

Meng Zhu

List of Publications by Year in descending order

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Version: 2024-02-01

98
papers

2,530
citations

257101

24
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101
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101
docs citations

101
times ranked

4142
citing authors

#	ARTICLE	IF	CITATIONS
1	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</i> , 2019, 7, 881-891.	5.2	167
2	Genomic Landscape Survey Identifies SRSF1 as a Key Oncodriver in Small Cell Lung Cancer. <i>PLoS Genetics</i> , 2016, 12, e1005895.	1.5	144
3	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.	2.5	133
4	Systematic identification of genes with a cancer-testis expression pattern in 19 cancer types. <i>Nature Communications</i> , 2016, 7, 10499.	5.8	124
5	Cancer incidence and mortality: A cohort study in China, 2008–2013. <i>International Journal of Cancer</i> , 2017, 141, 1315-1323.	2.3	124
6	Genetic risk, incident gastric cancer, and healthy lifestyle: a meta-analysis of genome-wide association studies and prospective cohort study. <i>Lancet Oncology</i> , 2020, 21, 1378-1386.	5.1	123
7	One-off low-dose CT for lung cancer screening in China: a multicentre, population-based, prospective cohort study. <i>Lancet Respiratory Medicine</i> , 2022, 10, 378-391.	5.2	69
8	Whole-genome sequencing reveals genomic signatures associated with the inflammatory microenvironments in Chinese NSCLC patients. <i>Nature Communications</i> , 2018, 9, 2054.	5.8	68
9	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.	2.3	66
10	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.	2.6	61
11	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.	4.3	60
12	Exome Array Analysis Identifies Variants in SPOCD1 and BTN3A2 That Affect Risk for Gastric Cancer. <i>Gastroenterology</i> , 2017, 152, 2011-2021.	0.6	58
13	Role of <i>ATG10</i> expression quantitative trait loci in non-small cell lung cancer survival. <i>International Journal of Cancer</i> , 2016, 139, 1564-1573.	2.3	55
14	Genetic Risk for Overall Cancer and the Benefit of Adherence to a Healthy Lifestyle. <i>Cancer Research</i> , 2021, 81, 4618-4627.	0.4	48
15	A genome-wide gene-environment interaction analysis for tobacco smoke and lung cancer susceptibility. <i>Carcinogenesis</i> , 2014, 35, 1528-1535.	1.3	47
16	A functional variant in miR-155 regulation region contributes to lung cancer risk and survival. <i>Oncotarget</i> , 2015, 6, 42781-42792.	0.8	47
17	Telomere length, genetic variants and gastric cancer risk in a Chinese population. <i>Carcinogenesis</i> , 2015, 36, 963-970.	1.3	46
18	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, 832-840.	2.6	41

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19	Chronic Effects of High Fine Particulate Matter Exposure on Lung Cancer in China. American Journal of Respiratory and Critical Care Medicine, 2020, 202, 1551-1559.	2.5	40
20	Diet and Risk of Incident Lung Cancer: A Large Prospective Cohort Study in UK Biobank. American Journal of Clinical Nutrition, 2021, 114, 2043-2051.	2.2	38
21	Meta-analysis of genome-wide association studies and functional assays decipher susceptibility genes for gastric cancer in Chinese populations. Gut, 2020, 69, 641-651.	6.1	36
22	Personal exposure to PM2.5, genetic variants and DNA damage: A multi-center population-based study in Chinese. Toxicology Letters, 2015, 235, 172-178.	0.4	34
23	Fine mapping the MHC region identified four independent variants modifying susceptibility to chronic hepatitis B in Han Chinese. Human Molecular Genetics, 2016, 25, 1225-1232.	1.4	33
24	Precision oncology of lung cancer: genetic and genomic differences in Chinese population. Npj Precision Oncology, 2019, 3, 14.	2.3	31
25	Effectiveness of inactivated COVID-19 vaccines against severe illness in B.1.617.2 (Delta) variant-infected patients in Jiangsu, China. International Journal of Infectious Diseases, 2022, 116, 204-209.	1.5	31
26	Genetic variants in regulatory regions of microRNAs are associated with lung cancer risk. Oncotarget, 2016, 7, 47966-47974.	0.8	28
27	A polymorphism in miR-1262 regulatory region confers the risk of lung cancer in Chinese population. International Journal of Cancer, 2017, 141, 958-966.	2.3	26
28	Relationships between sleep traits and lung cancer risk: a prospective cohort study in UK Biobank. Sleep, 2021, 44, .	0.6	26
29	MicroRNA expression profiles in muscle-invasive bladder cancer: identification of a four-microRNA signature associated with patient survival. Tumor Biology, 2015, 36, 8159-8166.	0.8	24
30	Genome-wide Association Study on Platinum-induced Hepatotoxicity in Non-Small Cell Lung Cancer Patients. Scientific Reports, 2015, 5, 11556.	1.6	23
31	Metabolome-wide association study identified the association between a circulating polyunsaturated fatty acids variant rs174548 and lung cancer. Carcinogenesis, 2017, 38, 1147-1154.	1.3	21
32	Fine-mapping the MHC region in Asian populations identified novel variants modifying susceptibility to lung cancer. Lung Cancer, 2017, 112, 169-175.	0.9	21
33	Comprehensive functional annotation of susceptibility variants identifies genetic heterogeneity between lung adenocarcinoma and squamous cell carcinoma. Frontiers of Medicine, 2021, 15, 275-291.	1.5	21
34	Genetically predicted high body mass index is associated with increased gastric cancer risk. European Journal of Human Genetics, 2017, 25, 1061-1066.	1.4	20
35	LINCO0961 restrains cancer progression via modulating epithelial-mesenchymal transition in renal cell carcinoma. Journal of Cellular Physiology, 2019, 234, 7257-7265.	2.0	20
36	Saturated fatty acids entrap PDX1 in stress granules and impede islet beta cell function. Diabetologia, 2021, 64, 1144-1157.	2.9	20

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37	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.	0.5	19
38	A Large-Scale Genome-Wide Gene-Gene Interaction Study of Lung Cancer Susceptibility in Europeans With a Trans-Ethnic Validation in Asians. <i>Journal of Thoracic Oncology</i> , 2022, 17, 974-990.	0.5	18
39	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.	2.3	17
40	Whole-exome sequencing identify a new mutation of MYH7 in a Chinese family with left ventricular noncompaction. <i>Gene</i> , 2015, 558, 138-142.	1.0	16
41	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.	1.6	16
42	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.	1.2	16
43	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.	0.6	16
44	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.	1.2	16
45	The eQTL-missense polymorphisms of APOBEC3H are associated with lung cancer risk in a Han Chinese population. <i>Scientific Reports</i> , 2015, 5, 14969.	1.6	15
46	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.	0.5	15
47	Mendelian randomization study of telomere length and lung cancer risk in East Asian population. <i>Cancer Medicine</i> , 2019, 8, 7469-7476.	1.3	15
48	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.	1.3	15
49	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.	2.3	15
50	Adherence to Healthy Lifestyle and Liver cancer in Chinese: a prospective cohort study of 0.5 million people. <i>British Journal of Cancer</i> , 2022, 126, 815-821.	2.9	15
51	Association Analysis Identifies New Risk Loci for Coal Workers' Pneumoconiosis in Han Chinese Men. <i>Toxicological Sciences</i> , 2018, 163, 206-213.	1.4	14
52	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.	2.3	14
53	Interaction analysis between germline susceptibility loci and somatic alterations in lung cancer. <i>International Journal of Cancer</i> , 2018, 143, 878-885.	2.3	13
54	Functional genetic variants in centrosome-related genes CEP72 and YWHAG confer susceptibility to gastric cancer. <i>Archives of Toxicology</i> , 2020, 94, 2861-2872.	1.9	13

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55	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.	1.1	13
56	Low-frequency nonsynonymous variants in <i>FKBP1</i> and <i>ARPC1B</i> genes are associated with breast cancer risk in Chinese women. <i>Molecular Carcinogenesis</i> , 2017, 56, 774-780.	1.3	12
57	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.	0.8	11
58	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, 478-486.	1.5	10
59	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.	0.5	10
60	Genetic variants, PM2.5 exposure level and global DNA methylation level: A multi-center population-based study in Chinese. <i>Toxicology Letters</i> , 2017, 269, 77-82.	0.4	10
61	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.	1.3	10
62	Integration of GWAS and eQTL Analysis to Identify Risk Loci and Susceptibility Genes for Gastric Cancer. <i>Frontiers in Genetics</i> , 2020, 11, 679.	1.1	10
63	Polymorphisms in alternative splicing associated genes are associated with lung cancer risk in a Chinese population. <i>Lung Cancer</i> , 2015, 89, 238-242.	0.9	9
64	Genetic variants in chromatin-remodeling pathway associated with lung cancer risk in a Chinese population. <i>Gene</i> , 2016, 587, 178-182.	1.0	9
65	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.	1.4	9
66	Multi-marker analysis of genomic annotation on gastric cancer GWAS data from Chinese populations. <i>Gastric Cancer</i> , 2019, 22, 60-68.	2.7	8
67	Limited Clinical Utility of Remote Ischemic Conditioning in Renal Transplantation: A Meta-Analysis of Randomized Controlled Trials. <i>PLoS ONE</i> , 2017, 12, e0170729.	1.1	8
68	Genetic variants in PPP2CA are associated with gastric cancer risk in a Chinese population. <i>Scientific Reports</i> , 2017, 7, 11499.	1.6	7
69	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.	1.8	7
70	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.	1.3	7
71	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.	0.5	7
72	Integrated gene-based and pathway analyses using UK Biobank data identify novel genes for chronic respiratory diseases. <i>Gene</i> , 2021, 767, 145287.	1.0	7

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73	Genetic variants associated with expression of TCF19 contribute to the risk of head and neck cancer in Chinese population. <i>Journal of Medical Genetics</i> , 2021, , jmedgenet-2020-107410.	1.5	7
74	Genetic variants in SMARC genes are associated with DNA damage levels in Chinese population. <i>Toxicology Letters</i> , 2014, 229, 327-332.	0.4	6
75	Potentially functional polymorphisms in PAK 1 are associated with risk of lung cancer in a Chinese population. <i>Cancer Medicine</i> , 2015, 4, 1781-1787.	1.3	6
76	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.	0.4	6
77	Effects of potentially functional polymorphisms in suppressor of cytokine signaling 3 (<i>SOCS3</i>) on the risk of head and neck squamous cancer. <i>Journal of Oral Pathology and Medicine</i> , 2017, 46, 598-602.	1.4	6
78	Association of expression quantitative trait loci for long noncoding RNAs with lung cancer risk in Asians. <i>Molecular Carcinogenesis</i> , 2019, 58, 1303-1313.	1.3	6
79	Transcriptome-wide association study for persistent hepatitis B virus infection and related hepatocellular carcinoma. <i>Liver International</i> , 2020, 40, 2117-2127.	1.9	6
80	Cross-Cancer Pleiotropic Analysis Reveals Novel Susceptibility Loci for Lung Cancer. <i>Frontiers in Oncology</i> , 2019, 9, 1492.	1.3	6
81	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.	1.1	6
82	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.	2.3	6
83	Genetic risk, metabolic syndrome, and gastrointestinal cancer risk: A prospective cohort study. <i>Cancer Medicine</i> , 2023, 12, 597-605.	1.3	6
84	Whole exome sequencing identifies novel candidate mutations in a Chinese family with left ventricular noncompaction. <i>Molecular Medicine Reports</i> , 2018, 17, 7325-7330.	1.1	5
85	Fine mapping in <i>TERT</i> region identified three independent lung cancer susceptibility signals: A large-scale multi-ethnic population study. <i>Molecular Carcinogenesis</i> , 2018, 57, 1289-1299.	1.3	5
86	<i>KIT</i> polymorphisms were associated with the risk for head and neck squamous carcinoma in Chinese population. <i>Molecular Carcinogenesis</i> , 2017, 56, 232-237.	1.3	4
87	Sex-Specific Associations of Testosterone and Genetic Factors With Health Span. <i>Frontiers in Endocrinology</i> , 2021, 12, 773464.	1.5	4
88	Polygenic risk scores: the future of cancer risk prediction, screening, and precision prevention. <i>Medical Review</i> , 2021, 1, 129-149.	0.3	4
89	Potentially Functional Polymorphisms in <i>POU5F1</i> Gene Are Associated with the Risk of Lung Cancer in Han Chinese. <i>BioMed Research International</i> , 2015, 2015, 1-7.	0.9	3
90	Genetic variants of H2AX gene were associated with P M 2.5 -modulated DNA damage levels in Chinese Han populations. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2015, 778, 41-45.	0.4	3

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91	Genome-wide association studies identified loci contribute to phenotypic variance of gastric cancer. <i>Gut</i> , 2018, 67, 1366-1368.	6.1	3
92	Genome-wide analysis of expression quantitative trait loci identified potential lung cancer susceptibility variants among Asian populations. <i>Carcinogenesis</i> , 2019, 40, 263-268.	1.3	3
93	Reply to Ward <i>et al.</i> : Air Pollution as a Risk Factor for Lung Cancer: Potential Mechanisms. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2022, 205, 367-368.	2.5	3
94	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.	1.2	1
95	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.	1.3	1
96	Association Between Neuroticism and Risk of Lung Cancer: Results From Observational and Mendelian Randomization Analyses. <i>Frontiers in Oncology</i> , 2022, 12, 836159.	1.3	1
97	Genetic variants in autophagy associated genes are associated with DNA damage levels in Chinese population. <i>Gene</i> , 2017, 626, 414-419.	1.0	0
98	Reply to: Contribution of COPD as a Mediator for the Association Between Air Pollution and Lung Cancer. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2022, , .	2.5	0