

Meng Zhu

List of Publications by Year in Descending Order

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Version: 2024-04-25

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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.

91
papers

1,294
citations

20
h-index

31
g-index

101
ext. papers

1,957
ext. citations

6.6
avg, IF

3.93
L-index

#	Paper	IF	Citations
91	Effectiveness of inactivated COVID-19 vaccines against severe illness in B.1.617.2 (Delta) variant-infected patients in Jiangsu, China.. <i>International Journal of Infectious Diseases</i> , 2022 ,	10.5	6
90	Circulating C-reactive protein increases lung cancer risk: Results from a prospective cohort of UK Biobank. <i>International Journal of Cancer</i> , 2022 , 150, 47-55	7.5	2
89	Association Between Neuroticism and Risk of Lung Cancer: Results From Observational and Mendelian Randomization Analyses.. <i>Frontiers in Oncology</i> , 2022 , 12, 836159	5.3	
88	One-off low-dose CT for lung cancer screening in China: a multicentre, population-based, prospective cohort study.. <i>Lancet Respiratory Medicine</i> , 2022 ,	35.1	4
87	Sex-Specific Associations of Testosterone and Genetic Factors With Health Span.. <i>Frontiers in Endocrinology</i> , 2021 , 12, 773464	5.7	1
86	Relationships between sleep traits and lung cancer risk: a prospective cohort study in UK Biobank. <i>Sleep</i> , 2021 , 44,	1.1	4
85	A cross-tissue transcriptome-wide association study identifies novel susceptibility genes for lung cancer in Chinese populations. <i>Human Molecular Genetics</i> , 2021 , 30, 1666-1676	5.6	0
84	Associations Between Sleep Quality and Health Span: A Prospective Cohort Study Based on 328,850 UK Biobank Participants. <i>Frontiers in Genetics</i> , 2021 , 12, 663449	4.5	4
83	Integrated gene-based and pathway analyses using UK Biobank data identify novel genes for chronic respiratory diseases. <i>Gene</i> , 2021 , 767, 145287	3.8	4
82	Comprehensive functional annotation of susceptibility variants identifies genetic heterogeneity between lung adenocarcinoma and squamous cell carcinoma. <i>Frontiers of Medicine</i> , 2021 , 15, 275-291	12	6
81	Saturated fatty acids entrap PDX1 in stress granules and impede islet beta cell function. <i>Diabetologia</i> , 2021 , 64, 1144-1157	10.3	2
80	Prediction and clinical utility of a liver cancer risk model in Chinese adults: A prospective cohort study of 0.5 million people. <i>International Journal of Cancer</i> , 2021 , 148, 2924-2934	7.5	1
79	Genome-wide gene-smoking interaction study identified novel susceptibility loci for non-small cell lung cancer in Chinese populations. <i>Carcinogenesis</i> , 2021 , 42, 1154-1161	4.6	0
78	Genetic Risk for Overall Cancer and the Benefit of Adherence to a Healthy Lifestyle. <i>Cancer Research</i> , 2021 , 81, 4618-4627	10.1	9
77	Air Pollution, Genetic Factors, and the Risk of Lung Cancer: A Prospective Study in the UK Biobank. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2021 , 204, 817-825	10.2	13
76	Diet and Risk of Incident Lung Cancer: A Large Prospective Cohort Study in UK Biobank. <i>American Journal of Clinical Nutrition</i> , 2021 ,	7	2
75	Functional genetic variants in centrosome-related genes CEP72 and YWHAG confer susceptibility to gastric cancer. <i>Archives of Toxicology</i> , 2020 , 94, 2861-2872	5.8	3

74	Transcriptome-wide association study for persistent hepatitis B virus infection and related hepatocellular carcinoma. <i>Liver International</i> , 2020 , 40, 2117-2127	7.9	1
73	Chronic Effects of High Fine Particulate Matter Exposure on Lung Cancer in China. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2020 , 202, 1551-1559	10.2	6
72	Systematic analyses of genetic variants in chromatin interaction regions identified four novel lung cancer susceptibility loci. <i>Journal of Cancer</i> , 2020 , 11, 1075-1081	4.5	6
71	Genetic risk, incident gastric cancer, and healthy lifestyle: a meta-analysis of genome-wide association studies and prospective cohort study. <i>Lancet Oncology, The</i> , 2020 , 21, 1378-1386	21.7	38
70	Integration of GWAS and eQTL Analysis to Identify Risk Loci and Susceptibility Genes for Gastric Cancer. <i>Frontiers in Genetics</i> , 2020 , 11, 679	4.5	2
69	Meta-analysis of genome-wide association studies and functional assays decipher susceptibility genes for gastric cancer in Chinese populations. <i>Gut</i> , 2020 , 69, 641-651	19.2	18
68	Tuberculosis infection and lung adenocarcinoma: Mendelian randomization and pathway analysis of genome-wide association study data from never-smoking Asian women. <i>Genomics</i> , 2020 , 112, 1223-1232	4.3	8
67	Association Analysis of Driver Gene-Related Genetic Variants Identified Novel Lung Cancer Susceptibility Loci with 20,871 Lung Cancer Cases and 15,971 Controls. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020 , 29, 1423-1429	4	2
66	Genome-wide analysis of expression quantitative trait loci identified potential lung cancer susceptibility variants among Asian populations. <i>Carcinogenesis</i> , 2019 , 40, 263-268	4.6	3
65	Identification of Novel T1D Risk Loci and Their Association With Age and Islet Function at Diagnosis in Autoantibody-Positive T1D Individuals: Based on a Two-Stage Genome-Wide Association Study. <i>Diabetes Care</i> , 2019 , 42, 1414-1421	14.6	30
64	Precision oncology of lung cancer: genetic and genomic differences in Chinese population. <i>Npj Precision Oncology</i> , 2019 , 3, 14	9.8	20
63	Association of expression quantitative trait loci for long noncoding RNAs with lung cancer risk in Asians. <i>Molecular Carcinogenesis</i> , 2019 , 58, 1303-1313	5	5
62	Genetic variations in miR-125 family and the survival of non-small cell lung cancer in Chinese population. <i>Cancer Medicine</i> , 2019 , 8, 2636-2645	4.8	5
61	Cross-Cancer Pleiotropic Analysis Reveals Novel Susceptibility Loci for Lung Cancer. <i>Frontiers in Oncology</i> , 2019 , 9, 1492	5.3	3
60	Multi-marker analysis of genomic annotation on gastric cancer GWAS data from Chinese populations. <i>Gastric Cancer</i> , 2019 , 22, 60-68	7.6	6
59	Identification of risk loci and a polygenic risk score for lung cancer: a large-scale prospective cohort study in Chinese populations. <i>Lancet Respiratory Medicine, the</i> , 2019 , 7, 881-891	35.1	58
58	Fine Mapping in Chromosome 3q28 Identified Two Variants Associated with Lung Cancer Risk in Asian Population. <i>Journal of Cancer</i> , 2019 , 10, 1862-1869	4.5	
57	Mendelian randomization study of telomere length and lung cancer risk in East Asian population. <i>Cancer Medicine</i> , 2019 , 8, 7469-7476	4.8	8

56	A nomogram to predict overall survival of patients with early stage non-small cell lung cancer. <i>Journal of Thoracic Disease</i> , 2019 , 11, 5407-5416	2.6	9
55	Association of Mosaic Loss of Chromosome Y with Lung Cancer Risk and Prognosis in a Chinese Population. <i>Journal of Thoracic Oncology</i> , 2019 , 14, 37-44	8.9	12
54	A cancer-testis non-coding RNA LIN28B-AS1 activates driver gene LIN28B by interacting with IGF2BP1 in lung adenocarcinoma. <i>Oncogene</i> , 2019 , 38, 1611-1624	9.2	45
53	LINC00961 restrains cancer progression via modulating epithelial-mesenchymal transition in renal cell carcinoma. <i>Journal of Cellular Physiology</i> , 2019 , 234, 7257-7265	7	17
52	Fine mapping the MHC region identified rs4997052 as a new variant associated with nonobstructive azoospermia in Han Chinese males. <i>Fertility and Sterility</i> , 2019 , 111, 61-68	4.8	4
51	Interaction analysis between germline susceptibility loci and somatic alterations in lung cancer. <i>International Journal of Cancer</i> , 2018 , 143, 878-885	7.5	10
50	Association Analysis Identifies New Risk Loci for Coal Workers' Pneumoconiosis in Han Chinese Men. <i>Toxicological Sciences</i> , 2018 , 163, 206-213	4.4	9
49	Genome-wide association studies identified loci contribute to phenotypic variance of gastric cancer. <i>Gut</i> , 2018 , 67, 1366-1368	19.2	3
48	Integrating expression-related SNPs into genome-wide gene- and pathway-based analyses identified novel lung cancer susceptibility genes. <i>International Journal of Cancer</i> , 2018 , 142, 1602-1610	7.5	9
47	Whole exome sequencing identifies novel candidate mutations in a Chinese family with left ventricular noncompaction. <i>Molecular Medicine Reports</i> , 2018 , 17, 7325-7330	2.9	4
46	Genetic variants in nuclear DNA along with environmental factors modify mitochondrial DNA copy number: a population-based exome-wide association study. <i>BMC Genomics</i> , 2018 , 19, 752	4.5	6
45	Fine mapping in TERT-CLPTM1L region identified three independent lung cancer susceptibility signals: A large-scale multi-ethnic population study. <i>Molecular Carcinogenesis</i> , 2018 , 57, 1289-1299	5	2
44	Whole-genome sequencing reveals genomic signatures associated with the inflammatory microenvironments in Chinese NSCLC patients. <i>Nature Communications</i> , 2018 , 9, 2054	17.4	43
43	KIT polymorphisms were associated with the risk for head and neck squamous carcinoma in Chinese population. <i>Molecular Carcinogenesis</i> , 2017 , 56, 232-237	5	4
42	Effects of potentially functional polymorphisms in suppressor of cytokine signaling 3 (SOCS3) on the risk of head and neck squamous cancer. <i>Journal of Oral Pathology and Medicine</i> , 2017 , 46, 598-602	3.3	4
41	Exome-Wide Association Study Identifies Low-Frequency Coding Variants in 2p23.2 and 7p11.2 Associated with Survival of Non-Small Cell Lung Cancer Patients. <i>Journal of Thoracic Oncology</i> , 2017 , 12, 644-656	8.9	8
40	Genetic variants, PM exposure level and global DNA methylation level: A multi-center population-based study in Chinese. <i>Toxicology Letters</i> , 2017 , 269, 77-82	4.4	10
39	Exome Array Analysis Identifies Variants in SPOCD1 and BTN3A2 That Affect Risk for Gastric Cancer. <i>Gastroenterology</i> , 2017 , 152, 2011-2021	13.3	32

38	A polymorphism in miR-1262 regulatory region confers the risk of lung cancer in Chinese population. <i>International Journal of Cancer</i> , 2017 , 141, 958-966	7.5	18
37	Genetic variants in autophagy associated genes are associated with DNA damage levels in Chinese population. <i>Gene</i> , 2017 , 626, 414-419	3.8	
36	Genetically predicted high body mass index is associated with increased gastric cancer risk. <i>European Journal of Human Genetics</i> , 2017 , 25, 1061-1066	5.3	15
35	Cancer incidence and mortality: A cohort study in China, 2008-2013. <i>International Journal of Cancer</i> , 2017 , 141, 1315-1323	7.5	78
34	Targeted sequencing of chromosome 15q25 identified novel variants associated with risk of lung cancer and smoking behavior in Chinese. <i>Carcinogenesis</i> , 2017 , 38, 552-558	4.6	7
33	Fine mapping of chromosome 5p15.33 identifies novel lung cancer susceptibility loci in Han Chinese. <i>International Journal of Cancer</i> , 2017 , 141, 447-456	7.5	9
32	Metabolome-wide association study identified the association between a circulating polyunsaturated fatty acids variant rs174548 and lung cancer. <i>Carcinogenesis</i> , 2017 , 38, 1147-1154	4.6	14
31	Genetic variants in PPP2CA are associated with gastric cancer risk in a Chinese population. <i>Scientific Reports</i> , 2017 , 7, 11499	4.9	6
30	Fine-mapping the MHC region in Asian populations identified novel variants modifying susceptibility to lung cancer. <i>Lung Cancer</i> , 2017 , 112, 169-175	5.9	8
29	Transcriptome-wide association study revealed two novel genes associated with nonobstructive azoospermia in a Chinese population. <i>Fertility and Sterility</i> , 2017 , 108, 1056-1062.e4	4.8	11
28	A cis-eQTL genetic variant of the cancer-testis gene CCDC116 is associated with risk of multiple cancers. <i>Human Genetics</i> , 2017 , 136, 987-997	6.3	4
27	Low-frequency nonsynonymous variants in FKBPL and ARPC1B genes are associated with breast cancer risk in Chinese women. <i>Molecular Carcinogenesis</i> , 2017 , 56, 774-780	5	9
26	Estimation of heritability for nine common cancers using data from genome-wide association studies in Chinese population. <i>International Journal of Cancer</i> , 2017 , 140, 329-336	7.5	43
25	Limited Clinical Utility of Remote Ischemic Conditioning in Renal Transplantation: A Meta-Analysis of Randomized Controlled Trials. <i>PLoS ONE</i> , 2017 , 12, e0170729	3.7	5
24	Risk assessment models for genetic risk predictors of lung cancer using two-stage replication for Asian and European populations. <i>Oncotarget</i> , 2017 , 8, 53959-53967	3.3	8
23	Genetic variants in chromatin-remodeling pathway associated with lung cancer risk in a Chinese population. <i>Gene</i> , 2016 , 587, 178-82	3.8	6
22	Role of ATG10 expression quantitative trait loci in non-small cell lung cancer survival. <i>International Journal of Cancer</i> , 2016 , 139, 1564-73	7.5	34
21	Systematic identification of genes with a cancer-testis expression pattern in 19 cancer types. <i>Nature Communications</i> , 2016 , 7, 10499	17.4	80

20	Genetic variants in multisynthetase complex genes are associated with DNA damage levels in Chinese populations. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2016 , 786, 8-13	3.3	6
19	Fine mapping the MHC region identified four independent variants modifying susceptibility to chronic hepatitis B in Han Chinese. <i>Human Molecular Genetics</i> , 2016 , 25, 1225-32	5.6	24
18	Genomic Landscape Survey Identifies SRSF1 as a Key Oncodriver in Small Cell Lung Cancer. <i>PLoS Genetics</i> , 2016 , 12, e1005895	6	87
17	Genetic variants in regulatory regions of microRNAs are associated with lung cancer risk. <i>Oncotarget</i> , 2016 , 7, 47966-47974	3.3	26
16	Genetic variants of H2AX gene were associated with PM2.5-modulated DNA damage levels in Chinese Han populations. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2015 , 778, 41-5	3.3	3
15	Personal exposure to PM2.5, genetic variants and DNA damage: a multi-center population-based study in Chinese. <i>Toxicology Letters</i> , 2015 , 235, 172-8	4.4	26
14	Low-frequency coding variants at 6p21.33 and 20q11.21 are associated with lung cancer risk in Chinese populations. <i>American Journal of Human Genetics</i> , 2015 , 96, 832-40	11	30
13	Polymorphisms in alternative splicing associated genes are associated with lung cancer risk in a Chinese population. <i>Lung Cancer</i> , 2015 , 89, 238-42	5.9	8
12	Telomere length, genetic variants and gastric cancer risk in a Chinese population. <i>Carcinogenesis</i> , 2015 , 36, 963-70	4.6	39
11	U-shaped association between telomere length and esophageal squamous cell carcinoma risk: a case-control study in Chinese population. <i>Frontiers of Medicine</i> , 2015 , 9, 478-86	12	8
10	Potentially functional polymorphisms in PAK1 are associated with risk of lung cancer in a Chinese population. <i>Cancer Medicine</i> , 2015 , 4, 1781-7	4.8	5
9	The eQTL-missense polymorphisms of APOBEC3H are associated with lung cancer risk in a Han Chinese population. <i>Scientific Reports</i> , 2015 , 5, 14969	4.9	11
8	Genome-wide Association Study on Platinum-induced Hepatotoxicity in Non-Small Cell Lung Cancer Patients. <i>Scientific Reports</i> , 2015 , 5, 11556	4.9	20
7	Potentially Functional Polymorphisms in POU5F1 Gene Are Associated with the Risk of Lung Cancer in Han Chinese. <i>BioMed Research International</i> , 2015 , 2015, 851320	3	2
6	MicroRNA expression profiles in muscle-invasive bladder cancer: identification of a four-microRNA signature associated with patient survival. <i>Tumor Biology</i> , 2015 , 36, 8159-66	2.9	21
5	Whole-exome sequencing identify a new mutation of MYH7 in a Chinese family with left ventricular noncompaction. <i>Gene</i> , 2015 , 558, 138-42	3.8	14
4	Systematical analyses of variants in CTCF-binding sites identified a novel lung cancer susceptibility locus among Chinese population. <i>Scientific Reports</i> , 2015 , 5, 7833	4.9	13
3	A functional variant in miR-155 regulation region contributes to lung cancer risk and survival. <i>Oncotarget</i> , 2015 , 6, 42781-92	3.3	36

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| 2 | A genome-wide gene-environment interaction analysis for tobacco smoke and lung cancer susceptibility. <i>Carcinogenesis</i> , 2014 , 35, 1528-35 | 4.6 | 35 |
| 1 | Genetic variants in SMARC genes are associated with DNA damage levels in Chinese population. <i>Toxicology Letters</i> , 2014 , 229, 327-32 | 4.4 | 5 |