

Yuzhuo Wang

List of Publications by Year in descending order

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Version: 2024-02-01

34
papers

581
citations

759233

12
h-index

677142

22
g-index

35
all docs

35
docs citations

35
times ranked

1117
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	5.1	15
2	Association Between Neuroticism and Risk of Lung Cancer: Results From Observational and Mendelian Randomization Analyses. <i>Frontiers in Oncology</i> , 2022, 12, 836159.	2.8	1
3	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.	1.1	18
4	Integrated gene-based and pathway analyses using UK Biobank data identify novel genes for chronic respiratory diseases. <i>Gene</i> , 2021, 767, 145287.	2.2	7
5	Relationships between sleep traits and lung cancer risk: a prospective cohort study in UK Biobank. <i>Sleep</i> , 2021, 44, .	1.1	26
6	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.	2.9	9
7	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.	2.8	1
8	Diet and Risk of Incident Lung Cancer: A Large Prospective Cohort Study in UK Biobank. <i>American Journal of Clinical Nutrition</i> , 2021, 114, 2043-2051.	4.7	38
9	Polygenic risk scores: the future of cancer risk prediction, screening, and precision prevention. <i>Medical Review</i> , 2021, 1, 129-149.	1.2	4
10	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.	2.9	15
11	Integration of GWAS and eQTL Analysis to Identify Risk Loci and Susceptibility Genes for Gastric Cancer. <i>Frontiers in Genetics</i> , 2020, 11, 679.	2.3	10
12	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.	2.5	6
13	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.	10.7	167
14	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.	2.5	1
15	Genome-wide analysis of expression quantitative trait loci identified potential lung cancer susceptibility variants among Asian populations. <i>Carcinogenesis</i> , 2019, 40, 263-268.	2.8	3
16	Association of expression quantitative trait loci for long noncoding RNAs with lung cancer risk in Asians. <i>Molecular Carcinogenesis</i> , 2019, 58, 1303-1313.	2.7	6
17	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.	2.8	7
18	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.	1.4	16

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19	Cross-Cancer Pleiotropic Analysis Reveals Novel Susceptibility Loci for Lung Cancer. <i>Frontiers in Oncology</i> , 2019, 9, 1492.	2.8	6
20	Interaction analysis between germline susceptibility loci and somatic alterations in lung cancer. <i>International Journal of Cancer</i> , 2018, 143, 878-885.	5.1	13
21	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.	5.1	14
22	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.	2.7	5
23	Whole-genome sequencing reveals genomic signatures associated with the inflammatory microenvironments in Chinese NSCLC patients. <i>Nature Communications</i> , 2018, 9, 2054.	12.8	68
24	Germline genetic variants were interactively associated with somatic alterations in gastric cancer. <i>Cancer Medicine</i> , 2018, 7, 3912-3920.	2.8	19
25	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.	1.1	10
26	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.	0.8	10
27	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.	2.8	10
28	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.	5.1	17
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.	1.0	15
30	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.	1.8	11
31	Genetic variants in chromatin-remodeling pathway associated with lung cancer risk in a Chinese population. <i>Gene</i> , 2016, 587, 178-182.	2.2	9
32	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.	1.0	6
33	The eQTL-missense polymorphisms of APOBEC3H are associated with lung cancer risk in a Han Chinese population. <i>Scientific Reports</i> , 2015, 5, 14969.	3.3	15
34	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.	1.9	3