Meng Zhou

List of Publications by Year
in descending order

90 papers	4,881 citations	147566 31 h-index	106150 65 g-index
96 all docs	96 docs citations	96 times ranked	3835 citing authors

#	Article	IF	Citations
1	Integrated immunogenomic analysis of single-cell and bulk tissue transcriptome profiling unravels a macrophage activation paradigm associated with immunologically and clinically distinct behaviors in ovarian cancer. Journal of Advanced Research, 2023, 44, 149-160.	4.4	8
2	Multiomics integration-based molecular characterizations of COVID-19. Briefings in Bioinformatics, 2022, 23, .	3.2	24
3	Deep learning-based advances and applications for single-cell RNA-sequencing data analysis. Briefings in Bioinformatics, 2022, 23, .	3.2	19
4	Immuno-genomic characterisation of high-grade serous ovarian cancer reveals immune evasion mechanisms and identifies an immunological subtype with a favourable prognosis and improved therapeutic efficacy. British Journal of Cancer, 2022, 126, 1570-1580.	2.9	18
5	Computational elucidation of spatial gene expression variation from spatially resolved transcriptomics data. Molecular Therapy - Nucleic Acids, 2022, 27, 404-411.	2.3	9
6	Transcriptional landscape of circulating platelets from patients with COVID-19 reveals key subnetworks and regulators underlying SARS-CoV-2 infection: implications for immunothrombosis. Cell and Bioscience, 2022, 12, 15.	2.1	8
7	Multi-omic characterization of genome-wide abnormal DNA methylation reveals diagnostic and prognostic markers for esophageal squamous-cell carcinoma. Signal Transduction and Targeted Therapy, 2022, 7, 53.	7.1	22
8	Bradykinin‐mediated estrogen‐dependent depressor response by direct activation of female‐specific distribution of myelinated A‐type baroreceptor neurons in rats. CNS Neuroscience and Therapeutics, 2022, 28, 435-447.	1.9	2
9	iUMRG: multi-layered network-guided propagation modeling for the inference of susceptibility genes and potential drugs against uveal melanoma. Npj Systems Biology and Applications, 2022, 8, .	1.4	3
10	Mechanistically derived patient-level framework for precision medicine identifies a personalized immune prognostic signature in high-grade serous ovarian cancer. Briefings in Bioinformatics, 2021, 22, .	3.2	14
11	Computational recognition of lncRNA signature of tumor-infiltrating B lymphocytes with potential implications in prognosis and immunotherapy of bladder cancer. Briefings in Bioinformatics, 2021, 22, .	3.2	126
12	Computational principles and practice for decoding immune contexture in the tumor microenvironment. Briefings in Bioinformatics, 2021, 22, .	3.2	33
13	Genomic instability-derived plasma extracellular vesicle-microRNA signature as a minimally invasive predictor of risk and unfavorable prognosis in breast cancer. Journal of Nanobiotechnology, 2021, 19, 22.	4.2	52
14	Genome-wide cell-free DNA methylation analyses improve accuracy of non-invasive diagnostic imaging for early-stage breast cancer. Molecular Cancer, 2021, 20, 36.	7.9	30
15	COVID-19 Quarantine Reveals That Behavioral Changes Have an Effect on Myopia Progression. Ophthalmology, 2021, 128, 1652-1654.	2.5	82
16	Circulating exosomal *miR‐363‐5p* inhibits lymph node metastasis by downregulating *PDGFB* and serves as a potential noninvasive biomarker for breast cancer. Molecular Oncology, 2021, 15, 2466-2479.	2.1	31
17	Pan-cancer characterization of lncRNA modifiers of immune microenvironment reveals clinically distinct de novo tumor subtypes. Npj Genomic Medicine, 2021, 6, 52.	1.7	15
18	The pan-cancer landscape of crosstalk between epithelial-mesenchymal transition and immune evasion relevant to prognosis and immunotherapy response. Npj Precision Oncology, 2021, 5, 56.	2.3	44

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19	Estrogen-dependent KCa1.1 modulation is essential for retaining neuroexcitation of female-specific subpopulation of myelinated Ah-type baroreceptor neurons in rats. Acta Pharmacologica Sinica, 2021, 42, 2173-2180.	2.8	4
20	Design, methodology, and baseline of whole city-million scale children and adolescents myopia survey (CAMS) in Wenzhou, China. Eye and Vision (London, England), 2021, 8, 31.	1.4	25
21	Machine learning-based integrative analysis of methylome and transcriptome identifies novel prognostic DNA methylation signature in uveal melanoma. Briefings in Bioinformatics, 2021, 22, .	3.2	17
22	Cell-free DNA 5-hydroxymethylcytosine profiles of long non-coding RNA genes enable early detection and progression monitoring of human cancers. Clinical Epigenetics, 2021, 13, 197.	1.8	6
23	A Novel Clinical Five-Risk Factor Panel for Individualized Recurrence Risk Assessment of Patients With Acute Anterior Uveitis. Translational Vision Science and Technology, 2021, 10, 29.	1.1	1
24	CFEA: a cell-free epigenome atlas in human diseases. Nucleic Acids Research, 2020, 48, D40-D44.	6.5	32
25	Computational identification of mutator-derived lncRNA signatures of genome instability for improving the clinical outcome of cancers: a case study in breast cancer. Briefings in Bioinformatics, 2020, 21, 1742-1755.	3.2	143
26	The Circular RNome of Developmental Retina in Mice. Molecular Therapy - Nucleic Acids, 2020, 19, 339-349.	2.3	24
27	Benchmarking algorithms for pathway activity transformation of single-cell RNA-seq data. Computational and Structural Biotechnology Journal, 2020, 18, 2953-2961.	1.9	43
28	Computational Methods and Applications for Identifying Disease-Associated lncRNAs as Potential Biomarkers and Therapeutic Targets. Molecular Therapy - Nucleic Acids, 2020, 21, 156-171.	2.3	30
29	scTPA: a web tool for single-cell transcriptome analysis of pathway activation signatures. Bioinformatics, 2020, 36, 4217-4219.	1.8	21
30	Mutational landscape and genetic signatures of cell‐free DNA in tumour‐induced osteomalacia. Journal of Cellular and Molecular Medicine, 2020, 24, 4931-4943.	1.6	4
31	Refined grains intake in high fat, high protein, low carbohydrate and low energy levels subgroups and higher likelihood of abdominal obesity in Chinese population. International Journal of Food Sciences and Nutrition, 2020, 71, 979-990.	1.3	1
32	Identification of tumor immune infiltration-associated lncRNAs for improving prognosis and immunotherapy response of patients with non-small cell lung cancer. , 2020, 8, e000110.		239
33	Large-scale integrated analysis of ovarian cancer tumors and cell lines identifies an individualized gene expression signature for predicting response to platinum-based chemotherapy. Cell Death and Disease, 2019, 10, 661.	2.7	18
34	Integrative analysis from multi‐centre studies identifies a function‐derived personalized multi‐gene signature of outcome in colorectal cancer. Journal of Cellular and Molecular Medicine, 2019, 23, 5270-5281.	1.6	27
35	MetSigDis: a manually curated resource for the metabolic signatures of diseases. Briefings in Bioinformatics, 2019, 20, 203-209.	3.2	106
36	Analysis of long noncoding RNAs highlights region-specific altered expression patterns and diagnostic roles in Alzheimer's disease. Briefings in Bioinformatics, 2019, 20, 598-608.	3.2	95

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37	An Immune-Related Six-lncRNA Signature to Improve Prognosis Prediction of Glioblastoma Multiforme. Molecular Neurobiology, 2018, 55, 3684-3697.	1.9	221
38	DincRNA: a comprehensive web-based bioinformatics toolkit for exploring disease associations and ncRNA function. Bioinformatics, 2018, 34, 1953-1956.	1.8	241
39	Landscape of SNPs-mediated lncRNA structural variations and their implication in human complex diseases. Briefings in Bioinformatics, 2018, , .	3.2	6
40	Bispecific affibody molecule targeting HPV16 and HPV18E7 oncoproteins for enhanced molecular imaging of cervical cancer. Applied Microbiology and Biotechnology, 2018, 102, 7429-7439.	1.7	16
41	A novel HPV16 E7-affitoxin for targeted therapy of HPV16-induced human cervical cancer. Theranostics, 2018, 8, 3544-3558.	4.6	21
42	InfAcrOnt: calculating cross-ontology term similarities using information flow by a random walk. BMC Genomics, 2018, 19, 919.	1.2	98
43	A novel lncRNA-focus expression signature for survival prediction in endometrial carcinoma. BMC Cancer, 2018, 18, 39.	1.1	64
44	Recurrence-Associated Long Non-coding RNA Signature for Determining the Risk of Recurrence in Patients with Colon Cancer. Molecular Therapy - Nucleic Acids, 2018, 12, 518-529.	2.3	139
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. Molecular Cancer, 2017, 16, 16.	7.9	227
46	Molecular classification of prostate adenocarcinoma by the integrated somatic mutation profiles and molecular network. Scientific Reports, 2017, 7, 738.	1.6	12
47	Measuring disease similarity and predicting disease-related ncRNAs by a novel method. BMC Medical Genomics, 2017, 10, 71.	0.7	49
48	Construction and analysis of dysregulated lncRNA-associated ceRNA network identified novel lncRNA biomarkers for early diagnosis of human pancreatic cancer. Oncotarget, 2016, 7, 56383-56394.	0.8	155
49	Characterization of long non-coding RNA-associated ceRNA network to reveal potential prognostic lncRNA biomarkers in human ovarian cancer. Oncotarget, 2016, 7, 12598-12611.	0.8	218
50	Relapse-related long non-coding RNA signature to improve prognosis prediction of lung adenocarcinoma. Oncotarget, 2016, 7, 29720-29738.	0.8	80
51	Integration of Multiple Genomic and Phenotype Data to Infer Novel miRNA-Disease Associations. PLoS ONE, 2016, 11, e0148521.	1.1	26
52	DisSim: an online system for exploring significant similar diseases and exhibiting potential therapeutic drugs. Scientific Reports, 2016, 6, 30024.	1.6	53
53	InfDisSim: A novel method for measuring disease similarity based on information flow. , 2016, , .		2
54	Characterize the relationship between essential and TATA-containing genes for S. cerevisiae by network topologies in the perturbation sensitivity network. Genomics, 2016, 108, 177-183.	1.3	1

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55	Characterization of BioPlex network by topological properties. Journal of Theoretical Biology, 2016, 409, 148-154.	0.8	0
56	Discovery of potential prognostic long non-coding RNA biomarkers for predicting the risk of tumor recurrence of breast cancer patients. Scientific Reports, 2016, 6, 31038.	1.6	103
57	A potential panel of six-long non-coding RNA signature to improve survival prediction of diffuse large-B-cell lymphoma. Scientific Reports, 2016, 6, 27842.	1.6	65
58	OAHG: an integrated resource for annotating human genes with multi-level ontologies. Scientific Reports, 2016, 6, 34820.	1.6	106
59	Comparative analysis of housekeeping and tissue-selective genes in human based on network topologies and biological properties. Molecular Genetics and Genomics, 2016, 291, 1227-1241.	1.0	8
60	IntNetLncSim: an integrative network analysis method to infer human lncRNA functional similarity. Oncotarget, 2016, 7, 47864-47874.	0.8	51
61	Comprehensive analysis of lncRNA expression profiles reveals a novel lncRNA signature to discriminate nonequivalent outcomes in patients with ovarian cancer. Oncotarget, 2016, 7, 32433-32448.	0.8	121
62	A potential prognostic long non-coding RNA signature to predict metastasis-free survival of breast cancer patients. Scientific Reports, 2015, 5, 16553.	1.6	99
63	Identification and validation of potential prognostic lncRNA biomarkers for predicting survival in patients with multiple myeloma. Journal of Experimental and Clinical Cancer Research, 2015, 34, 102.	3.5	207
64	A potential signature of eight long non-coding RNAs predicts survival in patients with non-small cell lung cancer. Journal of Translational Medicine, 2015, 13, 231.	1.8	207
65	Prioritizing candidate disease-related long non-coding RNAs by walking on the heterogeneous lncRNA and disease network. Molecular BioSystems, 2015, 11, 760-769.	2.9	173
66	Identification of Aberrant Chromosomal Regions in Human Breast Cancer Using Gene Expression Data and Related Gene Information. Medical Science Monitor, 2015, 21, 2557-2566.	0.5	4
67	MicroRNA and Transcription Factor Mediated Regulatory Network Analysis Reveals Critical Regulators and Regulatory Modules in Myocardial Infarction. PLoS ONE, 2015, 10, e0135339.	1.1	31
68	Correlation between gene expression and mutator phenotype predicts homologous recombination deficiency and outcome in ovarian cancer. Journal of Molecular Medicine, 2014, 92, 1159-1168.	1.7	31
69	A computational frame and resource for understanding the lncRNA-environmental factor associations and prediction of environmental factors implicated in diseases. Molecular BioSystems, 2014, 10, 3264-3271.	2.9	11
70	Systematic large-scale study of the inheritance mode of Mendelian disorders provides new insight into human diseasome. European Journal of Human Genetics, 2014, 22, 1260-1267.	1.4	4
71	Inferring novel lncRNA–disease associations based on a random walk model of a lncRNA functional similarity network. Molecular BioSystems, 2014, 10, 2074-2081.	2.9	296
72	Network-based analysis of genotype–phenotype correlations between different inheritance modes. Bioinformatics, 2014, 30, 3223-3231.	1.8	5

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73	The detection of risk pathways, regulated by miRNAs, via the integration of sample-matched miRNA-mRNA profiles and pathway structure. Journal of Biomedical Informatics, 2014, 49, 187-197.	2.5	9
74	Systematic analysis of genomic organization and structure of long non-coding RNAs in the human genome. FEBS Letters, 2013, 587, 976-982.	1.3	16
75	Comparative genomic analysis reveals evolutionary characteristics and patterns of microRNA clusters in vertebrates. Gene, 2013, 512, 383-391.	1.0	20
76	Allele-Specific Behavior of Molecular Networks: Understanding Small-Molecule Drug Response in Yeast. PLoS ONE, 2013, 8, e53581.	1.1	5
77	Inferring Potential microRNA-microRNA Associations Based on Targeting Propensity and Connectivity in the Context of Protein Interaction Network. PLoS ONE, 2013, 8, e69719.	1.1	22
78	Characterization and Evolution of microRNA Genes Derived from Repetitive Elements and Duplication Events in Plants. PLoS ONE, 2012, 7, e34092.	1.1	41
79	Systematic analysis of genomic organization and heterogeneities of miRNA cluster in vertebrates. Molecular Biology Reports, 2012, 39, 5143-5149.	1.0	4
80	Genome-wide analysis of clustering patterns and flanking characteristics for plant microRNA genes. FEBS Journal, 2011, 278, 929-940.	2.2	19
81	Systematic analysis of human microRNA divergence based on evolutionary emergence. FEBS Letters, 2011, 585, 240-248.	1.3	15
82	MicroRNA regulation constrains the organization of target genes on mammalian chromosomes. FEBS Letters, 2011, 585, 1897-1904.	1.3	5
83	A novel network-based method for measuring the functional relationship between gene sets. Bioinformatics, 2011, 27, 1521-1528.	1.8	19
84	Functional Homogeneity in microRNA Target Heterogeneity—a New Sight into Human microRNomics. OMICS A Journal of Integrative Biology, 2011, 15, 25-35.	1.0	10
85	Analysis of synonymous codon usage patterns in different plant mitochondrial genomes. Molecular Biology Reports, 2009, 36, 2039-2046.	1.0	53
86	In silico detection and characteristics of novel microRNA genes in the Equus caballus genome using an integrated ab initio and comparative genomic approach. Genomics, 2009, 94, 125-131.	1.3	52
87	Patterns of synonymous codon usage bias in chloroplast genomes of seed plants. Forestry Studies in China, 2008, 10, 235-242.	0.4	26
88	Analysis of synonymous codon usage in chloroplast genome of Populus alba. Journal of Forestry Research, 2008, 19, 293-297.	1.7	21
89	Analysis of Codon Usage Between Different Poplar Species. Journal of Genetics and Genomics, 2007, 34, 555-561.	1.7	16
90	Mutation of FGFR1 and MED12 of Cell-Free DNA Contribute to Early Diagnostics of Tumor-Induced Osteomalacia. SSRN Electronic Journal, 0, , .	0.4	0