

Meng Zhou

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.

86

papers

3,082

citations

29

h-index

54

g-index

96

ext. papers

4,346

ext. citations

7.7

avg, IF

5.63

L-index

#	Paper	IF	Citations
86	Transcriptional landscape of circulating platelets from patients with COVID-19 reveals key subnetworks and regulators underlying SARS-CoV-2 infection: implications for immunothrombosis.. <i>Cell and Bioscience</i> , 2022 , 12, 15	9.8	1
85	Computational elucidation of spatial gene expression variation from spatially resolved transcriptomics data.. <i>Molecular Therapy - Nucleic Acids</i> , 2022 , 27, 404-411	10.7	2
84	Multi-omic characterization of genome-wide abnormal DNA methylation reveals diagnostic and prognostic markers for esophageal squamous-cell carcinoma.. <i>Signal Transduction and Targeted Therapy</i> , 2022 , 7, 53	21	1
83	A Novel Clinical Five-Risk Factor Panel for Individualized Recurrence Risk Assessment of Patients With Acute Anterior Uveitis. <i>Translational Vision Science and Technology</i> , 2021 , 10, 29	3.3	0
82	Multomics integration-based molecular characterizations of COVID-19. <i>Briefings in Bioinformatics</i> , 2021 ,	13.4	4
81	Deep learning-based advances and applications for single-cell RNA-sequencing data analysis. <i>Briefings in Bioinformatics</i> , 2021 ,	13.4	2
80	Cell-free DNA 5-hydroxymethylcytosine profiles of long non-coding RNA genes enable early detection and progression monitoring of human cancers. <i>Clinical Epigenetics</i> , 2021 , 13, 197	7.7	2
79	Machine learning-based integrative analysis of methylome and transcriptome identifies novel prognostic DNA methylation signature in uveal melanoma. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	3
78	COVID-19 Quarantine Reveals That Behavioral Changes Have an Effect on Myopia Progression. <i>Ophthalmology</i> , 2021 , 128, 1652-1654	7.3	15
77	Circulating exosomal miR-363-5p inhibits lymph node metastasis by downregulating PDGFB and serves as a potential noninvasive biomarker for breast cancer. <i>Molecular Oncology</i> , 2021 , 15, 2466-2479	7.9	5
76	Pan-cancer characterization of lncRNA modifiers of immune microenvironment reveals clinically distinct de novo tumor subtypes. <i>Npj Genomic Medicine</i> , 2021 , 6, 52	6.2	5
75	The pan-cancer landscape of crosstalk between epithelial-mesenchymal transition and immune evasion relevant to prognosis and immunotherapy response. <i>Npj Precision Oncology</i> , 2021 , 5, 56	9.8	7
74	Mechanistically derived patient-level framework for precision medicine identifies a personalized immune prognostic signature in high-grade serous ovarian cancer. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	7
73	Computational recognition of lncRNA signature of tumor-infiltrating B lymphocytes with potential implications in prognosis and immunotherapy of bladder cancer. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	60
72	Computational principles and practice for decoding immune contexture in the tumor microenvironment. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	19
71	Genomic instability-derived plasma extracellular vesicle-microRNA signature as a minimally invasive predictor of risk and unfavorable prognosis in breast cancer. <i>Journal of Nanobiotechnology</i> , 2021 , 19, 22	9.4	20
70	Genome-wide cell-free DNA methylation analyses improve accuracy of non-invasive diagnostic imaging for early-stage breast cancer. <i>Molecular Cancer</i> , 2021 , 20, 36	42.1	7

69	Estrogen-dependent KCa1.1 modulation is essential for retaining neuroexcitation of female-specific subpopulation of myelinated Ah-type baroreceptor neurons in rats. <i>Acta Pharmacologica Sinica</i> , 2021 , 42, 2173-2180	8	1
68	Design, methodology, and baseline of whole city-million scale children and adolescents myopia survey (CAMS) in Wenzhou, China. <i>Eye and Vision (London, England)</i> , 2021 , 8, 31	4.9	5
67	Bradykinin-mediated estrogen-dependent depressor response by direct activation of female-specific distribution of myelinated Ah-type baroreceptor neurons in rats.. <i>CNS Neuroscience and Therapeutics</i> , 2021 ,	6.8	1
66	scTPA: a web tool for single-cell transcriptome analysis of pathway activation signatures. <i>Bioinformatics</i> , 2020 , 36, 4217-4219	7.2	6
65	Computational identification of mutator-derived lncRNA signatures of genome instability for improving the clinical outcome of cancers: a case study in breast cancer. <i>Briefings in Bioinformatics</i> , 2020 , 21, 1742-1755	13.4	73
64	The Circular RNome of Developmental Retina in Mice. <i>Molecular Therapy - Nucleic Acids</i> , 2020 , 19, 339-349.	10.7	16
63	Benchmarking algorithms for pathway activity transformation of single-cell RNA-seq data. <i>Computational and Structural Biotechnology Journal</i> , 2020 , 18, 2953-2961	6.8	9
62	Computational Methods and Applications for Identifying Disease-Associated lncRNAs as Potential Biomarkers and Therapeutic Targets. <i>Molecular Therapy - Nucleic Acids</i> , 2020 , 21, 156-171	10.7	18
61	CFEA: a cell-free epigenome atlas in human diseases. <i>Nucleic Acids Research</i> , 2020 , 48, D40-D44	20.1	10
60	Mutational landscape and genetic signatures of cell-free DNA in tumour-induced osteomalacia. <i>Journal of Cellular and Molecular Medicine</i> , 2020 , 24, 4931-4943	5.6	1
59	Refined grains intake in high fat, high protein, low carbohydrate and low energy levels subgroups and higher likelihood of abdominal obesity in Chinese population. <i>International Journal of Food Sciences and Nutrition</i> , 2020 , 71, 979-990	3.7	1
58	Identification of tumor immune infiltration-associated lncRNAs for improving prognosis and immunotherapy response of patients with non-small cell lung cancer 2020 , 8,		116
57	Large-scale integrated analysis of ovarian cancer tumors and cell lines identifies an individualized gene expression signature for predicting response to platinum-based chemotherapy. <i>Cell Death and Disease</i> , 2019 , 10, 661	9.8	11
56	Integrative analysis from multi-centre studies identifies a function-derived personalized multi-gene signature of outcome in colorectal cancer. <i>Journal of Cellular and Molecular Medicine</i> , 2019 , 23, 5270-5281	5.6	12
55	MetSigDis: a manually curated resource for the metabolic signatures of diseases. <i>Briefings in Bioinformatics</i> , 2019 , 20, 203-209	13.4	82
54	Analysis of long noncoding RNAs highlights region-specific altered expression patterns and diagnostic roles in Alzheimer's disease. <i>Briefings in Bioinformatics</i> , 2019 , 20, 598-608	13.4	51
53	An Immune-Related Six-lncRNA Signature to Improve Prognosis Prediction of Glioblastoma Multiforme. <i>Molecular Neurobiology</i> , 2018 , 55, 3684-3697	6.2	130
52	DincRNA: a comprehensive web-based bioinformatics toolkit for exploring disease associations and ncRNA function. <i>Bioinformatics</i> , 2018 , 34, 1953-1956	7.2	168

51	A novel HPV16 E7-affitoxin for targeted therapy of HPV16-induced human cervical cancer. <i>Theranostics</i> , 2018 , 8, 3544-3558	12.1	12
50	InfAcrOnt: calculating cross-ontology term similarities using information flow by a random walk. <i>BMC Genomics</i> , 2018 , 19, 919	4.5	76
49	A novel lncRNA-focus expression signature for survival prediction in endometrial carcinoma. <i>BMC Cancer</i> , 2018 , 18, 39	4.8	44
48	Recurrence-Associated Long Non-coding RNA Signature for Determining the Risk of Recurrence in Patients with Colon Cancer. <i>Molecular Therapy - Nucleic Acids</i> , 2018 , 12, 518-529	10.7	74
47	Landscape of SNPs-mediated lncRNA structural variations and their implication in human complex diseases. <i>Briefings in Bioinformatics</i> , 2018 ,	13.4	5
46	Bispecific affibody molecule targeting HPV16 and HPV18E7 oncoproteins for enhanced molecular imaging of cervical cancer. <i>Applied Microbiology and Biotechnology</i> , 2018 , 102, 7429-7439	5.7	8
45	Discovery and validation of immune-associated long non-coding RNA biomarkers associated with clinically molecular subtype and prognosis in diffuse large B cell lymphoma. <i>Molecular Cancer</i> , 2017 , 16, 16	42.1	138
44	Molecular classification of prostate adenocarcinoma by the integrated somatic mutation profiles and molecular network. <i>Scientific Reports</i> , 2017 , 7, 738	4.9	7
43	Measuring disease similarity and predicting disease-related ncRNAs by a novel method. <i>BMC Medical Genomics</i> , 2017 , 10, 71	3.7	29
42	Characterization of BioPlex network by topological properties. <i>Journal of Theoretical Biology</i> , 2016 , 409, 148-154	2.3	
41	Discovery of potential prognostic long non-coding RNA biomarkers for predicting the risk of tumor recurrence of breast cancer patients. <i>Scientific Reports</i> , 2016 , 6, 31038	4.9	70
40	A potential panel of six-long non-coding RNA signature to improve survival prediction of diffuse large-B-cell lymphoma. <i>Scientific Reports</i> , 2016 , 6, 27842	4.9	56
39	OAHG: an integrated resource for annotating human genes with multi-level ontologies. <i>Scientific Reports</i> , 2016 , 6, 34820	4.9	68
38	Comparative analysis of housekeeping and tissue-selective genes in human based on network topologies and biological properties. <i>Molecular Genetics and Genomics</i> , 2016 , 291, 1227-41	3.1	6
37	IntNetLncSim: an integrative network analysis method to infer human lncRNA functional similarity. <i>Oncotarget</i> , 2016 , 7, 47864-47874	3.3	42
36	Comprehensive analysis of lncRNA expression profiles reveals a novel lncRNA signature to discriminate nonequivalent outcomes in patients with ovarian cancer. <i>Oncotarget</i> , 2016 , 7, 32433-48	3.3	110
35	Construction and analysis of dysregulated lncRNA-associated ceRNA network identified novel lncRNA biomarkers for early diagnosis of human pancreatic cancer. <i>Oncotarget</i> , 2016 , 7, 56383-56394	3.3	109
34	Characterization of long non-coding RNA-associated ceRNA network to reveal potential prognostic lncRNA biomarkers in human ovarian cancer. <i>Oncotarget</i> , 2016 , 7, 12598-611	3.3	190

33	Relapse-related long non-coding RNA signature to improve prognosis prediction of lung adenocarcinoma. <i>Oncotarget</i> , 2016 , 7, 29720-38	3.3	70
32	Integration of Multiple Genomic and Phenotype Data to Infer Novel miRNA-Disease Associations. <i>PLoS ONE</i> , 2016 , 11, e0148521	3.7	21
31	DisSim: an online system for exploring significant similar diseases and exhibiting potential therapeutic drugs. <i>Scientific Reports</i> , 2016 , 6, 30024	4.9	42
30	Characterize the relationship between essential and TATA-containing genes for <i>S. cerevisiae</i> by network topologies in the perturbation sensitivity network. <i>Genomics</i> , 2016 , 108, 177-183	4.3	1
29	A potential signature of eight long non-coding RNAs predicts survival in patients with non-small cell lung cancer. <i>Journal of Translational Medicine</i> , 2015 , 13, 231	8.5	143
28	Prioritizing candidate disease-related long non-coding RNAs by walking on the heterogeneous lncRNA and disease network. <i>Molecular BioSystems</i> , 2015 , 11, 760-9		140
27	A potential prognostic long non-coding RNA signature to predict metastasis-free survival of breast cancer patients. <i>Scientific Reports</i> , 2015 , 5, 16553	4.9	81
26	Identification and validation of potential prognostic lncRNA biomarkers for predicting survival in patients with multiple myeloma. <i>Journal of Experimental and Clinical Cancer Research</i> , 2015 , 34, 102	12.8	141
25	Identification of Aberrant Chromosomal Regions in Human Breast Cancer Using Gene Expression Data and Related Gene Information. <i>Medical Science Monitor</i> , 2015 , 21, 2557-66	3.2	4
24	MicroRNA and transcription factor mediated regulatory network analysis reveals critical regulators and regulatory modules in myocardial infarction. <i>PLoS ONE</i> , 2015 , 10, e0135339	3.7	26
23	Systematic large-scale study of the inheritance mode of Mendelian disorders provides new insight into human disease. <i>European Journal of Human Genetics</i> , 2014 , 22, 1260-7	5.3	4
22	Inferring novel lncRNA-disease associations based on a random walk model of a lncRNA functional similarity network. <i>Molecular BioSystems</i> , 2014 , 10, 2074-81		188
21	Network-based analysis of genotype-phenotype correlations between different inheritance modes. <i>Bioinformatics</i> , 2014 , 30, 3223-31	7.2	4
20	The detection of risk pathways, regulated by miRNAs, via the integration of sample-matched miRNA-mRNA profiles and pathway structure. <i>Journal of Biomedical Informatics</i> , 2014 , 49, 187-97	10.2	8
19	Correlation between gene expression and mutator phenotype predicts homologous recombination deficiency and outcome in ovarian cancer. <i>Journal of Molecular Medicine</i> , 2014 , 92, 1159-68	5.5	11
18	A computational frame and resource for understanding the lncRNA-environmental factor associations and prediction of environmental factors implicated in diseases. <i>Molecular BioSystems</i> , 2014 , 10, 3264-71		8
17	Systematic analysis of genomic organization and structure of long non-coding RNAs in the human genome. <i>FEBS Letters</i> , 2013 , 587, 976-82	3.8	11
16	Comparative genomic analysis reveals evolutionary characteristics and patterns of microRNA clusters in vertebrates. <i>Gene</i> , 2013 , 512, 383-91	3.8	19

15	Allele-specific behavior of molecular networks: understanding small-molecule drug response in yeast. <i>PLoS ONE</i> , 2013 , 8, e53581	3.7	3
14	Inferring potential microRNA-microRNA associations based on targeting propensity and connectivity in the context of protein interaction network. <i>PLoS ONE</i> , 2013 , 8, e69719	3.7	15
13	Characterization and evolution of microRNA genes derived from repetitive elements and duplication events in plants. <i>PLoS ONE</i> , 2012 , 7, e34092	3.7	35
12	Systematic analysis of genomic organization and heterogeneities of miRNA cluster in vertebrates. <i>Molecular Biology Reports</i> , 2012 , 39, 5143-9	2.8	4
11	Genome-wide analysis of clustering patterns and flanking characteristics for plant microRNA genes. <i>FEBS Journal</i> , 2011 , 278, 929-40	5.7	19
10	Systematic analysis of human microRNA divergence based on evolutionary emergence. <i>FEBS Letters</i> , 2011 , 585, 240-8	3.8	13
9	MicroRNA regulation constrains the organization of target genes on mammalian chromosomes. <i>FEBS Letters</i> , 2011 , 585, 1897-904	3.8	5
8	A novel network-based method for measuring the functional relationship between gene sets. <i>Bioinformatics</i> , 2011 , 27, 1521-8	7.2	18
7	Functional homogeneity in microRNA target heterogeneity--a new sight into human microRNomics. <i>OMICS A Journal of Integrative Biology</i> , 2011 , 15, 25-35	3.8	8
6	Analysis of synonymous codon usage patterns in different plant mitochondrial genomes. <i>Molecular Biology Reports</i> , 2009 , 36, 2039-46	2.8	39
5	In silico detection and characteristics of novel microRNA genes in the Equus caballus genome using an integrated ab initio and comparative genomic approach. <i>Genomics</i> , 2009 , 94, 125-31	4.3	42
4	Patterns of synonymous codon usage bias in chloroplast genomes of seed plants. <i>Forestry Studies in China</i> , 2008 , 10, 235-242		13
3	Analysis of synonymous codon usage in chloroplast genome of Populus alba. <i>Journal of Forestry Research</i> , 2008 , 19, 293-297	2	17
2	Analysis of codon usage between different poplar species. <i>Journal of Genetics and Genomics</i> , 2007 , 34, 555-61	4	11
1	scTPA: A web tool for single-cell transcriptome analysis of pathway activation signatures		1