

Luonan Chen

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.

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	Deep latent space fusion for adaptive representation of heterogeneous multi-omics data.. <i>Briefings in Bioinformatics</i> , 2022 ,	13.4	1
202	Dynamical network biomarkers: Theory and applications. <i>Gene</i> , 2022 , 808, 145997	3.8	1
201	Single-cell RNA sequencing data analysis based on non-uniform β -neighborhood network.. <i>Bioinformatics</i> , 2022 ,	7.2	1
200	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> , 2022 , 98, 102057	7.6	2
199	Embedding entropy: a nonlinear measure of dynamical causality.. <i>Journal of the Royal Society Interface</i> , 2022 , 19, 20210766	4.1	0
198	Integrated profiling of human pancreatic cancer organoids reveals chromatin accessibility features associated with drug sensitivity.. <i>Nature Communications</i> , 2022 , 13, 2169	17.4	0
197	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> , 2022 , 13, 2555	17.4	2
196	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> , 2022 , 294, 115324	5	0
195	Revealing dynamic regulations and the related key proteins of myeloma-initiating cells by integrating experimental data into a systems biological model. <i>Bioinformatics</i> , 2021 , 37, 1554-1561	7.2	10
194	Interpreting Functional Impact of Genetic Variations by Network QTL for Genotype-Phenotype Association Study.. <i>Frontiers in Cell and Developmental Biology</i> , 2021 , 9, 720321	5.7	0
193	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> , 2021 , 9, 749963	5.7	0
192	EPCO-31. GERMLINE AND SOMATIC MUTATIONS IN PEDIATRIC GERM CELL TUMORS. <i>Neuro-Oncology</i> , 2021 , 23, vi8-vi9	1	
191	Deep-joint-learning analysis model of single cell transcriptome and open chromatin accessibility data. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	14
190	Identifying Critical States of Complex Diseases by Single-Sample Jensen-Shannon Divergence. <i>Frontiers in Oncology</i> , 2021 , 11, 684781	5.3	1
189	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> , 2021 , 210, 105859	5.1	4
188	Potential transmission chains of variant B.1.1.7 and co-mutations of SARS-CoV-2. <i>Cell Discovery</i> , 2021 , 7, 44	22.3	8
187	Single-cell RNA-sequencing atlas reveals an MDK-dependent immunosuppressive environment in ErbB pathway-mutated gallbladder cancer. <i>Journal of Hepatology</i> , 2021 , 75, 1128-1141	13.4	4

186	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> , 2021 , 37, 103-107	2.1	3
185	Disease characterization using a partial correlation-based sample-specific network. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	5
184	Tgfb3 and Mmp13 regulated the initiation of liver fibrosis progression as dynamic network biomarkers. <i>Journal of Cellular and Molecular Medicine</i> , 2021 , 25, 867-879	5.6	5
183	Mutational Landscape and Evolutionary Pattern of Liver and Brain Metastasis in Lung Adenocarcinoma. <i>Journal of Thoracic Oncology</i> , 2021 , 16, 237-249	8.9	6
182	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> , 2021 , 76, 601-610	6.4	4
181	scDA: Single cell discriminant analysis for single-cell RNA sequencing data. <i>Computational and Structural Biotechnology Journal</i> , 2021 , 19, 3234-3244	6.8	0
180	Network controllability-based algorithm to target personalized driver genes for discovering combinatorial drugs of individual patients. <i>Nucleic Acids Research</i> , 2021 , 49, e37	20.1	6
179	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> , 2021 , PP,	3	3
178	Dynamics-based data science in biology. <i>National Science Review</i> , 2021 , 8, nwab029	10.8	2
177	c-CSN: Single-cell RNA Sequencing Data Analysis by Conditional Cell-specific Network. <i>Genomics, Proteomics and Bioinformatics</i> , 2021 , 19, 319-329	6.5	3
176	Facial Skin Microbiota-Mediated Host Response to Pollution Stress Revealed by Microbiome Networks of Individual. <i>MSystems</i> , 2021 , 6, e0031921	7.6	2
175	Dynamic network biomarker analysis discovers IbNAC083 in the initiation and regulation of sweet potato root tuberization. <i>Plant Journal</i> , 2021 , 108, 793-813	6.9	4
174	Predicting local COVID-19 outbreaks and infectious disease epidemics based on landscape network entropy. <i>Science Bulletin</i> , 2021 , 66, 2265-2270	10.6	6
173	Targeting HSPA1A in ARID2-deficient lung adenocarcinoma. <i>National Science Review</i> , 2021 , 8, nwab014	10.8	1
172	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> , 2021 , 11, e620	5.7	1
171	Large-scale Generation of Functional and Transplantable Hepatocytes and Cholangiocytes from Human Endoderm Stem Cells. <i>Cell Reports</i> , 2020 , 33, 108455	10.6	12
170	Partial cross mapping eliminates indirect causal influences. <i>Nature Communications</i> , 2020 , 11, 2632	17.4	16
169	CIDO, a community-based ontology for coronavirus disease knowledge and data integration, sharing, and analysis. <i>Scientific Data</i> , 2020 , 7, 181	8.2	41

168	Gene expression analysis reveals the tipping points during infant brain development for human and chimpanzee. <i>BMC Genomics</i> , 2020 , 21, 74	4.5	3
167	A plausible accelerating function of intermediate states in cancer metastasis. <i>PLoS Computational Biology</i> , 2020 , 16, e1007682	5	18
166	Predicting future dynamics from short-term time series using an Anticipated Learning Machine. <i>National Science Review</i> , 2020 , 7, 1079-1091	10.8	6
165	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> , 2020 , 75, 858-866	6.4	1
164	Analysis on gene modular network reveals morphogen-directed development robustness in. <i>Cell Discovery</i> , 2020 , 6, 43	22.3	2
163	Evolution and transition of expression trajectory during human brain development. <i>BMC Evolutionary Biology</i> , 2020 , 20, 72	3	3
162	Personalized Early-Warning Signals during Progression of Human Coronary Atherosclerosis by Landscape Dynamic Network Biomarker. <i>Genes</i> , 2020 , 11,	4.2	1
161	Different effects of fast and slow input fluctuations on output in gene regulation. <i>Chaos</i> , 2020 , 30, 023104	9.4	1
160	"Dysfunctions" induced by Roux-en-Y gastric bypass surgery are concomitant with metabolic improvement independent of weight loss. <i>Cell Discovery</i> , 2020 , 6, 4	22.3	16
159	A multi-omics investigation of the molecular characteristics and classification of six metabolic syndrome relevant diseases. <i>Theranostics</i> , 2020 , 10, 2029-2046	12.1	14
158	Oleic Acid Attenuates Ang II (Angiotensin II)-Induced Cardiac Remodeling by Inhibiting FGF23 (Fibroblast Growth Factor 23) Expression in Mice. <i>Hypertension</i> , 2020 , 75, 680-692	8.5	6
157	SMAD7 and SERPINE1 as novel dynamic network biomarkers detect and regulate the tipping point of TGF-beta induced EMT. <i>Science Bulletin</i> , 2020 , 65, 842-853	10.6	7
156	Kinase-substrate Edge Biomarkers Provide a More Accurate Prognostic Prediction in ER-negative Breast Cancer. <i>Genomics, Proteomics and Bioinformatics</i> , 2020 , 18, 525-538	6.5	
155	Network control principles for identifying personalized driver genes in cancer. <i>Briefings in Bioinformatics</i> , 2020 , 21, 1641-1662	13.4	4
154	Nerve Injury-Induced Neuronal PAP-I Maintains Neuropathic Pain by Activating Spinal Microglia. <i>Journal of Neuroscience</i> , 2020 , 40, 297-310	6.6	8
153	Improved Human Age Prediction by Using Gene Expression Profiles From Multiple Tissues. <i>Frontiers in Genetics</i> , 2020 , 11, 1025	4.5	3
152	Genomic insights of body plan transitions from bilateral to pentameral symmetry in Echinoderms. <i>Communications Biology</i> , 2020 , 3, 371	6.7	5
151	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> , 2020 , 2020, 9129134	2.3	5

150	Identification of Key Genes for the Ultrahigh Yield of Rice Using Dynamic Cross-tissue Network Analysis. <i>Genomics, Proteomics and Bioinformatics</i> , 2020 , 18, 256-270	6.5	6
149	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> , 2020 , 108, 101940	7.4	5
148	Critical transitions and tipping points in EMT. <i>Quantitative Biology</i> , 2020 , 8, 195-202	3.9	2
147	Autoreservoir computing for multistep ahead prediction based on the spatiotemporal information transformation. <i>Nature Communications</i> , 2020 , 11, 4568	17.4	15
146	Single-cell transcriptomics identifies a distinct luminal progenitor cell type in distal prostate invagination tips. <i>Nature Genetics</i> , 2020 , 52, 908-918	36.3	30
145	Quantifying Direct Dependencies in Biological Networks by Multiscale Association Analysis. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020 , 17, 449-458	3	5
144	Single-sample landscape entropy reveals the imminent phase transition during disease progression. <i>Bioinformatics</i> , 2020 , 36, 1522-1532	7.2	20
143	Predicting protein-ligand interactions based on bow-pharmacological space and Bayesian additive regression trees. <i>Scientific Reports</i> , 2019 , 9, 7703	4.9	17
142	High-Order Correlation Integration for Single-Cell or Bulk RNA-seq Data Analysis. <i>Frontiers in Genetics</i> , 2019 , 10, 371	4.5	5
141	A vitamin-C-derived DNA modification catalysed by an algal TET homologue. <i>Nature</i> , 2019 , 569, 581-585	50.4	41
140	Cell-specific network constructed by single-cell RNA sequencing data. <i>Nucleic Acids Research</i> , 2019 , 47, e62	20.1	43
139	The onset mechanism of Parkinson's beta oscillations: A theoretical analysis. <i>Journal of Theoretical Biology</i> , 2019 , 470, 1-16	2.3	
138	Competitive endogenous RNA is an intrinsic component of EMT regulatory circuits and modulates EMT. <i>Nature Communications</i> , 2019 , 10, 1637	17.4	50
137	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> , 2019 , 11, 665-677	6.3	11
136	Genome-wide dynamic network analysis reveals a critical transition state of flower development in Arabidopsis. <i>BMC Plant Biology</i> , 2019 , 19, 11	5.3	5
135	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> , 2019 , 116, 3646-3655	11.5	21
134	Hierarchical graphical model reveals HFR1 bridging circadian rhythm and flower development in. <i>Npj Systems Biology and Applications</i> , 2019 , 5, 28	5	2
133	Branched-Chain Amino Acid Metabolic Reprogramming Orchestrates Drug Resistance to EGFR Tyrosine Kinase Inhibitors. <i>Cell Reports</i> , 2019 , 28, 512-525.e6	10.6	32

132	Identifying pre-disease signals before metabolic syndrome in mice by dynamical network biomarkers. <i>Scientific Reports</i> , 2019 , 9, 8767	4.9	9
131	Targeted genetic screening in mice through haploid embryonic stem cells identifies critical genes in bone development. <i>PLoS Biology</i> , 2019 , 17, e3000350	9.7	12
130	Quantifying pluripotency landscape of cell differentiation from scRNA-seq data by continuous birth-death process. <i>PLoS Computational Biology</i> , 2019 , 15, e1007488	5	5
129	Cullin5 deficiency promotes small-cell lung cancer metastasis by stabilizing integrin β . <i>Journal of Clinical Investigation</i> , 2019 , 129, 972-987	15.9	32
128	A novel network control model for identifying personalized driver genes in cancer. <i>PLoS Computational Biology</i> , 2019 , 15, e1007520	5	20
127	Chronic hepatitis B: dynamic change in Traditional Chinese Medicine syndrome by dynamic network biomarkers. <i>Chinese Medicine</i> , 2019 , 14, 52	4.7	9
126	Associating lncRNAs with small molecules via bilevel optimization reveals cancer-related lncRNAs. <i>PLoS Computational Biology</i> , 2019 , 15, e1007540	5	6
125	Detecting direct associations in a network by information theoretic approaches. <i>Science China Mathematics</i> , 2019 , 62, 823-838	0.8	8
124	Detection for disease tipping points by landscape dynamic network biomarkers. <i>National Science Review</i> , 2019 , 6, 775-785	10.8	41
123	Detecting early-warning signals of influenza outbreak based on dynamic network marker. <i>Journal of Cellular and Molecular Medicine</i> , 2019 , 23, 395-404	5.6	25
122	Victors: a web-based knowledge base of virulence factors in human and animal pathogens. <i>Nucleic Acids Research</i> , 2019 , 47, D693-D700	20.1	53
121	Hunt for the tipping point during endocrine resistance process in breast cancer by dynamic network biomarkers. <i>Journal of Molecular Cell Biology</i> , 2019 , 11, 649-664	6.3	33
120	A novel network control model for identifying personalized driver genes in cancer 2019 , 15, e1007520		
119	A novel network control model for identifying personalized driver genes in cancer 2019 , 15, e1007520		
118	A novel network control model for identifying personalized driver genes in cancer 2019 , 15, e1007520		
117	A novel network control model for identifying personalized driver genes in cancer 2019 , 15, e1007520		
116	A novel network control model for identifying personalized driver genes in cancer 2019 , 15, e1007520		
115	A novel algorithm for finding optimal driver nodes to target control complex networks and its applications for drug targets identification. <i>BMC Genomics</i> , 2018 , 19, 924	4.5	17

114	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> , 2018 , 115, E3978-E3986	11.5	45
113	Dynamic network biomarker indicates pulmonary metastasis at the tipping point of hepatocellular carcinoma. <i>Nature Communications</i> , 2018 , 9, 678	17.4	83
112	Impaired Functional Criticality of Human Brain during Alzheimer's Disease Progression. <i>Scientific Reports</i> , 2018 , 8, 1324	4.9	15
111	Discovering personalized driver mutation profiles of single samples in cancer by network control strategy. <i>Bioinformatics</i> , 2018 , 34, 1893-1903	7.2	44
110	The oscillatory boundary conditions of different frequency bands in Parkinson's disease. <i>Journal of Theoretical Biology</i> , 2018 , 451, 67-79	2.3	3
109	The generation mechanism of spike-and-slow wave discharges appearing on thalamic relay nuclei. <i>Scientific Reports</i> , 2018 , 8, 4953	4.9	2
108	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> , 2018 , 73, 279-288	6.4	11
107	Improved flower pollination algorithm for identifying essential proteins. <i>BMC Systems Biology</i> , 2018 , 12, 46	3.5	13
106	Unravelling miRNA regulation in yield of rice (<i>Oryza sativa</i>) based on differential network model. <i>Scientific Reports</i> , 2018 , 8, 8498	4.9	17
105	Efficient Mining Multi-mers in a Variety of Biological Sequences. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018 ,	3	2
104	Quantifying Waddington's epigenetic landscape: a comparison of single-cell potency measures. <i>Briefings in Bioinformatics</i> , 2018 ,	13.4	12
103	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> , 2018 , 115, E9994-E10002	11.5	22
102	PWCDA: Path Weighted Method for Predicting circRNA-Disease Associations. <i>International Journal of Molecular Sciences</i> , 2018 , 19,	6.3	48
101	Single cell clustering based on cell-pair differentiability correlation and variance analysis. <i>Bioinformatics</i> , 2018 , 34, 3684-3694	7.2	30
100	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> , 2017 , 16, 529-540	9.9	32
99	Differential function analysis: identifying structure and activation variations in dysregulated pathways. <i>Science China Information Sciences</i> , 2017 , 60, 1	3.4	1
98	SIDeseq: A Cell Similarity Measure Defined by Shared Identified Differentially Expressed Genes for Single-Cell RNA sequencing Data. <i>Statistics in Biosciences</i> , 2017 , 9, 200-216	1.5	9
97	Pattern fusion analysis by adaptive alignment of multiple heterogeneous omics data. <i>Bioinformatics</i> , 2017 , 33, 2706-2714	7.2	39

96	Comparative network stratification analysis for identifying functional interpretable network biomarkers. <i>BMC Bioinformatics</i> , 2017 , 18, 48	3.6	5
95	Individual-specific edge-network analysis for disease prediction. <i>Nucleic Acids Research</i> , 2017 , 45, e170	20.1	38
94	Network Biomarkers Constructed from Gene Expression and Protein-Protein Interaction Data for Accurate Prediction of Leukemia. <i>Journal of Cancer</i> , 2017 , 8, 278-286	4.5	14
93	Quantifying critical states of complex diseases using single-sample dynamic network biomarkers. <i>PLoS Computational Biology</i> , 2017 , 13, e1005633	5	51
92	Detecting causality from short time-series data based on prediction of topologically equivalent attractors. <i>BMC Systems Biology</i> , 2017 , 11, 128	3.5	5
91	Local network component analysis for quantifying transcription factor activities. <i>Methods</i> , 2017 , 124, 25-35	4.6	6
90	Dysfunction of PLA2G6 and CYP2C44-associated network signals imminent carcinogenesis from chronic inflammation to hepatocellular carcinoma. <i>Journal of Molecular Cell Biology</i> , 2017 , 9, 489-503	6.3	41
89	Constrained target controllability of complex networks. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2017 , 2017, 063402	1.9	16
88	Nanodiamonds Interfere with Wnt-Regulated Cell Migration and Adipocyte Differentiation in Cells and Embryonic Development In Vivo. <i>Particle and Particle Systems Characterization</i> , 2017 , 34, 1600208	3.1	4
87	Low-Grade Dysplastic Nodules Revealed as the Tipping Point during Multistep Hepatocarcinogenesis by Dynamic Network Biomarkers. <i>Genes</i> , 2017 , 8,	4.2	6
86	Molecular dynamics simulation reveals how phosphorylation of tyrosine 26 of phosphoglycerate mutase 1 upregulates glycolysis and promotes tumor growth. <i>Oncotarget</i> , 2017 , 8, 12093-12107	3.3	10
85	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> , 2017 , 8, 17453-17474	3.3	20
84	Hyperlipidemia-associated gene variations and expression patterns revealed by whole-genome and transcriptome sequencing of rabbit models. <i>Scientific Reports</i> , 2016 , 6, 26942	4.9	21
83	Towards a critical transition theory under different temporal scales and noise strengths. <i>Physical Review E</i> , 2016 , 93, 032137	2.4	17
82	Personalized characterization of diseases using sample-specific networks. <i>Nucleic Acids Research</i> , 2016 , 44, e164	20.1	128
81	CMIP: a software package capable of reconstructing genome-wide regulatory networks using gene expression data. <i>BMC Bioinformatics</i> , 2016 , 17, 535	3.6	15
80	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> , 2016 , 9, 2		17
79	Gene expression profiling of selenophosphate synthetase 2 knockdown in <i>Drosophila melanogaster</i> . <i>Metallomics</i> , 2016 , 8, 354-65	4.5	

78	Detecting critical state before phase transition of complex biological systems by hidden Markov model. <i>Bioinformatics</i> , 2016 , 32, 2143-50	7.2	36
77	Discovering a critical transition state from nonalcoholic hepatosteatois to nonalcoholic steatohepatitis by lipidomics and dynamical network biomarkers. <i>Journal of Molecular Cell Biology</i> , 2016 , 8, 195-206	6.3	24
76	Interferon-microRNA signalling drives liver precancerous lesion formation and hepatocarcinogenesis. <i>Gut</i> , 2016 , 65, 1186-201	19.2	31
75	Modelling biochemical reaction systems by stochastic differential equations with reflection. <i>Journal of Theoretical Biology</i> , 2016 , 396, 90-104	2.3	7
74	PPIM: A Protein-Protein Interaction Database for Maize. <i>Plant Physiology</i> , 2016 , 170, 618-26	6.6	62
73	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> , 2016 , 8, 642-63	5.6	20
72	The effects of graded levels of calorie restriction: VII. Topological rearrangement of hypothalamic aging networks. <i>Aging</i> , 2016 , 8, 917-32	5.6	15
71	Prediction and Dissection of Protein-RNA Interactions by Molecular Descriptors. <i>Current Topics in Medicinal Chemistry</i> , 2016 , 16, 604-15	3	4
70	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> , 2016 , 7, 19147-70	3.3	30
69	Uncovering Driver DNA Methylation Events in Nonsmoking Early Stage Lung Adenocarcinoma. <i>BioMed Research International</i> , 2016 , 2016, 2090286	3	3
68	Inference of Gene Regulatory Network Based on Local Bayesian Networks. <i>PLoS Computational Biology</i> , 2016 , 12, e1005024	5	73
67	Identifying joint biomarker panel from multiple level dataset by an optimization model. <i>Biomarkers in Medicine</i> , 2016 , 10, 567-75	2.3	1
66	Knowledge-Guided Bioinformatics Model for Identifying Autism Spectrum Disorder Diagnostic MicroRNA Biomarkers. <i>Scientific Reports</i> , 2016 , 6, 39663	4.9	36
65	Biomarker MicroRNAs for Diagnosis, Prognosis and Treatment of Hepatocellular Carcinoma: A Functional Survey and Comparison. <i>Scientific Reports</i> , 2016 , 6, 38311	4.9	59
64	Integration of multiple heterogeneous omics data 2016 ,		1
63	Part mutual information for quantifying direct associations in networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 5130-5	11.5	118
62	Comparison of Chromosome 4 gene expression profile between lung telocytes and other local cell types. <i>Journal of Cellular and Molecular Medicine</i> , 2016 , 20, 71-80	5.6	33
61	A novel mixed integer programming for multi-biomarker panel identification by distinguishing malignant from benign colorectal tumors. <i>Methods</i> , 2015 , 83, 3-17	4.6	18

60	Diagnosing phenotypes of single-sample individuals by edge biomarkers. <i>Journal of Molecular Cell Biology</i> , 2015 , 7, 231-41	6.3	48
59	Identifying module biomarker in type 2 diabetes mellitus by discriminative area of functional activity. <i>BMC Bioinformatics</i> , 2015 , 16, 92	3.6	14
58	Conditional mutual inclusive information enables accurate quantification of associations in gene regulatory networks. <i>Nucleic Acids Research</i> , 2015 , 43, e31	20.1	90
57	Single amino acid changes in naked mole rat may reveal new anti-cancer mechanisms in mammals. <i>Gene</i> , 2015 , 572, 101-107	3.8	5
56	Identifying cancer-related microRNAs based on gene expression data. <i>Bioinformatics</i> , 2015 , 31, 1226-34	7.2	66
55	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> , 2015 , 5, 13198	4.9	15
54	Identifying early-warning signals of critical transitions with strong noise by dynamical network markers. <i>Scientific Reports</i> , 2015 , 5, 17501	4.9	64
53	Unravelling personalized dysfunctional gene network of complex diseases based on differential network model. <i>Journal of Translational Medicine</i> , 2015 , 13, 189	8.5	24
52	Identifying critical differentiation state of MCF-7 cells for breast cancer by dynamical network biomarkers. <i>Frontiers in Genetics</i> , 2015 , 6, 252	4.5	19
51	Analysing the Effect of Mutation on Protein Function and Discovering Potential Inhibitors of CDK4: Molecular Modelling and Dynamics Studies. <i>PLoS ONE</i> , 2015 , 10, e0133969	3.7	36
50	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> , 2015 , 6, 15902-30	3.3	65
49	Serum chemokine network correlates with chemotherapy in non-small cell lung cancer. <i>Cancer Letters</i> , 2015 , 365, 57-67	9.9	15
48	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> , 2015 , 16, 97	3.6	7
47	Comparative genomics reveals new candidate genes involved in selenium metabolism in prokaryotes. <i>Genome Biology and Evolution</i> , 2015 , 7, 664-76	3.9	27
46	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> , 2015 , 6, 23213-37	3.3	56
45	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> , 2015 , 6, 18314-37	3.3	38
44	Detecting causality from nonlinear dynamics with short-term time series. <i>Scientific Reports</i> , 2014 , 4, 7464	4.9	43
43	Prediction of dynamical drug sensitivity and resistance by module network rewiring-analysis based on transcriptional profiling. <i>Drug Resistance Updates</i> , 2014 , 17, 64-76	23.2	33

42	Early diagnosis of complex diseases by molecular biomarkers, network biomarkers, and dynamical network biomarkers. <i>Medicinal Research Reviews</i> , 2014 , 34, 455-78	14.4	172
41	Network biomarkers, interaction networks and dynamical network biomarkers in respiratory diseases. <i>Clinical and Translational Medicine</i> , 2014 , 3, 16	5.7	41
40	EdgeMarker: Identifying differentially correlated molecule pairs as edge-biomarkers. <i>Journal of Theoretical Biology</i> , 2014 , 362, 35-43	2.3	52
39	Deciphering early development of complex diseases by progressive module network. <i>Methods</i> , 2014 , 67, 334-43	4.6	36
38	Network analysis reveals roles of inflammatory factors in different phenotypes of kidney transplant patients. <i>Journal of Theoretical Biology</i> , 2014 , 362, 62-8	2.3	8
37	Identifying critical transitions of complex diseases based on a single sample. <i>Bioinformatics</i> , 2014 , 30, 1579-86	7.2	57
36	Transittability of complex networks and its applications to regulatory biomolecular networks. <i>Scientific Reports</i> , 2014 , 4, 4819	4.9	40
35	Big biological data: challenges and opportunities. <i>Genomics, Proteomics and Bioinformatics</i> , 2014 , 12, 187-9	6.5	57
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