

List of Publications by Citations

**Source:** <https://exaly.com/author-pdf/4291722/luonan-chen-publications-by-citations.pdf>  
**Version:** 2024-04-10

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.  
The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

203 papers	4,339 citations	39 h-index	57 g-index
243 ext. papers	6,264 ext. citations	7.1 avg, IF	5.96 L-index

#	Paper	IF	Citations
203	Detecting early-warning signals for sudden deterioration of complex diseases by dynamical network biomarkers. <i>Scientific Reports</i> , <b>2012</b> , 2, 342	4.9	329
202	Early diagnosis of complex diseases by molecular biomarkers, network biomarkers, and dynamical network biomarkers. <i>Medicinal Research Reviews</i> , <b>2014</b> , 34, 455-78	14.4	172
201	Personalized characterization of diseases using sample-specific networks. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, e164	20.1	128
200	Part mutual information for quantifying direct associations in networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, 5130-5	11.5	118
199	Identifying critical transitions and their leading biomolecular networks in complex diseases. <i>Scientific Reports</i> , <b>2012</b> , 2, 813	4.9	112
198	NARROMI: a noise and redundancy reduction technique improves accuracy of gene regulatory network inference. <i>Bioinformatics</i> , <b>2013</b> , 29, 106-13	7.2	99
197	Conditional mutual inclusive information enables accurate quantification of associations in gene regulatory networks. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, e31	20.1	90
196	Detecting tissue-specific early warning signals for complex diseases based on dynamical network biomarkers: study of type 2 diabetes by cross-tissue analysis. <i>Briefings in Bioinformatics</i> , <b>2014</b> , 15, 229-43	13.4	85
195	Dynamic network biomarker indicates pulmonary metastasis at the tipping point of hepatocellular carcinoma. <i>Nature Communications</i> , <b>2018</b> , 9, 678	17.4	83
194	Inference of Gene Regulatory Network Based on Local Bayesian Networks. <i>PLoS Computational Biology</i> , <b>2016</b> , 12, e1005024	5	73
193	Identifying cancer-related microRNAs based on gene expression data. <i>Bioinformatics</i> , <b>2015</b> , 31, 1226-34	7.2	66
192	The effects of graded levels of calorie restriction: I. impact of short term calorie and protein restriction on body composition in the C57BL/6 mouse. <i>Oncotarget</i> , <b>2015</b> , 6, 15902-30	3.3	65
191	Identifying early-warning signals of critical transitions with strong noise by dynamical network markers. <i>Scientific Reports</i> , <b>2015</b> , 5, 17501	4.9	64
190	PPIM: A Protein-Protein Interaction Database for Maize. <i>Plant Physiology</i> , <b>2016</b> , 170, 618-26	6.6	62
189	Biomarker MicroRNAs for Diagnosis, Prognosis and Treatment of Hepatocellular Carcinoma: A Functional Survey and Comparison. <i>Scientific Reports</i> , <b>2016</b> , 6, 38311	4.9	59
188	Identifying critical transitions of complex diseases based on a single sample. <i>Bioinformatics</i> , <b>2014</b> , 30, 1579-86	7.2	57
187	Big biological data: challenges and opportunities. <i>Genomics, Proteomics and Bioinformatics</i> , <b>2014</b> , 12, 187-9	6.5	57

186	The effects of graded levels of calorie restriction: II. Impact of short term calorie and protein restriction on circulating hormone levels, glucose homeostasis and oxidative stress in male C57BL/6 mice. <i>Oncotarget</i> , <b>2015</b> , 6, 23213-37	3.3	56
185	Victors: a web-based knowledge base of virulence factors in human and animal pathogens. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, D693-D700	20.1	53
184	EdgeMarker: Identifying differentially correlated molecule pairs as edge-biomarkers. <i>Journal of Theoretical Biology</i> , <b>2014</b> , 362, 35-43	2.3	52
183	Quantifying critical states of complex diseases using single-sample dynamic network biomarkers. <i>PLoS Computational Biology</i> , <b>2017</b> , 13, e1005633	5	51
182	Detecting early-warning signals of type 1 diabetes and its leading biomolecular networks by dynamical network biomarkers. <i>BMC Medical Genomics</i> , <b>2013</b> , 6 Suppl 2, S8	3.7	51
181	Competitive endogenous RNA is an intrinsic component of EMT regulatory circuits and modulates EMT. <i>Nature Communications</i> , <b>2019</b> , 10, 1637	17.4	50
180	Network biomarkers reveal dysfunctional gene regulations during disease progression. <i>FEBS Journal</i> , <b>2013</b> , 280, 5682-95	5.7	49
179	Diagnosing phenotypes of single-sample individuals by edge biomarkers. <i>Journal of Molecular Cell Biology</i> , <b>2015</b> , 7, 231-41	6.3	48
178	PWCDA: Path Weighted Method for Predicting circRNA-Disease Associations. <i>International Journal of Molecular Sciences</i> , <b>2018</b> , 19,	6.3	48
177	In vivo CRISPR screening unveils histone demethylase UTX as an important epigenetic regulator in lung tumorigenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2018</b> , 115, E3978-E3986	11.5	45
176	Discovering personalized driver mutation profiles of single samples in cancer by network control strategy. <i>Bioinformatics</i> , <b>2018</b> , 34, 1893-1903	7.2	44
175	Cell-specific network constructed by single-cell RNA sequencing data. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, e62	20.1	43
174	Detecting causality from nonlinear dynamics with short-term time series. <i>Scientific Reports</i> , <b>2014</b> , 4, 7464	4.9	43
173	The dynamics of DNA methylation covariation patterns in carcinogenesis. <i>PLoS Computational Biology</i> , <b>2014</b> , 10, e1003709	5	43
172	A vitamin-C-derived DNA modification catalysed by an algal TET homologue. <i>Nature</i> , <b>2019</b> , 569, 581-585	50.4	41
171	CIDO, a community-based ontology for coronavirus disease knowledge and data integration, sharing, and analysis. <i>Scientific Data</i> , <b>2020</b> , 7, 181	8.2	41
170	Network biomarkers, interaction networks and dynamical network biomarkers in respiratory diseases. <i>Clinical and Translational Medicine</i> , <b>2014</b> , 3, 16	5.7	41
169	Dysfunction of PLA2G6 and CYP2C44-associated network signals imminent carcinogenesis from chronic inflammation to hepatocellular carcinoma. <i>Journal of Molecular Cell Biology</i> , <b>2017</b> , 9, 489-503	6.3	41

168	Detection for disease tipping points by landscape dynamic network biomarkers. <i>National Science Review</i> , <b>2019</b> , 6, 775-785	10.8	41
167	Transittability of complex networks and its applications to regulatory biomolecular networks. <i>Scientific Reports</i> , <b>2014</b> , 4, 4819	4.9	40
166	Pattern fusion analysis by adaptive alignment of multiple heterogeneous omics data. <i>Bioinformatics</i> , <b>2017</b> , 33, 2706-2714	7.2	39
165	Evolution- and structure-based computational strategy reveals the impact of deleterious missense mutations on MODY 2 (maturity-onset diabetes of the young, type 2). <i>Theranostics</i> , <b>2014</b> , 4, 366-85	12.1	39
164	Individual-specific edge-network analysis for disease prediction. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, e170	20.1	38
163	The effects of graded levels of calorie restriction: III. Impact of short term calorie and protein restriction on mean daily body temperature and torpor use in the C57BL/6 mouse. <i>Oncotarget</i> , <b>2015</b> , 6, 18314-37	3.3	38
162	Detecting critical state before phase transition of complex biological systems by hidden Markov model. <i>Bioinformatics</i> , <b>2016</b> , 32, 2143-50	7.2	36
161	Deciphering early development of complex diseases by progressive module network. <i>Methods</i> , <b>2014</b> , 67, 334-43	4.6	36
160	Analysing the Effect of Mutation on Protein Function and Discovering Potential Inhibitors of CDK4: Molecular Modelling and Dynamics Studies. <i>PLoS ONE</i> , <b>2015</b> , 10, e0133969	3.7	36
159	Knowledge-Guided Bioinformatics Model for Identifying Autism Spectrum Disorder Diagnostic MicroRNA Biomarkers. <i>Scientific Reports</i> , <b>2016</b> , 6, 39663	4.9	36
158	Prediction of dynamical drug sensitivity and resistance by module network rewiring-analysis based on transcriptional profiling. <i>Drug Resistance Updates</i> , <b>2014</b> , 17, 64-76	23.2	33
157	Comparison of Chromosome 4 gene expression profile between lung telocytes and other local cell types. <i>Journal of Cellular and Molecular Medicine</i> , <b>2016</b> , 20, 71-80	5.6	33
156	Hunt for the tipping point during endocrine resistance process in breast cancer by dynamic network biomarkers. <i>Journal of Molecular Cell Biology</i> , <b>2019</b> , 11, 649-664	6.3	33
155	The effects of graded levels of calorie restriction: IX. Global metabolomic screen reveals modulation of carnitines, sphingolipids and bile acids in the liver of C57BL/6 mice. <i>Aging Cell</i> , <b>2017</b> , 16, 529-540	9.9	32
154	Branched-Chain Amino Acid Metabolic Reprogramming Orchestrates Drug Resistance to EGFR Tyrosine Kinase Inhibitors. <i>Cell Reports</i> , <b>2019</b> , 28, 512-525.e6	10.6	32
153	Cullin5 deficiency promotes small-cell lung cancer metastasis by stabilizing integrin $\beta$ . <i>Journal of Clinical Investigation</i> , <b>2019</b> , 129, 972-987	15.9	32
152	Interferon-microRNA signalling drives liver precancerous lesion formation and hepatocarcinogenesis. <i>Gut</i> , <b>2016</b> , 65, 1186-201	19.2	31
151	Single-cell transcriptomics identifies a distinct luminal progenitor cell type in distal prostate invagination tips. <i>Nature Genetics</i> , <b>2020</b> , 52, 908-918	36.3	30

150	The effects of graded levels of calorie restriction: V. Impact of short term calorie and protein restriction on physical activity in the C57BL/6 mouse. <i>Oncotarget</i> , <b>2016</b> , 7, 19147-70	3.3	30
149	Single cell clustering based on cell-pair differentiability correlation and variance analysis. <i>Bioinformatics</i> , <b>2018</b> , 34, 3684-3694	7.2	30
148	Integrating in silico prediction methods, molecular docking, and molecular dynamics simulation to predict the impact of ALK missense mutations in structural perspective. <i>BioMed Research International</i> , <b>2014</b> , 2014, 895831	3	29
147	Comparative genomics reveals new candidate genes involved in selenium metabolism in prokaryotes. <i>Genome Biology and Evolution</i> , <b>2015</b> , 7, 664-76	3.9	27
146	Detecting early-warning signals of influenza outbreak based on dynamic network marker. <i>Journal of Cellular and Molecular Medicine</i> , <b>2019</b> , 23, 395-404	5.6	25
145	Discovering a critical transition state from nonalcoholic hepatosteatosis to nonalcoholic steatohepatitis by lipidomics and dynamical network biomarkers. <i>Journal of Molecular Cell Biology</i> , <b>2016</b> , 8, 195-206	6.3	24
144	Unravelling personalized dysfunctional gene network of complex diseases based on differential network model. <i>Journal of Translational Medicine</i> , <b>2015</b> , 13, 189	8.5	24
143	Randomly distributed embedding making short-term high-dimensional data predictable. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2018</b> , 115, E9994-E10002 <sup>1.5</sup>	11.5	22
142	Genomic and transcriptomic investigations of the evolutionary transition from oviparity to viviparity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2019</b> , 116, 3646-3655	11.5	21
141	Hyperlipidemia-associated gene variations and expression patterns revealed by whole-genome and transcriptome sequencing of rabbit models. <i>Scientific Reports</i> , <b>2016</b> , 6, 26942	4.9	21
140	A network biology study on circadian rhythm by integrating various omics data. <i>OMICS A Journal of Integrative Biology</i> , <b>2009</b> , 13, 313-24	3.8	20
139	The effects of graded levels of calorie restriction: VI. Impact of short-term graded calorie restriction on transcriptomic responses of the hypothalamic hunger and circadian signaling pathways. <i>Aging</i> , <b>2016</b> , 8, 642-63	5.6	20
138	The effects of graded levels of calorie restriction: VIII. Impact of short term calorie and protein restriction on basal metabolic rate in the C57BL/6 mouse. <i>Oncotarget</i> , <b>2017</b> , 8, 17453-17474	3.3	20
137	A novel network control model for identifying personalized driver genes in cancer. <i>PLoS Computational Biology</i> , <b>2019</b> , 15, e1007520	5	20
136	Single-sample landscape entropy reveals the imminent phase transition during disease progression. <i>Bioinformatics</i> , <b>2020</b> , 36, 1522-1532	7.2	20
135	Identifying critical differentiation state of MCF-7 cells for breast cancer by dynamical network biomarkers. <i>Frontiers in Genetics</i> , <b>2015</b> , 6, 252	4.5	19
134	A novel mixed integer programming for multi-biomarker panel identification by distinguishing malignant from benign colorectal tumors. <i>Methods</i> , <b>2015</b> , 83, 3-17	4.6	18
133	A plausible accelerating function of intermediate states in cancer metastasis. <i>PLoS Computational Biology</i> , <b>2020</b> , 16, e1007682	5	18

132	Predicting protein-ligand interactions based on bow-pharmacological space and Bayesian additive regression trees. <i>Scientific Reports</i> , <b>2019</b> , 9, 7703	4.9	17
131	A novel algorithm for finding optimal driver nodes to target control complex networks and its applications for drug targets identification. <i>BMC Genomics</i> , <b>2018</b> , 19, 924	4.5	17
130	Towards a critical transition theory under different temporal scales and noise strengths. <i>Physical Review E</i> , <b>2016</b> , 93, 032137	2.4	17
129	Transcriptomic analysis of the effects of Toll-like receptor 4 and its ligands on the gene expression network of hepatic stellate cells. <i>Fibrogenesis and Tissue Repair</i> , <b>2016</b> , 9, 2		17
128	Unravelling miRNA regulation in yield of rice ( <i>Oryza sativa</i> ) based on differential network model. <i>Scientific Reports</i> , <b>2018</b> , 8, 8498	4.9	17
127	Partial cross mapping eliminates indirect causal influences. <i>Nature Communications</i> , <b>2020</b> , 11, 2632	17.4	16
126	"Dysfunctions" induced by Roux-en-Y gastric bypass surgery are concomitant with metabolic improvement independent of weight loss. <i>Cell Discovery</i> , <b>2020</b> , 6, 4	22.3	16
125	Constrained target controllability of complex networks. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , <b>2017</b> , 2017, 063402	1.9	16
124	Impaired Functional Criticality of Human Brain during Alzheimer's Disease Progression. <i>Scientific Reports</i> , <b>2018</b> , 8, 1324	4.9	15
123	CMIP: a software package capable of reconstructing genome-wide regulatory networks using gene expression data. <i>BMC Bioinformatics</i> , <b>2016</b> , 17, 535	3.6	15
122	The effects of graded levels of calorie restriction: IV. Non-linear change in behavioural phenotype of mice in response to short-term calorie restriction. <i>Scientific Reports</i> , <b>2015</b> , 5, 13198	4.9	15
121	Serum chemokine network correlates with chemotherapy in non-small cell lung cancer. <i>Cancer Letters</i> , <b>2015</b> , 365, 57-67	9.9	15
120	The effects of graded levels of calorie restriction: VII. Topological rearrangement of hypothalamic aging networks. <i>Aging</i> , <b>2016</b> , 8, 917-32	5.6	15
119	Autoreservoir computing for multistep ahead prediction based on the spatiotemporal information transformation. <i>Nature Communications</i> , <b>2020</b> , 11, 4568	17.4	15
118	Identifying module biomarker in type 2 diabetes mellitus by discriminative area of functional activity. <i>BMC Bioinformatics</i> , <b>2015</b> , 16, 92	3.6	14
117	A multi-omics investigation of the molecular characteristics and classification of six metabolic syndrome relevant diseases. <i>Theranostics</i> , <b>2020</b> , 10, 2029-2046	12.1	14
116	Network Biomarkers Constructed from Gene Expression and Protein-Protein Interaction Data for Accurate Prediction of Leukemia. <i>Journal of Cancer</i> , <b>2017</b> , 8, 278-286	4.5	14
115	Deep-joint-learning analysis model of single cell transcriptome and open chromatin accessibility data. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,	13.4	14

114	Improved flower pollination algorithm for identifying essential proteins. <i>BMC Systems Biology</i> , <b>2018</b> , 12, 46	3.5	13
113	Large-scale Generation of Functional and Transplantable Hepatocytes and Cholangiocytes from Human Endoderm Stem Cells. <i>Cell Reports</i> , <b>2020</b> , 33, 108455	10.6	12
112	Targeted genetic screening in mice through haploid embryonic stem cells identifies critical genes in bone development. <i>PLoS Biology</i> , <b>2019</b> , 17, e3000350	9.7	12
111	Predicting Time Series from Short-Term High-Dimensional Data. <i>International Journal of Bifurcation and Chaos in Applied Sciences and Engineering</i> , <b>2014</b> , 24, 1430033	2	12
110	Parallel clustering algorithm for large-scale biological data sets. <i>PLoS ONE</i> , <b>2014</b> , 9, e91315	3.7	12
109	Quantifying Waddington's epigenetic landscape: a comparison of single-cell potency measures. <i>Briefings in Bioinformatics</i> , <b>2018</b> ,	13.4	12
108	Dynamic edge-based biomarker non-invasively predicts hepatocellular carcinoma with hepatitis B virus infection for individual patients based on blood testing. <i>Journal of Molecular Cell Biology</i> , <b>2019</b> , 11, 665-677	6.3	11
107	The Effects of Graded Levels of Calorie Restriction: X. Transcriptomic Responses of Epididymal Adipose Tissue. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , <b>2018</b> , 73, 279-288	6.4	11
106	Revealing dynamic regulations and the related key proteins of myeloma-initiating cells by integrating experimental data into a systems biological model. <i>Bioinformatics</i> , <b>2021</b> , 37, 1554-1561	7.2	10
105	On the robust stability of time-varying uncertain genetic regulatory networks. <i>International Journal of Robust and Nonlinear Control</i> , <b>2011</b> , 21, 1778-1790	3.6	10
104	Molecular dynamics simulation reveals how phosphorylation of tyrosine 26 of phosphoglycerate mutase 1 upregulates glycolysis and promotes tumor growth. <i>Oncotarget</i> , <b>2017</b> , 8, 12093-12107	3.3	10
103	SIDeseq: A Cell Similarity Measure Defined by Shared Identified Differentially Expressed Genes for Single-Cell RNA sequencing Data. <i>Statistics in Biosciences</i> , <b>2017</b> , 9, 200-216	1.5	9
102	Identifying pre-disease signals before metabolic syndrome in mice by dynamical network biomarkers. <i>Scientific Reports</i> , <b>2019</b> , 9, 8767	4.9	9
101	Chronic hepatitis B: dynamic change in Traditional Chinese Medicine syndrome by dynamic network biomarkers. <i>Chinese Medicine</i> , <b>2019</b> , 14, 52	4.7	9
100	Network analysis reveals roles of inflammatory factors in different phenotypes of kidney transplant patients. <i>Journal of Theoretical Biology</i> , <b>2014</b> , 362, 62-8	2.3	8
99	Nerve Injury-Induced Neuronal PAP-I Maintains Neuropathic Pain by Activating Spinal Microglia. <i>Journal of Neuroscience</i> , <b>2020</b> , 40, 297-310	6.6	8
98	Potential transmission chains of variant B.1.1.7 and co-mutations of SARS-CoV-2. <i>Cell Discovery</i> , <b>2021</b> , 7, 44	22.3	8
97	Detecting direct associations in a network by information theoretic approaches. <i>Science China Mathematics</i> , <b>2019</b> , 62, 823-838	0.8	8

96	SMAD7 and SERPINE1 as novel dynamic network biomarkers detect and regulate the tipping point of TGF-beta induced EMT. <i>Science Bulletin</i> , <b>2020</b> , 65, 842-853	10.6	7
95	Modelling biochemical reaction systems by stochastic differential equations with reflection. <i>Journal of Theoretical Biology</i> , <b>2016</b> , 396, 90-104	2.3	7
94	Systematic computation with functional gene-sets among leukemic and hematopoietic stem cells reveals a favorable prognostic signature for acute myeloid leukemia. <i>BMC Bioinformatics</i> , <b>2015</b> , 16, 97	3.6	7
93	Predicting future dynamics from short-term time series using an Anticipated Learning Machine. <i>National Science Review</i> , <b>2020</b> , 7, 1079-1091	10.8	6
92	Oleic Acid Attenuates Ang II (Angiotensin II)-Induced Cardiac Remodeling by Inhibiting FGF23 (Fibroblast Growth Factor 23) Expression in Mice. <i>Hypertension</i> , <b>2020</b> , 75, 680-692	8.5	6
91	Local network component analysis for quantifying transcription factor activities. <i>Methods</i> , <b>2017</b> , 124, 25-35	4.6	6
90	Low-Grade Dysplastic Nodules Revealed as the Tipping Point during Multistep Hepatocarcinogenesis by Dynamic Network Biomarkers. <i>Genes</i> , <b>2017</b> , 8,	4.2	6
89	Identification of Key Genes for the Ultrahigh Yield of Rice Using Dynamic Cross-tissue Network Analysis. <i>Genomics, Proteomics and Bioinformatics</i> , <b>2020</b> , 18, 256-270	6.5	6
88	Associating lncRNAs with small molecules via bilevel optimization reveals cancer-related lncRNAs. <i>PLoS Computational Biology</i> , <b>2019</b> , 15, e1007540	5	6
87	Mutational Landscape and Evolutionary Pattern of Liver and Brain Metastasis in Lung Adenocarcinoma. <i>Journal of Thoracic Oncology</i> , <b>2021</b> , 16, 237-249	8.9	6
86	Network controllability-based algorithm to target personalized driver genes for discovering combinatorial drugs of individual patients. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, e37	20.1	6
85	Predicting local COVID-19 outbreaks and infectious disease epidemics based on landscape network entropy. <i>Science Bulletin</i> , <b>2021</b> , 66, 2265-2270	10.6	6
84	Comparative network stratification analysis for identifying functional interpretable network biomarkers. <i>BMC Bioinformatics</i> , <b>2017</b> , 18, 48	3.6	5
83	High-Order Correlation Integration for Single-Cell or Bulk RNA-seq Data Analysis. <i>Frontiers in Genetics</i> , <b>2019</b> , 10, 371	4.5	5
82	Genome-wide dynamic network analysis reveals a critical transition state of flower development in Arabidopsis. <i>BMC Plant Biology</i> , <b>2019</b> , 19, 11	5.3	5
81	Single amino acid changes in naked mole rat may reveal new anti-cancer mechanisms in mammals. <i>Gene</i> , <b>2015</b> , 572, 101-107	3.8	5
80	Detecting causality from short time-series data based on prediction of topologically equivalent attractors. <i>BMC Systems Biology</i> , <b>2017</b> , 11, 128	3.5	5
79	Quantifying pluripotency landscape of cell differentiation from scRNA-seq data by continuous birth-death process. <i>PLoS Computational Biology</i> , <b>2019</b> , 15, e1007488	5	5

78	Genomic insights of body plan transitions from bilateral to pentameral symmetry in Echinoderms. <i>Communications Biology</i> , <b>2020</b> , 3, 371	6.7	5
77	Suppression of Dynamical Network Biomarker Signals at the Predisease State () before Metabolic Syndrome in Mice by a Traditional Japanese Medicine (Kampo Formula) Bofutsushosan. <i>Evidence-based Complementary and Alternative Medicine</i> , <b>2020</b> , 2020, 9129134	2.3	5
76	Identification of Alzheimer's disease based on wavelet transformation energy feature of the structural MRI image and NN classifier. <i>Artificial Intelligence in Medicine</i> , <b>2020</b> , 108, 101940	7.4	5
75	Quantifying Direct Dependencies in Biological Networks by Multiscale Association Analysis. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2020</b> , 17, 449-458	3	5
74	Disease characterization using a partial correlation-based sample-specific network. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,	13.4	5
73	Tgfb3 and Mmp13 regulated the initiation of liver fibrosis progression as dynamic network biomarkers. <i>Journal of Cellular and Molecular Medicine</i> , <b>2021</b> , 25, 867-879	5.6	5
72	Nanodiamonds Interfere with Wnt-Regulated Cell Migration and Adipocyte Differentiation in Cells and Embryonic Development In Vivo. <i>Particle and Particle Systems Characterization</i> , <b>2017</b> , 34, 1600208	3.1	4
71	Reinitiation enhances reliable transcriptional responses in eukaryotes. <i>Journal of the Royal Society Interface</i> , <b>2014</b> , 11, 20140326	4.1	4
70	Visualization of biomolecular networks' comparison on cytoscape. <i>Tsinghua Science and Technology</i> , <b>2013</b> , 18, 515--521	3.4	4
69	A parameter condition for ruling out multiple equilibria of the photosynthetic carbon metabolism. <i>Asian Journal of Control</i> , <b>2011</b> , 13, 611-624	1.7	4
68	Prediction and Dissection of Protein-RNA Interactions by Molecular Descriptors. <i>Current Topics in Medicinal Chemistry</i> , <b>2016</b> , 16, 604-15	3	4
67	Network control principles for identifying personalized driver genes in cancer. <i>Briefings in Bioinformatics</i> , <b>2020</b> , 21, 1641-1662	13.4	4
66	Tracing steroidogenesis in prostate biopsy samples to unveil prostate tissue androgen metabolism characteristics and potential clinical application. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , <b>2021</b> , 210, 105859	5.1	4
65	Single-cell RNA-sequencing atlas reveals an MDK-dependent immunosuppressive environment in ErbB pathway-mutated gallbladder cancer. <i>Journal of Hepatology</i> , <b>2021</b> , 75, 1128-1141	13.4	4
64	The Effects of Graded Levels of Calorie Restriction: XVI. Metabolomic Changes in the Cerebellum Indicate Activation of Hypothalamocerebellar Connections Driven by Hunger Responses. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , <b>2021</b> , 76, 601-610	6.4	4
63	Dynamic network biomarker analysis discovers IbNAC083 in the initiation and regulation of sweet potato root tuberization. <i>Plant Journal</i> , <b>2021</b> , 108, 793-813	6.9	4
62	Gene expression analysis reveals the tipping points during infant brain development for human and chimpanzee. <i>BMC Genomics</i> , <b>2020</b> , 21, 74	4.5	3
61	Evolution and transition of expression trajectory during human brain development. <i>BMC Evolutionary Biology</i> , <b>2020</b> , 20, 72	3	3

60	The oscillatory boundary conditions of different frequency bands in Parkinson's disease. <i>Journal of Theoretical Biology</i> , <b>2018</b> , 451, 67-79	2.3	3
59	Multi-equilibrium property of metabolic networks: Exclusion of multi-stability for SSN metabolic modules. <i>International Journal of Robust and Nonlinear Control</i> , <b>2011</b> , 21, 1791-1806	3.6	3
58	A new method to identify repositioned drugs for prostate cancer <b>2012</b> ,		3
57	Improved Human Age Prediction by Using Gene Expression Profiles From Multiple Tissues. <i>Frontiers in Genetics</i> , <b>2020</b> , 11, 1025	4.5	3
56	Collective fluctuation implies imminent state transition: Comment on "Dynamic and thermodynamic models of adaptation" by A.N. Gorban et al. <i>Physics of Life Reviews</i> , <b>2021</b> , 37, 103-107	2.1	3
55	Uncovering Driver DNA Methylation Events in Nonsmoking Early Stage Lung Adenocarcinoma. <i>BioMed Research International</i> , <b>2016</b> , 2016, 2090286	3	3
54	Extracting ROI-Based Contourlet Subband Energy Feature from the sMRI Image for Alzheimer's Disease Classification. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2021</b> , PP,	3	3
53	c-CSN: Single-cell RNA Sequencing Data Analysis by Conditional Cell-specific Network. <i>Genomics, Proteomics and Bioinformatics</i> , <b>2021</b> , 19, 319-329	6.5	3
52	Analysis on gene modular network reveals morphogen-directed development robustness in. <i>Cell Discovery</i> , <b>2020</b> , 6, 43	22.3	2
51	The generation mechanism of spike-and-slow wave discharges appearing on thalamic relay nuclei. <i>Scientific Reports</i> , <b>2018</b> , 8, 4953	4.9	2
50	Hierarchical graphical model reveals HFR1 bridging circadian rhythm and flower development in. <i>Npj Systems Biology and Applications</i> , <b>2019</b> , 5, 28	5	2
49	in silico identification of novel cancer-related genes by comparative genomics of naked mole rat and rat <b>2012</b> ,		2
48	Quantifying Waddington's epigenetic landscape: a comparison of single-cell potency measures		2
47	Critical transitions and tipping points in EMT. <i>Quantitative Biology</i> , <b>2020</b> , 8, 195-202	3.9	2
46	Efficient Mining Multi-mers in a Variety of Biological Sequences. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2018</b> ,	3	2
45	Dynamics-based data science in biology. <i>National Science Review</i> , <b>2021</b> , 8, nwab029	10.8	2
44	Facial Skin Microbiota-Mediated Host Response to Pollution Stress Revealed by Microbiome Networks of Individual. <i>MSystems</i> , <b>2021</b> , 6, e0031921	7.6	2
43	Detection of Alzheimer's disease using features of brain region-of-interest-based individual network constructed with the sMRI image.. <i>Computerized Medical Imaging and Graphics</i> , <b>2022</b> , 98, 102057	7.6	2

42	A randomized controlled trial for response of microbiome network to exercise and diet intervention in patients with nonalcoholic fatty liver disease.. <i>Nature Communications</i> , <b>2022</b> , 13, 2555	17.4	2
41	Differential function analysis: identifying structure and activation variations in dysregulated pathways. <i>Science China Information Sciences</i> , <b>2017</b> , 60, 1	3.4	1
40	The Effects of Graded Levels of Calorie Restriction XV: Phase Space Attractors Reveal Distinct Behavioral Phenotypes. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , <b>2020</b> , 75, 858-866	6.4	1
39	Personalized Early-Warning Signals during Progression of Human Coronary Atherosclerosis by Landscape Dynamic Network Biomarker. <i>Genes</i> , <b>2020</b> , 11,	4.2	1
38	Identifying rice arsenic stress response pathways based on molecular interaction network <b>2012</b> ,		1
37	Comparative analysis of protein-coding genes and long non-coding RNAs of prostate cancer between Caucasian and Chinese populations <b>2012</b> ,		1
36	A fixed-point blind source extraction algorithm and its application to ECG data analysis <b>2012</b> ,		1
35	Adaptation of simple molecular networks to time-dependent stimulus. <i>Asian Journal of Control</i> , <b>2011</b> , 13, 701-712	1.7	1
34	Detecting coherent local patterns from time series gene expression data by a temporal biclustering method <b>2011</b> ,		1
33	Protein interaction prediction for mouse pdz domains using dipeptide composition features <b>2011</b> ,		1
32	Identifying temporal trace of biological process during phase transition <b>2011</b> ,		1
31	Dynamical modeling of chronic myeloid leukemia progression and the development of mutations <b>2012</b> ,		1
30	Reconstructing dynamic gene regulatory network for the development process of hepatocellular carcinoma <b>2012</b> ,		1
29	Deep latent space fusion for adaptive representation of heterogeneous multi-omics data.. <i>Briefings in Bioinformatics</i> , <b>2022</b> ,	13.4	1
28	Dynamical network biomarkers: Theory and applications. <i>Gene</i> , <b>2022</b> , 808, 145997	3.8	1
27	MeSSII interplays the amylose and amylopectin biosynthesis by protein interactions in cassava storage root		1
26	Identifying Critical States of Complex Diseases by Single-Sample Jensen-Shannon Divergence. <i>Frontiers in Oncology</i> , <b>2021</b> , 11, 684781	5.3	1
25	Identifying joint biomarker panel from multiple level dataset by an optimization model. <i>Biomarkers in Medicine</i> , <b>2016</b> , 10, 567-75	2.3	1

24	Integration of multiple heterogeneous omics data <b>2016</b> ,		1
23	Targeting HSPA1A in ARID2-deficient lung adenocarcinoma. <i>National Science Review</i> , <b>2021</b> , 8, nwab014	10.8	1
22	Single-cell RNA sequencing data analysis based on non-uniform neighborhood network.. <i>Bioinformatics</i> , <b>2022</b> ,	7.2	1
21	Integrative analysis of multi-omics data reveals the heterogeneity and signatures of immune therapy for small cell lung cancer.. <i>Clinical and Translational Medicine</i> , <b>2021</b> , 11, e620	5.7	1
20	Interpreting Functional Impact of Genetic Variations by Network QTL for Genotype-Phenotype Association Study.. <i>Frontiers in Cell and Developmental Biology</i> , <b>2021</b> , 9, 720321	5.7	0
19	Derivedness Index for Estimating Degree of Phenotypic Evolution of Embryos: A Study of Comparative Transcriptomic Analyses of Chordates and Echinoderms.. <i>Frontiers in Cell and Developmental Biology</i> , <b>2021</b> , 9, 749963	5.7	0
18	scDA: Single cell discriminant analysis for single-cell RNA sequencing data. <i>Computational and Structural Biotechnology Journal</i> , <b>2021</b> , 19, 3234-3244	6.8	0
17	Embedding entropy: a nonlinear measure of dynamical causality.. <i>Journal of the Royal Society Interface</i> , <b>2022</b> , 19, 20210766	4.1	0
16	Integrated profiling of human pancreatic cancer organoids reveals chromatin accessibility features associated with drug sensitivity.. <i>Nature Communications</i> , <b>2022</b> , 13, 2169	17.4	0
15	Dynamic network biomarker analysis and system pharmacology methods to explore the therapeutic effects and targets of Xiaoyaosan against liver cirrhosis.. <i>Journal of Ethnopharmacology</i> , <b>2022</b> , 294, 115324	5	0
14	The onset mechanism of Parkinson's beta oscillations: A theoretical analysis. <i>Journal of Theoretical Biology</i> , <b>2019</b> , 470, 1-16	2.3	
13	Different effects of fast and slow input fluctuations on output in gene regulation. <i>Chaos</i> , <b>2020</b> , 30, 023104	10.4	
12	Gene expression profiling of selenophosphate synthetase 2 knockdown in Drosophila melanogaster. <i>Metallomics</i> , <b>2016</b> , 8, 354-65	4.5	
11	Spice simulation of intracellular transport: Free diffusion. <i>Asian Journal of Control</i> , <b>2011</b> , 13, 738-748	1.7	
10	Computational Models for Condition-Specific Gene and Pathway Inference <b>2010</b> , 665-689		
9	Protein Function Prediction with Data-Mining Techniques <b>2010</b> , 479-499		
8	The effect of coupled feedback on noise filtering in signal transduction networks. <i>Journal of Systems Science and Complexity</i> , <b>2010</b> , 23, 942-950		1
7	Kinase-substrate Edge Biomarkers Provide a More Accurate Prognostic Prediction in ER-negative Breast Cancer. <i>Genomics, Proteomics and Bioinformatics</i> , <b>2020</b> , 18, 525-538	6.5	

6 EPCO-31. GERMLINE AND SOMATIC MUTATIONS IN PEDIATRIC GERM CELL TUMORS. *Neuro-Oncology*, **2021**, 23, vi8-vi9 1

5 A novel network control model for identifying personalized driver genes in cancer **2019**, 15, e1007520

4 A novel network control model for identifying personalized driver genes in cancer **2019**, 15, e1007520

3 A novel network control model for identifying personalized driver genes in cancer **2019**, 15, e1007520

2 A novel network control model for identifying personalized driver genes in cancer **2019**, 15, e1007520

1 A novel network control model for identifying personalized driver genes in cancer **2019**, 15, e1007520