

Tao Zeng

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.

107 papers	1,484 citations	24 h-index	33 g-index
130 ext. papers	2,269 ext. citations	6.3 avg, IF	5.19 L-index

#	Paper	IF	Citations
107	Deep latent space fusion for adaptive representation of heterogeneous multi-omics data.. <i>Briefings in Bioinformatics</i> , 2022 ,	13.4	1
106	Identifying luminal and basal mammary cell specific genes and their expression patterns during pregnancy.. <i>PLoS ONE</i> , 2022 , 17, e0267211	3.7	
105	Detecting Brain Structure-Specific Methylation Signatures and Rules for Alzheimer's Disease.. <i>Frontiers in Neuroscience</i> , 2022 , 16, 895181	5.1	0
104	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
103	Predicting Human Protein Subcellular Locations by Using a Combination of Network and Function Features. <i>Frontiers in Genetics</i> , 2021 , 12, 783128	4.5	1
102	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
101	Exploring Somatic Alteration Associating With Aggressive Behaviors of Papillary Thyroid Carcinomas by Targeted Sequencing. <i>Frontiers in Oncology</i> , 2021 , 11, 722814	5.3	0
100	Identifying the Signatures and Rules of Circulating Extracellular MicroRNA for Distinguishing Cancer Subtypes. <i>Frontiers in Genetics</i> , 2021 , 12, 651610	4.5	6
99	Investigating gene methylation signatures for fetal intolerance prediction. <i>PLoS ONE</i> , 2021 , 16, e0250037	3.7	
98	Predicting gene phenotype by multi-label multi-class model based on essential functional features. <i>Molecular Genetics and Genomics</i> , 2021 , 296, 905-918	3.1	4
97	Applying artificial intelligence in the microbiome for gastrointestinal diseases: A review. <i>Journal of Gastroenterology and Hepatology (Australia)</i> , 2021 , 36, 832-840	4	2
96	Identifying Infliximab- (IFX-) Responsive Blood Signatures for the Treatment of Rheumatoid Arthritis. <i>BioMed Research International</i> , 2021 , 2021, 1-10	3	
95	Performance assessment of sample-specific network control methods for bulk and single-cell biological data analysis. <i>PLoS Computational Biology</i> , 2021 , 17, e1008962	5	1
94	Determining protein-protein functional associations by functional rules based on gene ontology and KEGG pathway. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2021 , 1869, 140621	4	31
93	Analysis of the Sequence Characteristics of Antifreeze Protein. <i>Life</i> , 2021 , 11,	3	1
92	Identifying COVID-19-Specific Transcriptomic Biomarkers with Machine Learning Methods. <i>BioMed Research International</i> , 2021 , 2021, 9939134	3	2
91	Identification of Microbiota Biomarkers With Orthologous Gene Annotation for Type 2 Diabetes. <i>Frontiers in Microbiology</i> , 2021 , 12, 711244	5.7	2

90	Repurpose Analysis Expanding Biomedical Benefits by Omics Data Integration 2021 , 94-102		2
89	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
88	Identifying the Immunological Gene Signatures of Immune Cell Subtypes. <i>BioMed Research International</i> , 2021 , 2021, 1-10	3	1
87	Recognizing Pattern and Rule of Mutation Signatures Corresponding to Cancer Types. <i>Frontiers in Cell and Developmental Biology</i> , 2021 , 9, 712931	5.7	
86	Facial Skin Microbiota-Mediated Host Response to Pollution Stress Revealed by Microbiome Networks of Individual. <i>MSystems</i> , 2021 , 6, e0031921	7.6	2
85	Identifying Cell-Type Specific Genes and Expression Rules Based on Single-Cell Transcriptomic Atlas Data. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020 , 8, 350	5.8	7
84	Discriminating Origin Tissues of Tumor Cell Lines by Methylation Signatures and Dys-Methylated Rules. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020 , 8, 507	5.8	8
83	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
82	Alternative Polyadenylation Modification Patterns Reveal Essential Posttranscription Regulatory Mechanisms of Tumorigenesis in Multiple Tumor Types. <i>BioMed Research International</i> , 2020 , 2020, 6384120	3.1	4
81	Analysis on gene modular network reveals morphogen-directed development robustness in. <i>Cell Discovery</i> , 2020 , 6, 43	22.3	2
80	Evolution and transition of expression trajectory during human brain development. <i>BMC Evolutionary Biology</i> , 2020 , 20, 72	3	3
79	Efficient Mining Closed k-Mers from DNA and Protein Sequences 2020 ,		3
78	Essential gene expression pattern of head and neck squamous cell carcinoma revealed by tumor-specific expression rule based on single-cell RNA sequencing. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2020 , 1866, 165791	6.9	2
77	Network control principles for identifying personalized driver genes in cancer. <i>Briefings in Bioinformatics</i> , 2020 , 21, 1641-1662	13.4	4
76	Screening Dys-Methylation Genes and Rules for Cancer Diagnosis by Using the Pan-Cancer Study. <i>IEEE Access</i> , 2020 , 8, 489-501	3.5	5
75	Identifying Robust Microbiota Signatures and Interpretable Rules to Distinguish Cancer Subtypes. <i>Frontiers in Molecular Biosciences</i> , 2020 , 7, 604794	5.6	7
74	Identifying the RNA signatures of coronary artery disease from combined lncRNA and mRNA expression profiles. <i>Genomics</i> , 2020 , 112, 4945-4958	4.3	7
73	Investigation and Prediction of Human Interactome Based on Quantitative Features. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020 , 8, 730	5.8	10

72	Identifying Essential Methylation Patterns and Genes Associated With Stroke. <i>IEEE Access</i> , 2020 , 8, 96669-96676	3.9	5
71	Genomic insights of body plan transitions from bilateral to pentameral symmetry in Echinoderms. <i>Communications Biology</i> , 2020 , 3, 371	6.7	5
70	Identification of COVID-19 Infection-Related Human Genes Based on a Random Walk Model in a Virus-Human Protein Interaction Network. <i>BioMed Research International</i> , 2020 , 2020, 4256301	3	12
69	Distinguishing Glioblastoma Subtypes by Methylation Signatures. <i>Frontiers in Genetics</i> , 2020 , 11, 604336	4.5	8
68	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
67	Disease Cluster Detection and Functional Characterization. <i>IEEE Access</i> , 2020 , 8, 141958-141966	3.5	2
66	Roles of TGF β 1 in the expression of phosphoinositide 3-kinase isoform genes and sensitivity and response of lung telocytes to PI3K inhibitors. <i>Cell Biology and Toxicology</i> , 2020 , 36, 51-64	7.4	16
65	Detecting the Multiomics Signatures of Factor-Specific Inflammatory Effects on Airway Smooth Muscles. <i>Frontiers in Genetics</i> , 2020 , 11, 599970	4.5	21
64	Identifying Transcriptomic Signatures and Rules for SARS-CoV-2 Infection. <i>Frontiers in Cell and Developmental Biology</i> , 2020 , 8, 627302	5.7	31
63	Identification of Protein Subcellular Localization With Network and Functional Embeddings. <i>Frontiers in Genetics</i> , 2020 , 11, 626500	4.5	29
62	Assessment of network module identification across complex diseases. <i>Nature Methods</i> , 2019 , 16, 843-852	2.6	91
61	Identifying Methylation Pattern and Genes Associated with Breast Cancer Subtypes. <i>International Journal of Molecular Sciences</i> , 2019 , 20,	6.3	23
60	Identifying Essential Signature Genes and Expression Rules Associated With Distinctive Development Stages of Early Embryonic Cells. <i>IEEE Access</i> , 2019 , 7, 128570-128578	3.5	9
59	Single-Cell RNA Sequencing-Based Computational Analysis to Describe Disease Heterogeneity. <i>Frontiers in Genetics</i> , 2019 , 10, 629	4.5	12
58	Values of integration between lipidomics and clinical phenomes in patients with acute lung infection, pulmonary embolism, or acute exacerbation of chronic pulmonary diseases: a preliminary study. <i>Journal of Translational Medicine</i> , 2019 , 17, 162	8.5	10
57	High-Order Correlation Integration for Single-Cell or Bulk RNA-seq Data Analysis. <i>Frontiers in Genetics</i> , 2019 , 10, 371	4.5	5
56	Cell-specific network constructed by single-cell RNA sequencing data. <i>Nucleic Acids Research</i> , 2019 , 47, e62	20.1	43
55	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

54	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
53	Multi-view Subspace Clustering Analysis for Aggregating Multiple Heterogeneous Omics Data. <i>Frontiers in Genetics</i> , 2019 , 10, 744	4.5	5
52	eGPS 1.0: comprehensive software for multi-omic and evolutionary analyses. <i>National Science Review</i> , 2019 , 6, 867-869	10.8	17
51	Copy Number Variation Pattern for Discriminating MACROD2 States of Colorectal Cancer Subtypes. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019 , 7, 407	5.8	15
50	Roles of transforming growth factor- β and phosphatidylinositol 3-kinase isoforms in integrin α -mediated bio-behaviors of mouse lung telocytes. <i>Journal of Translational Medicine</i> , 2019 , 17, 431	8.5	7
49	A novel network control model for identifying personalized driver genes in cancer. <i>PLoS Computational Biology</i> , 2019 , 15, e1007520	5	20
48	Chronic hepatitis B: dynamic change in Traditional Chinese Medicine syndrome by dynamic network biomarkers. <i>Chinese Medicine</i> , 2019 , 14, 52	4.7	9
47	Screening of Methylation Signature and Gene Functions Associated With the Subtypes of Isocitrate Dehydrogenase-Mutation Gliomas. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019 , 7, 339	5.8	13
46	Immunosignature Screening for Multiple Cancer Subtypes Based on Expression Rule. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019 , 7, 370	5.8	7
45	Dynamically characterizing individual clinical change by the steady state of disease-associated pathway. <i>BMC Bioinformatics</i> , 2019 , 20, 697	3.6	2
44	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
43	Discovering personalized driver mutation profiles of single samples in cancer by network control strategy. <i>Bioinformatics</i> , 2018 , 34, 1893-1903	7.2	44
42	Revisit of Machine Learning Supported Biological and Biomedical Studies. <i>Methods in Molecular Biology</i> , 2018 , 1754, 183-204	1.4	2
41	Integrative Analysis of Omics Big Data. <i>Methods in Molecular Biology</i> , 2018 , 1754, 109-135	1.4	26
40	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
39	Detecting Personalized Determinants During Drug Treatment from Omics Big Data. <i>Current Pharmaceutical Design</i> , 2018 , 24, 3727-3738	3.3	8
38	Characterizing and Discriminating Individual Steady State of Disease-Associated Pathway. <i>Lecture Notes in Computer Science</i> , 2018 , 533-538	0.9	
37	Efficient Mining Multi-mers in a Variety of Biological Sequences. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018 ,	3	2

36	Differential function analysis: identifying structure and activation variations in dysregulated pathways. <i>Science China Information Sciences</i> , 2017 , 60, 1	3.4	1
35	Pattern fusion analysis by adaptive alignment of multiple heterogeneous omics data. <i>Bioinformatics</i> , 2017 , 33, 2706-2714	7.2	39
34	Comparative network stratification analysis for identifying functional interpretable network biomarkers. <i>BMC Bioinformatics</i> , 2017 , 18, 48	3.6	5
33	Individual-specific edge-network analysis for disease prediction. <i>Nucleic Acids Research</i> , 2017 , 45, e170	20.1	38
32	Local network component analysis for quantifying transcription factor activities. <i>Methods</i> , 2017 , 124, 25-35	4.6	6
31	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
30	Constrained target controllability of complex networks. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2017 , 2017, 063402	1.9	16
29	Mining K-mers of Various Lengths in Biological Sequences. <i>Lecture Notes in Computer Science</i> , 2017 , 10519, 186-195	19.5	2
28	Interferon-microRNA signalling drives liver precancerous lesion formation and hepatocarcinogenesis. <i>Gut</i> , 2016 , 65, 1186-201	19.2	31
27	Big-data-based edge biomarkers: study on dynamical drug sensitivity and resistance in individuals. <i>Briefings in Bioinformatics</i> , 2016 , 17, 576-92	13.4	33
26	Integration of multiple heterogeneous omics data 2016 ,		1
25	Diagnosing phenotypes of single-sample individuals by edge biomarkers. <i>Journal of Molecular Cell Biology</i> , 2015 , 7, 231-41	6.3	48
24	Inferring Sequential Order of Somatic Mutations during Tumorigenesis based on Markov Chain Model. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015 , 12, 1094-103	3	6
23	Measuring the quality of linear patterns in biclusters. <i>Methods</i> , 2015 , 83, 18-27	4.6	6
22	Integrative enrichment analysis: a new computational method to detect dysregulated pathways in heterogeneous samples. <i>BMC Genomics</i> , 2015 , 16, 918	4.5	12
21	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
20	Serum chemokine network correlates with chemotherapy in non-small cell lung cancer. <i>Cancer Letters</i> , 2015 , 365, 57-67	9.9	15
19	Detecting disease genes of non-small lung cancer based on consistently differential interactions. <i>Cancer and Metastasis Reviews</i> , 2015 , 34, 195-208	9.6	1

18	MCentridFS: a tool for identifying module biomarkers for multi-phenotypes from high-throughput data. <i>Molecular BioSystems</i> , 2014 , 10, 2870-5		10
17	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
16	EdgeMarker: Identifying differentially correlated molecule pairs as edge-biomarkers. <i>Journal of Theoretical Biology</i> , 2014 , 362, 35-43	2.3	52
15	Deciphering early development of complex diseases by progressive module network. <i>Methods</i> , 2014 , 67, 334-43	4.6	36
14	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> , 2014 , 15, 229-43	13.4	85
13	Negative correlation based gene markers identification in integrative gene expression data. <i>International Journal of Data Mining and Bioinformatics</i> , 2014 , 10, 1-17	0.5	3
12	Edge biomarkers for classification and prediction of phenotypes. <i>Science China Life Sciences</i> , 2014 , 57, 1103-14	8.5	26
11	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, 5202-11	3.3	2
10	Network biomarkers reveal dysfunctional gene regulations during disease progression. <i>FEBS Journal</i> , 2013 , 280, 5682-95	5.7	49
9	Spatio-temporal analysis of type 2 diabetes mellitus based on differential expression networks. <i>Scientific Reports</i> , 2013 , 3, 2268	4.9	50
8	Prediction of heme binding residues from protein sequences with integrative sequence profiles. <i>Proteome Science</i> , 2012 , 10 Suppl 1, S20	2.6	29
7	Tracing dynamic biological processes during phase transition. <i>BMC Systems Biology</i> , 2012 , 6 Suppl 1, S12	3.5	5
6	Reconstructing dynamic gene regulatory networks from sample-based transcriptional data. <i>Nucleic Acids Research</i> , 2012 , 40, 10657-67	20.1	24
5	Distinct interfacial biclique patterns between ssDNA-binding proteins and those with dsDNAs. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011 , 79, 598-610	4.2	4
4	Identifying temporal trace of biological process during phase transition 2011 ,		1
3	Maximization of negative correlations in time-course gene expression data for enhancing understanding of molecular pathways. <i>Nucleic Acids Research</i> , 2010 , 38, e1	20.1	22
2	Mixture classification model based on clinical markers for breast cancer prognosis. <i>Artificial Intelligence in Medicine</i> , 2010 , 48, 129-37	7.4	27
1	Structure-function analysis of mutant RNA-dependent RNA polymerase complexes with VPg. <i>Biochemistry (Moscow)</i> , 2009 , 74, 1132-41	2.9	3

