

Zhi-Ping Liu

List of Publications by Year in descending order

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Version: 2024-02-01

100
papers

4,196
citations

172457

29
h-index

118850

62
g-index

102
all docs

102
docs citations

102
times ranked

5376
citing authors

#	ARTICLE	IF	CITATIONS
1	Network-based prioritization of cancer biomarkers by phenotype-driven module detection and ranking. Computational and Structural Biotechnology Journal, 2022, 20, 206-217.	4.1	6
2	PST-PRNA: prediction of RNA-binding sites using protein surface topography and deep learning. Bioinformatics, 2022, 38, 2162-2168.	4.1	12
3	tensorGSEA: Detecting Differential Pathways in Type 2 Diabetes via Tensor-Based Data Reconstruction. Interdisciplinary Sciences, Computational Life Sciences, 2022, 14, 520-531.	3.6	2
4	Predicting multiple types of MicroRNA-disease associations based on tensor factorization and label propagation. Computers in Biology and Medicine, 2022, 146, 105558.	7.0	8
5	Predicting Box-Office Markets with Machine Learning Methods. Entropy, 2022, 24, 711.	2.2	5
6	Prioritizing Type 2 Diabetes Genes by Weighted PageRank on Bilayer Heterogeneous Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 336-346.	3.0	12
7	Academic background of Nobel prize laureates reveals the importance of multidisciplinary education in medicine. Social Sciences & Humanities Open, 2021, 3, 100114.	2.2	2
8	Predicting lncRNA-protein Interactions by Machine Learning Methods: A Review. Current Bioinformatics, 2021, 15, 831-840.	1.5	14
9	Identifying Biomarkers of HCV-induced Dysplasia and Hepatocellular Carcinoma Based on Network Centrality. , 2021, , .		0
10	Predicting coastal algal blooms with environmental factors by machine learning methods. Ecological Indicators, 2021, 123, 107334.	6.3	41
11	Prediction of cardiovascular diseases by integrating multi-modal features with machine learning methods. Biomedical Signal Processing and Control, 2021, 66, 102474.	5.7	29
12	PEPRF: Identification of Essential Proteins by Integrating Topological Features of PPI Network and Sequence-based Features via Random Forest. Current Bioinformatics, 2021, 16, 1161-1168.	1.5	10
13	Mechanism of noncoding RNA-associated N6-methyladenosine recognition by an RNA processing complex during IgH DNA recombination. Molecular Cell, 2021, 81, 3949-3964.e7.	9.7	28
14	Robust biomarker discovery for hepatocellular carcinoma from high-throughput data by multiple feature selection methods. BMC Medical Genomics, 2021, 14, 112.	1.5	13
15	Inference of Gene Regulatory Network from Time Series Expression Data by Combining Local Geometric Similarity and Multivariate Regression. Lecture Notes in Computer Science, 2021, , 345-355.	1.3	0
16	Identifying biomarkers for breast cancer by gene regulatory network rewiring. BMC Bioinformatics, 2021, 22, 308.	2.6	6
17	Predicting lncRNA-Protein Interactions by Heterogenous Network Embedding. Frontiers in Genetics, 2021, 12, 814073.	2.3	5
18	Detecting prognostic biomarkers of breast cancer by regularized Cox proportional hazards models. Journal of Translational Medicine, 2021, 19, 514.	4.4	12

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19	Biomarker discovery for predicting spontaneous preterm birth from gene expression data by regularized logistic regression. Computational and Structural Biotechnology Journal, 2020, 18, 3434-3446.	4.1	18
20	Noncoding RNA transcription alters chromosomal topology to promote isotype-specific class switch recombination. Science Immunology, 2020, 5, .	11.9	28
21	Network-based prioritization of cancer genes by integrative ranks from multi-omics data. Computers in Biology and Medicine, 2020, 119, 103692.	7.0	16
22	iNOA. , 2020, , .		0
23	Detecting Diagnostic Biomarkers of Alzheimer's Disease by Integrating Gene Expression Data in Six Brain Regions. Frontiers in Genetics, 2019, 10, 157.	2.3	21
24	Analysis of Topological Parameters of Complex Disease Genes Reveals the Importance of Location in a Biomolecular Network. Genes, 2019, 10, 143.	2.4	32
25	Prioritizing Congenital Heart Disease Genes from Transcriptome and Interactome via PageRank. , 2018, , .		1
26	Towards precise reconstruction of gene regulatory networks by data integration. Quantitative Biology, 2018, 6, 113-128.	0.5	4
27	Detecting pathway biomarkers of diabetic progression with differential entropy. Journal of Biomedical Informatics, 2018, 82, 143-153.	4.3	16
28	Gene essentiality prediction based on fractal features and machine learning. Molecular BioSystems, 2017, 13, 577-584.	2.9	17
29	Multi-dimensional data representation using linear tensor coding. IET Image Processing, 2017, 11, 492-501.	2.5	2
30	Structure alignment-based classification of RNA-binding pockets reveals regional RNA recognition motifs on protein surfaces. BMC Bioinformatics, 2017, 18, 27.	2.6	7
31	Identification of candidate genes for Rituximab response in rheumatoid arthritis with weighted gene co-expression network analysis. , 2017, , .		0
32	Identifying biomarkers of diabetes with gene coexpression networks. , 2017, , .		2
33	Identifying module biomarkers of hepatocellular carcinoma from gene expression data. , 2017, , .		2
34	Quantifying Gene Regulatory Relationships with Association Measures: A Comparative Study. Frontiers in Genetics, 2017, 8, 96.	2.3	26
35	Uncovering Driver DNA Methylation Events in Nonsmoking Early Stage Lung Adenocarcinoma. BioMed Research International, 2016, 2016, 1-10.	1.9	5
36	Prediction of protein-RNA interactions using sequence and structure descriptors. Neurocomputing, 2016, 206, 28-34.	5.9	19

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37	CMIP: a software package capable of reconstructing genome-wide regulatory networks using gene expression data. BMC Bioinformatics, 2016, 17, 535.	2.6	26
38	Type 1 Interferons Induce Changes in Core Metabolism that Are Critical for Immune Function. Immunity, 2016, 44, 1325-1336.	14.3	248
39	Exploring the relationship between fractal features and bacterial essential genes. Chinese Physics B, 2016, 25, 060503.	1.4	3
40	Identifying network-based biomarkers of complex diseases from high-throughput data. Biomarkers in Medicine, 2016, 10, 633-650.	1.4	35
41	Multiscale modeling biological systems. IET Systems Biology, 2016, 10, 1-1.	1.5	1
42	Prediction of Protein-RNA Interactions Using Sequence and Structure Descriptors**This work was partially supported by the National Natural Science Foundation of China (NSFC) Grant No. 31100949, the Scientific Research Foundation for the Returned Overseas Chinese Scholars, Ministry of Education of China, the Fundamental Research Funds of Shandong University Grant No. 2014TB006, University of Rochester Center for AIDS Research Grant P30 AI078498 (NIH/NIAID) and NIH R01 Grant GM100788-01.. IFAC-PapersOnLine, 2015, 48, 1-6.	0.9	2
43	RegNetwork: an integrated database of transcriptional and post-transcriptional regulatory networks in human and mouse. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav095.	3.0	338
44	Diversity in Compartmental Dynamics of Gene Regulatory Networks: The Immune Response in Primary Influenza A Infection in Mice. PLoS ONE, 2015, 10, e0138110.	2.5	8
45	Reverse Engineering of Genome-wide Gene Regulatory Networks from Gene Expression Data. Current Genomics, 2015, 16, 3-22.	1.6	79
46	Identifying module biomarker in type 2 diabetes mellitus by discriminative area of functional activity. BMC Bioinformatics, 2015, 16, 92.	2.6	20
47	RNA Exosome-Regulated Long Non-Coding RNA Transcription Controls Super-Enhancer Activity. Cell, 2015, 161, 774-789.	28.9	370
48	Prediction and Dissection of Protein-RNA Interactions by Molecular Descriptors. Current Topics in Medicinal Chemistry, 2015, 16, 604-615.	2.1	4
49	Modeling Genome-Wide Dynamic Regulatory Network in Mouse Lungs with Influenza Infection Using High-Dimensional Ordinary Differential Equations. PLoS ONE, 2014, 9, e95276.	2.5	16
50	Systematic identification of transcriptional and post-transcriptional regulations in human respiratory epithelial cells during influenza A virus infection. BMC Bioinformatics, 2014, 15, 336.	2.6	35
51	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
52	A sequence-based computational approach to predicting PDZ domain-peptide interactions. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 165-170.	2.3	14
53	Selected papers from The 7th IEEE International Conference on Systems Biology (ISB 2013). IET Systems Biology, 2014, 8, 127-128.	1.5	0
54	Systematic identification of local structure binding motifs in protein-RNA recognition. , 2014, , .		2

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55	Predicting Protein-Ligand Interactions Based on Chemical Preference Features with its Application to New D-Amino Acid Oxidase Inhibitor Discovery. <i>Current Pharmaceutical Design</i> , 2014, 20, 5202-5211.	1.9	4
56	NARROMI: a noise and redundancy reduction technique improves accuracy of gene regulatory network inference. <i>Bioinformatics</i> , 2013, 29, 106-113.	4.1	133
57	De novo prediction of RNA-protein interactions from sequence information. <i>Molecular BioSystems</i> , 2013, 9, 133-142.	2.9	102
58	An integrated approach to identify causal network modules of complex diseases with application to colorectal cancer. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2013, 20, 659-667.	4.4	58
59	Spatio-temporal analysis of type 2 diabetes mellitus based on differential expression networks. <i>Scientific Reports</i> , 2013, 3, 2268.	3.3	60
60	Construction and analysis of single nucleotide polymorphism-single nucleotide polymorphism interaction networks. <i>IET Systems Biology</i> , 2013, 7, 170-181.	1.5	0
61	Gaussian graphical model for identifying significantly responsive regulatory networks from time course high-throughput data. <i>IET Systems Biology</i> , 2013, 7, 143-152.	1.5	17
62	High-Dimensional Ordinary Differential Equation Models for Reconstructing Genome-Wide Dynamic Regulatory Networks. <i>Springer Proceedings in Mathematics and Statistics</i> , 2013, , 173-190.	0.2	2
63	Prediction of hot spots in protein interfaces using a random forest model with hybrid features. <i>Protein Engineering, Design and Selection</i> , 2012, 25, 119-126.	2.1	60
64	Identifying critical transitions and their leading biomolecular networks in complex diseases. <i>Scientific Reports</i> , 2012, 2, 813.	3.3	155
65	Coexpression network analysis in chronic hepatitis B and C hepatic lesions reveals distinct patterns of disease progression to hepatocellular carcinoma. <i>Journal of Molecular Cell Biology</i> , 2012, 4, 140-152.	3.3	95
66	Identification of overlapping communities in protein interaction networks using multi-scale local information expansion. , 2012, , .		1
67	Community structure detection based on Potts model and network's spectral characterization. <i>Europhysics Letters</i> , 2012, 97, 48005.	2.0	47
68	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
69	A Gaussian graphical model for identifying significantly responsive regulatory networks from time series gene expression data. , 2012, , .		0
70	Identifying dysregulated pathways in cancers from pathway interaction networks. <i>BMC Bioinformatics</i> , 2012, 13, 126.	2.6	109
71	A computational procedure for identifying master regulator candidates: a case study on diabetes progression in Goto-Kakizaki rats. <i>BMC Systems Biology</i> , 2012, 6, S2.	3.0	16
72	Detecting early-warning signals for sudden deterioration of complex diseases by dynamical network biomarkers. <i>Scientific Reports</i> , 2012, 2, 342.	3.3	494

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73	Inferring gene regulatory networks from gene expression data by path consistency algorithm based on conditional mutual information. <i>Bioinformatics</i> , 2012, 28, 98-104.	4.1	265
74	Proteome-wide prediction of protein-protein interactions from high-throughput data. <i>Protein and Cell</i> , 2012, 3, 508-520.	11.0	36
75	Detecting thermophilic proteins through selecting amino acid and dipeptide composition features. <i>Amino Acids</i> , 2012, 42, 1947-1953.	2.7	25
76	Multiple-resource and multiple-depot emergency response problem considering secondary disasters. <i>Expert Systems With Applications</i> , 2012, 39, 11066-11071.	7.6	137
77	Network-based analysis of complex diseases. <i>IET Systems Biology</i> , 2012, 6, 22.	1.5	71
78	Identifying overlapping communities in social networks using multi-scale local information expansion. <i>European Physical Journal B</i> , 2012, 85, 1.	1.5	21
79	Inferring a protein interaction map of <i>Mycobacterium tuberculosis</i> based on sequences and interologs. <i>BMC Bioinformatics</i> , 2012, 13, S6.	2.6	19
80	Identifying Responsive Modules by Mathematical Programming: An Application to Budding Yeast Cell Cycle. <i>PLoS ONE</i> , 2012, 7, e41854.	2.5	8
81	Inferring Protein-Protein Interactions Based on Sequences and Interologs in <i>Mycobacterium Tuberculosis</i> . <i>Lecture Notes in Computer Science</i> , 2012, , 91-96.	1.3	1
82	DIPOS: database of interacting proteins in <i>Oryza sativa</i> . <i>Molecular BioSystems</i> , 2011, 7, 2615.	2.9	25
83	Protein interaction prediction for mouse pdz domains using dipeptide composition features. , 2011, , .		1
84	A dynamical method to extract communities induced by low or middle-degree nodes. , 2011, , .		0
85	Identification of master regulator candidates for diabetes progression in Goto-Kakizaki Rat by a computational procedure. , 2011, , .		1
86	Detecting and analyzing differentially activated pathways in brain regions of Alzheimer's disease patients. <i>Molecular BioSystems</i> , 2011, 7, 1441.	2.9	30
87	Network screening of Goto-Kakizaki rat liver microarray data during diabetic progression. <i>BMC Systems Biology</i> , 2011, 5, S16.	3.0	23
88	Identification of dysfunctional modules and disease genes in congenital heart disease by a network-based approach. <i>BMC Genomics</i> , 2011, 12, 592.	2.8	46
89	Phenotype-difference oriented identification of molecular functions for diabetes progression in Goto-Kakizaki rat. , 2011, , .		0
90	NOA: a novel Network Ontology Analysis method. <i>Nucleic Acids Research</i> , 2011, 39, e87-e87.	14.5	101

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91	Protein structure alignment based on internal coordinates. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2010, 2, 308-319.	3.6	3
92	Identifying dysfunctional crosstalk of pathways in various regions of Alzheimer's disease brains. <i>BMC Systems Biology</i> , 2010, 4, S11.	3.0	80
93	Prediction of protein-RNA binding sites by a random forest method with combined features. <i>Bioinformatics</i> , 2010, 26, 1616-1622.	4.1	133
94	Inferring gene regulatory networks from expression data with prior knowledge by linear programming. , 2010, , .		0
95	Dynamically dysfunctional protein interactions in the development of Alzheimer's disease. , 2009, , .		7
96	Bridging protein local structures and protein functions. <i>Amino Acids</i> , 2008, 35, 627-650.	2.7	37
97	Protein cavity clustering based on community structure of pocket similarity network. <i>International Journal of Bioinformatics Research and Applications</i> , 2008, 4, 445.	0.2	5
98	Analysis of Protein Surface Patterns by Pocket Similarity Network. <i>Protein and Peptide Letters</i> , 2008, 15, 448-455.	0.9	9
99	Predicting gene ontology functions from protein's regional surface structures. <i>BMC Bioinformatics</i> , 2007, 8, 475.	2.6	19
100	A connected network-regularized logistic regression model for feature selection. <i>Applied Intelligence</i> , 0, , 1.	5.3	6