	3
116	Computational Detection of piRNA in Human Using Support Vector Machine. <i>Avicenna Journal of Medical Biotechnology</i> , 2016, 8, 36-41.	0.3	3
117	SCAN-Toolbox: Structural COBRA Add-on (SCAN) for Analysing Large Metabolic Networks. <i>Current Bioinformatics</i> , 2018, 13, 100-107.	1.5	2
118	Appropriate time to apply control input to complex dynamical systems. <i>Scientific Reports</i> , 2020, 10, 22035.	3.3	2
119	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
120	Informative Bayesian Model Selection: a method for identifying interactions in genome-wide data. <i>Molecular BioSystems</i> , 2014, 10, 2654-2662.	2.9	1
121	Extracting a cancer model by enhanced ant colony optimisation algorithm. <i>International Journal of Data Mining and Bioinformatics</i> , 2014, 10, 83.	0.1	1
122	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
123	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
124	Sequence-based 5-mers highly correlated to epigenetic modifications in genes interactions. <i>Genes and Genomics</i> , 2018, 40, 1363-1371.	1.4	1
125	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
126	C-element: A New Clustering Algorithm to Find High Quality Functional Modules in PPI Networks. <i>PLoS ONE</i> , 2013, 8, e72366.	2.5	1

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127	Analysis of Genome-scale Expression Network in Four Major Bacterial Residents of Cystic Fibrosis Lung. <i>Current Genomics</i> , 2014, 15, 408-418.	1.6	1
128	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
129	Hubs and Non-hubs in Protein-Protein Interaction Networks: A Biophysical Interpretation. , 2012, , .		0
130	Flow of Information in Biological Systems. <i>Seminars in Cell and Developmental Biology</i> , 2016, 51, 1-2.	5.0	0
131	Formalisms for Molecular Modeling and Simulation. <i>SpringerBriefs in Systems Biology</i> , 2015, , 1-39.	0.3	0
132	Case Study: Modeling and Comparison of NSCLC and Normal EGFR Signaling. <i>SpringerBriefs in Systems Biology</i> , 2015, , 63-77.	0.3	0
133	Cancer Modeling. <i>SpringerBriefs in Systems Biology</i> , 2015, , 41-61.	0.3	0
134	ParaKavosh: A Parallel Algorithm for Finding Biological Network Motifs. , 2020, , .		0