

Xiaoping Liu

List of Publications by Year in descending order

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Version: 2024-02-01

42
papers

1,605
citations

304368

22
h-index

301761

39
g-index

44
all docs

44
docs citations

44
times ranked

1773
citing authors

#	ARTICLE	IF	CITATIONS
1	Personalized characterization of diseases using sample-specific networks. <i>Nucleic Acids Research</i> , 2016, 44, e164-e164.	6.5	226
2	A real-time electrochemical technique for measurement of cellular hydrogen peroxide generation and consumption: evaluation in human polymorphonuclear leukocytes. <i>Free Radical Biology and Medicine</i> , 2001, 31, 894-901.	1.3	101
3	Identifying disease genes and module biomarkers by differential interactions. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2012, 19, 241-248.	2.2	99
4	Detection for disease tipping points by landscape dynamic network biomarkers. <i>National Science Review</i> , 2019, 6, 775-785.	4.6	94
5	Quantifying critical states of complex diseases using single-sample dynamic network biomarkers. <i>PLoS Computational Biology</i> , 2017, 13, e1005633.	1.5	90
6	Identifying critical transitions of complex diseases based on a single sample. <i>Bioinformatics</i> , 2014, 30, 1579-1586.	1.8	82
7	Detecting early-warning signals of type 1 diabetes and its leading biomolecular networks by dynamical network biomarkers. <i>BMC Medical Genomics</i> , 2013, 6, S8.	0.7	74
8	Diagnosing phenotypes of single-sample individuals by edge biomarkers. <i>Journal of Molecular Cell Biology</i> , 2015, 7, 231-241.	1.5	69
9	Feature selection of gene expression data for Cancer classification using double RBF-kernels. <i>BMC Bioinformatics</i> , 2018, 19, 396.	1.2	59
10	Big-data-based edge biomarkers: study on dynamical drug sensitivity and resistance in individuals. <i>Briefings in Bioinformatics</i> , 2016, 17, 576-592.	3.2	57
11	The heterogeneity of pore structure in lacustrine shales: Insights from multifractal analysis using N ₂ adsorption and mercury intrusion. <i>Marine and Petroleum Geology</i> , 2020, 114, 104150.	1.5	54
12	The Dynamics of DNA Methylation Covariation Patterns in Carcinogenesis. <i>PLoS Computational Biology</i> , 2014, 10, e1003709.	1.5	52
13	In vitro inhibition of postharvest pathogens of fruit and control of gray mold of strawberry and green mold of citrus by aureobasidin A. <i>International Journal of Food Microbiology</i> , 2007, 119, 223-229.	2.1	48
14	A Network Approach to Predict Pathogenic Genes for <i>Fusarium graminearum</i> . <i>PLoS ONE</i> , 2010, 5, e13021.	1.1	47
15	Insights in the pore structure, fluid mobility and oiliness in oil shales of Paleogene Funing Formation in Subei Basin, China. <i>Marine and Petroleum Geology</i> , 2020, 114, 104228.	1.5	46
16	A Gene Signature of Survival Prediction for Kidney Renal Cell Carcinoma by Multi-Omic Data Analysis. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5720.	1.8	44
17	Multicellular gene network analysis identifies a macrophage-related gene signature predictive of therapeutic response and prognosis of gliomas. <i>Journal of Translational Medicine</i> , 2019, 17, 159.	1.8	40
18	Detecting the tipping points in a three-state model of complex diseases by temporal differential networks. <i>Journal of Translational Medicine</i> , 2017, 15, 217.	1.8	37

#	ARTICLE	IF	CITATIONS
19	Edge biomarkers for classification and prediction of phenotypes. <i>Science China Life Sciences</i> , 2014, 57, 1103-1114.	2.3	30
20	Dynamical network biomarkers: Theory and applications. <i>Gene</i> , 2022, 808, 145997.	1.0	29
21	Whole-exome sequencing reveals recurrent somatic mutation networks in cancer. <i>Cancer Letters</i> , 2013, 340, 270-276.	3.2	28
22	DIPOS: database of interacting proteins in <i>Oryza sativa</i> . <i>Molecular BioSystems</i> , 2011, 7, 2615.	2.9	25
23	Inference of gene regulatory networks using pseudo-time series data. <i>Bioinformatics</i> , 2021, 37, 2423-2431.	1.8	18
24	Genome-wide dynamic network analysis reveals a critical transition state of flower development in <i>Arabidopsis</i> . <i>BMC Plant Biology</i> , 2019, 19, 11.	1.6	17
25	Integrating subpathway analysis to identify candidate agents for hepatocellular carcinoma. <i>OncoTargets and Therapy</i> , 2016, 9, 1221.	1.0	16
26	Disease characterization using a partial correlation-based sample-specific network. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	16
27	TransBorrow: genome-guided transcriptome assembly by borrowing assemblies from different assemblers. <i>Genome Research</i> , 2020, 30, 1181-1190.	2.4	15
28	Network analysis reveals roles of inflammatory factors in different phenotypes of kidney transplant patients. <i>Journal of Theoretical Biology</i> , 2014, 362, 62-68.	0.8	11
29	Identifying module biomarkers from gastric cancer by differential correlation network. <i>OncoTargets and Therapy</i> , 2016, Volume 9, 5701-5711.	1.0	11
30	Predicting Functional Modules of Liver Cancer Based on Differential Network Analysis. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2019, 11, 636-644.	2.2	10
31	A simple, SIR-like but individual-based epidemic model: Application in comparison of COVID-19 in New York City and Wuhan. <i>Results in Physics</i> , 2021, 20, 103712.	2.0	10
32	Quantifying Direct Dependencies in Biological Networks by Multiscale Association Analysis. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 17, 449-458.	1.9	9
33	Detecting causality from short time-series data based on prediction of topologically equivalent attractors. <i>BMC Systems Biology</i> , 2017, 11, 128.	3.0	8
34	Personalized Early-Warning Signals during Progression of Human Coronary Atherosclerosis by Landscape Dynamic Network Biomarker. <i>Genes</i> , 2020, 11, 676.	1.0	7
35	eFG: an electronic resource for <i>Fusarium graminearum</i> . <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat042-bat042.	1.4	5
36	Network-based identification of biomarkers for colon adenocarcinoma. <i>BMC Cancer</i> , 2020, 20, 668.	1.1	5

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37	Differential network inference via the fused D-trace loss with cross variables. <i>Electronic Journal of Statistics</i> , 2020, 14, .	0.4	5
38	Identification of HCC-Related Genes Based on Differential Partial Correlation Network. <i>Frontiers in Genetics</i> , 2021, 12, 672117.	1.1	4
39	Identifying network biomarkers of cancer by sample-specific differential network. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	3
40	Detecting disease genes of non-small lung cancer based on consistently differential interactions. <i>Cancer and Metastasis Reviews</i> , 2015, 34, 195-208.	2.7	1
41	Effect of pore structure on oil-bearing property in the third member of Paleogene Funing Formation in Subei Basin, East China. <i>Energy Science and Engineering</i> , 2020, 8, 2187-2202.	1.9	1
42	Transcriptome analysis method based on differential distribution evaluation. <i>Briefings in Bioinformatics</i> , 2022, , .	3.2	1