

# Xiaoping Liu

## List of Publications by Year in descending order

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Version: 2024-02-01

42  
papers

1,605  
citations

304743

22  
h-index

302126

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.	14.5	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.	2.9	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.	4.4	99
4	Detection for disease tipping points by landscape dynamic network biomarkers. <i>National Science Review</i> , 2019, 6, 775-785.	9.5	94
5	Quantifying critical states of complex diseases using single-sample dynamic network biomarkers. <i>PLoS Computational Biology</i> , 2017, 13, e1005633.	3.2	90
6	Identifying critical transitions of complex diseases based on a single sample. <i>Bioinformatics</i> , 2014, 30, 1579-1586.	4.1	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.	1.5	74
8	Diagnosing phenotypes of single-sample individuals by edge biomarkers. <i>Journal of Molecular Cell Biology</i> , 2015, 7, 231-241.	3.3	69
9	Feature selection of gene expression data for Cancer classification using double RBF-kernels. <i>BMC Bioinformatics</i> , 2018, 19, 396.	2.6	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.	6.5	57
11	The heterogeneity of pore structure in lacustrine shales: Insights from multifractal analysis using N <sub>2</sub> adsorption and mercury intrusion. <i>Marine and Petroleum Geology</i> , 2020, 114, 104150.	3.3	54
12	The Dynamics of DNA Methylation Covariation Patterns in Carcinogenesis. <i>PLoS Computational Biology</i> , 2014, 10, e1003709.	3.2	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.	4.7	48
14	A Network Approach to Predict Pathogenic Genes for <i>Fusarium graminearum</i> . <i>PLoS ONE</i> , 2010, 5, e13021.	2.5	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.	3.3	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.	4.1	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.	4.4	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.	4.4	37

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19	Edge biomarkers for classification and prediction of phenotypes. Science China Life Sciences, 2014, 57, 1103-1114.	4.9	30
20	Dynamical network biomarkers: Theory and applications. Gene, 2022, 808, 145997.	2.2	29
21	Whole-exome sequencing reveals recurrent somatic mutation networks in cancer. Cancer Letters, 2013, 340, 270-276.	7.2	28
22	DIPOS: database of interacting proteins in Oryza sativa. Molecular BioSystems, 2011, 7, 2615.	2.9	25
23	Inference of gene regulatory networks using pseudo-time series data. Bioinformatics, 2021, 37, 2423-2431.	4.1	18
24	Genome-wide dynamic network analysis reveals a critical transition state of flower development in Arabidopsis. BMC Plant Biology, 2019, 19, 11.	3.6	17
25	Integrating subpathway analysis to identify candidate agents for hepatocellular carcinoma. OncoTargets and Therapy, 2016, 9, 1221.	2.0	16
26	Disease characterization using a partial correlation-based sample-specific network. Briefings in Bioinformatics, 2021, 22, .	6.5	16
27	TransBorrow: genome-guided transcriptome assembly by borrowing assemblies from different assemblers. Genome Research, 2020, 30, 1181-1190.	5.5	15
28	Network analysis reveals roles of inflammatory factors in different phenotypes of kidney transplant patients. Journal of Theoretical Biology, 2014, 362, 62-68.	1.7	11
29	Identifying module biomarkers from gastric cancer by differential correlation network. OncoTargets and Therapy, 2016, Volume 9, 5701-5711.	2.0	11
30	Predicting Functional Modules of Liver Cancer Based on Differential Network Analysis. Interdisciplinary Sciences, Computational Life Sciences, 2019, 11, 636-644.	3.6	10
31	A simple, SIR-like but individual-based epidemic model: Application in comparison of COVID-19 in New York City and Wuhan. Results in Physics, 2021, 20, 103712.	4.1	10
32	Quantifying Direct Dependencies in Biological Networks by Multiscale Association Analysis. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 449-458.	3.0	9
33	Detecting causality from short time-series data based on prediction of topologically equivalent attractors. BMC Systems Biology, 2017, 11, 128.	3.0	8
34	Personalized Early-Warning Signals during Progression of Human Coronary Atherosclerosis by Landscape Dynamic Network Biomarker. Genes, 2020, 11, 676.	2.4	7
35	eFG: an electronic resource for Fusarium graminearum. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat042-bat042.	3.0	5
36	Network-based identification of biomarkers for colon adenocarcinoma. BMC Cancer, 2020, 20, 668.	2.6	5

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37	Differential network inference via the fused D-trace loss with cross variables. Electronic Journal of Statistics, 2020, 14, .	0.7	5
38	Identification of HCC-Related Genes Based on Differential Partial Correlation Network. Frontiers in Genetics, 2021, 12, 672117.	2.3	4
39	Identifying network biomarkers of cancer by sample-specific differential network. BMC Bioinformatics, 2022, 23, .	2.6	3
40	Detecting disease genes of non-small lung cancer based on consistently differential interactions. Cancer and Metastasis Reviews, 2015, 34, 195-208.	5.9	1
41	Effect of pore structure on oil-bearing property in the third member of Paleogene Funing Formation in Subei Basin, East China. Energy Science and Engineering, 2020, 8, 2187-2202.	4.0	1
42	Transcriptome analysis method based on differential distribution evaluation. Briefings in Bioinformatics, 2022, , .	6.5	1