Meng Zhou

List of Publications by Citations

86	3,082	29	54
papers	citations	h-index	g-index

96	4,346	7.7	5.63
ext. papers	ext. citations	avg, IF	L-index

#	Paper	IF	Citations
86	Characterization of long non-coding RNA-associated ceRNA network to reveal potential prognostic lncRNA biomarkers in human ovarian cancer. *Oncotarget*, **2016**, 7, 12598-611	3.3	190
85	Inferring novel lncRNA-disease associations based on a random walk model of a lncRNA functional similarity network. *Molecular BioSystems*, **2014**, 10, 2074-81		188
84	DincRNA: a comprehensive web-based bioinformatics toolkit for exploring disease associations and ncRNA function. *Bioinformatics*, **2018**, 34, 1953-1956	7.2	168
83	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	8.5	143
82	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	12.8	141
81	Prioritizing candidate disease-related long non-coding RNAs by walking on the heterogeneous lncRNA and disease network. *Molecular BioSystems*, **2015**, 11, 760-9		140
80	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	42.1	138
79	An Immune-Related Six-lncRNA Signature to Improve Prognosis Prediction of Glioblastoma Multiforme. *Molecular Neurobiology*, **2018**, 55, 3684-3697	6.2	130
78	Identification of tumor immune infiltration-associated lncRNAs for improving prognosis and immunotherapy response of patients with non-small cell lung cancer **2020**, 8,		116
77	Comprehensive analysis of lncRNA expression profiles reveals a novel lncRNA signature to discriminate nonequivalent outcomes in patients with ovarian cancer. *Oncotarget*, **2016**, 7, 32433-48	3.3	110
76	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	3.3	109
75	MetSigDis: a manually curated resource for the metabolic signatures of diseases. *Briefings in Bioinformatics*, **2019**, 20, 203-209	13.4	82
74	A potential prognostic long non-coding RNA signature to predict metastasis-free survival of breast cancer patients. *Scientific Reports*, **2015**, 5, 16553	4.9	81
73	InfAcrOnt: calculating cross-ontology term similarities using information flow by a random walk. *BMC Genomics*, **2018**, 19, 919	4.5	76
72	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	10.7	74
71	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	13.4	73
70	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	4.9	70

69	Relapse-related long non-coding RNA signature to improve prognosis prediction of lung adenocarcinoma. *Oncotarget*, **2016**, 7, 29720-38	3.3	70
68	OAHG: an integrated resource for annotating human genes with multi-level ontologies. *Scientific Reports*, **2016**, 6, 34820	4.9	68
67	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,	13.4	60
66	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	4.9	56
65	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	13.4	51
64	A novel lncRNA-focus expression signature for survival prediction in endometrial carcinoma. *BMC Cancer*, **2018**, 18, 39	4.8	44
63	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, 125-31	4.3	42
62	IntNetLncSim: an integrative network analysis method to infer human lncRNA functional similarity. *Oncotarget*, **2016**, 7, 47864-47874	3.3	42
61	DisSim: an online system for exploring significant similar diseases and exhibiting potential therapeutic drugs. *Scientific Reports*, **2016**, 6, 30024	4.9	42
60	Analysis of synonymous codon usage patterns in different plant mitochondrial genomes. *Molecular Biology Reports*, **2009**, 36, 2039-46	2.8	39
59	Characterization and evolution of microRNA genes derived from repetitive elements and duplication events in plants. *PLoS ONE*, **2012**, 7, e34092	3.7	35
58	Measuring disease similarity and predicting disease-related ncRNAs by a novel method. *BMC Medical Genomics*, **2017**, 10, 71	3.7	29
57	MicroRNA and transcription factor mediated regulatory network analysis reveals critical regulators and regulatory modules in myocardial infarction. *PLoS ONE*, **2015**, 10, e0135339	3.7	26
56	Integration of Multiple Genomic and Phenotype Data to Infer Novel miRNA-Disease Associations. *PLoS ONE*, **2016**, 11, e0148521	3.7	21
55	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	9.4	20
54	Comparative genomic analysis reveals evolutionary characteristics and patterns of microRNA clusters in vertebrates. *Gene*, **2013**, 512, 383-91	3.8	19
53	Genome-wide analysis of clustering patterns and flanking characteristics for plant microRNA genes. *FEBS Journal*, **2011**, 278, 929-40	5.7	19
52	Computational principles and practice for decoding immune contexture in the tumor microenvironment. *Briefings in Bioinformatics*, **2021**, 22,	13.4	19

51 A novel network-based method for measuring the functional relationship between gene sets. *Bioinformatics*, **2011**, 27, 1521-8 — 7.2 — 18

50 Computational Methods and Applications for Identifying Disease-Associated lncRNAs as Potential Biomarkers and Therapeutic Targets. *Molecular Therapy - Nucleic Acids*, **2020**, 21, 156-171 — 10.7 — 18

49 Analysis of synonymous codon usage in chloroplast genome of Populus alba. *Journal of Forestry Research*, **2008**, 19, 293-297 — 2 — 17

48 The Circular RNome of Developmental Retina in Mice. *Molecular Therapy - Nucleic Acids*, **2020**, 19, 339-349 — 10.7 — 16

47 Inferring potential microRNA-microRNA associations based on targeting propensity and connectivity in the context of protein interaction network. *PLoS ONE*, **2013**, 8, e69719 — 3.7 — 15

46 COVID-19 Quarantine Reveals That Behavioral Changes Have an Effect on Myopia Progression. *Ophthalmology*, **2021**, 128, 1652-1654 — 7.3 — 15

45 Systematic analysis of human microRNA divergence based on evolutionary emergence. *FEBS Letters*, **2011**, 585, 240-8 — 3.8 — 13

44 Patterns of synonymous codon usage bias in chloroplast genomes of seed plants. *Forestry Studies in China*, **2008**, 10, 235-242 — 13

43 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 — 5.6 — 12

42 A novel HPV16 E7-affitoxin for targeted therapy of HPV16-induced human cervical cancer. *Theranostics*, **2018**, 8, 3544-3558 — 12.1 — 12

41 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 — 9.8 — 11

40 Correlation between gene expression and mutator phenotype predicts homologous recombination deficiency and outcome in ovarian cancer. *Journal of Molecular Medicine*, **2014**, 92, 1159-68 — 5.5 — 11

39 Systematic analysis of genomic organization and structure of long non-coding RNAs in the human genome. *FEBS Letters*, **2013**, 587, 976-82 — 3.8 — 11

38 Analysis of codon usage between different poplar species. *Journal of Genetics and Genomics*, **2007**, 34, 555-61 — 4 — 11

37 CFEA: a cell-free epigenome atlas in human diseases. *Nucleic Acids Research*, **2020**, 48, D40-D44 — 20.1 — 10

36 Benchmarking algorithms for pathway activity transformation of single-cell RNA-seq data. *Computational and Structural Biotechnology Journal*, **2020**, 18, 2953-2961 — 6.8 — 9

35 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, 187-97 — 10.2 — 8

34 A computational frame and resource for understanding the lncRNA-environmental factor associations and prediction of environmental factors implicated in diseases. *Molecular BioSystems*, **2014**, 10, 3264-71 — 8

33	Functional homogeneity in microRNA target heterogeneity--a new sight into human microRNomics. *OMICS A Journal of Integrative Biology*, **2011**, 15, 25-35	3.8	8
32	Bispecific affibody molecule targeting HPV16 and HPV18E7 oncoproteins for enhanced molecular imaging of cervical cancer. *Applied Microbiology and Biotechnology*, **2018**, 102, 7429-7439	5.7	8
31	Molecular classification of prostate adenocarcinoma by the integrated somatic mutation profiles and molecular network. *Scientific Reports*, **2017**, 7, 738	4.9	7
30	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	9.8	7
29	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,	13.4	7
28	Genome-wide cell-free DNA methylation analyses improve accuracy of non-invasive diagnostic imaging for early-stage breast cancer. *Molecular Cancer*, **2021**, 20, 36	42.1	7
27	scTPA: a web tool for single-cell transcriptome analysis of pathway activation signatures. *Bioinformatics*, **2020**, 36, 4217-4219	7.2	6
26	Comparative analysis of housekeeping and tissue-selective genes in human based on network topologies and biological properties. *Molecular Genetics and Genomics*, **2016**, 291, 1227-41	3.1	6
25	MicroRNA regulation constrains the organization of target genes on mammalian chromosomes. *FEBS Letters*, **2011**, 585, 1897-904	3.8	5
24	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	7.9	5
23	Pan-cancer characterization of lncRNA modifiers of immune microenvironment reveals clinically distinct de novo tumor subtypes. *Npj Genomic Medicine*, **2021**, 6, 52	6.2	5
22	Landscape of SNPs-mediated lncRNA structural variations and their implication in human complex diseases. *Briefings in Bioinformatics*, **2018**,	13.4	5
21	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	4.9	5
20	Systematic large-scale study of the inheritance mode of Mendelian disorders provides new insight into human diseasome. *European Journal of Human Genetics*, **2014**, 22, 1260-7	5.3	4
19	Network-based analysis of genotype-phenotype correlations between different inheritance modes. *Bioinformatics*, **2014**, 30, 3223-31	7.2	4
18	Systematic analysis of genomic organization and heterogeneities of miRNA cluster in vertebrates. *Molecular Biology Reports*, **2012**, 39, 5143-9	2.8	4
17	Identification of Aberrant Chromosomal Regions in Human Breast Cancer Using Gene Expression Data and Related Gene Information. *Medical Science Monitor*, **2015**, 21, 2557-66	3.2	4
16	Multiomics integration-based molecular characterizations of COVID-19. *Briefings in Bioinformatics*, **2021**,	13.4	4

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15	Allele-specific behavior of molecular networks: understanding small-molecule drug response in yeast. *PLoS ONE*, **2013**, 8, e53581	3.7	3
14	Machine learning-based integrative analysis of methylome and transcriptome identifies novel prognostic DNA methylation signature in uveal melanoma. *Briefings in Bioinformatics*, **2021**, 22,	13.4	3
13	Computational elucidation of spatial gene expression variation from spatially resolved transcriptomics data.. *Molecular Therapy - Nucleic Acids*, **2022**, 27, 404-411	10.7	2
12	Deep learning-based advances and applications for single-cell RNA-sequencing data analysis. *Briefings in Bioinformatics*, **2021**,	13.4	2
11	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	7.7	2
10	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	9.8	1
9	scTPA: A web tool for single-cell transcriptome analysis of pathway activation signatures		1
8	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	4.3	1
7	Mutational landscape and genetic signatures of cell-free DNA in tumour-induced osteomalacia. *Journal of Cellular and Molecular Medicine*, **2020**, 24, 4931-4943	5.6	1
6	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	3.7	1
5	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	8	1
4	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	21	1
3	Bradykinin-mediated estrogen-dependent depressor response by direct activation of female-specific distribution of myelinated Ah-type baroreceptor neurons in rats.. *CNS Neuroscience and Therapeutics*, **2021**,	6.8	1
2	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	3.3	0
1	Characterization of BioPlex network by topological properties. *Journal of Theoretical Biology*, **2016**, 409, 148-154	2.3	