Ruyang Zhang

List of Publications by Year
in descending order

58 papers	1,838 citations	361296 20 h-index	302012 39 g-index
59 all docs	59 docs citations	59 times ranked	3806 citing authors

#	Article	IF	Citations
1	Comprehensive estimation for the length and dispersion of COVID-19 incubation period: a systematic review and meta-analysis. Infection, 2022, 50, 803-813.	2.3	12
2	Global COVID-19 Pandemic Waves: Limited Lessons Learned Worldwide over the Past Year. Engineering, 2022, 13, 91-98.	3.2	10
3	Epigenome‐wide three‐way interaction study identifies a complex pattern between *TRIM27*, *KIAA0226*, and smoking associated with overall survival of early‐stage NSCLC. Molecular Oncology, 2022, 16, 717-731.	2.1	4
4	A two-phase comprehensive NSCLC prognostic study identifies lncRNAs with significant main effect and interaction. Molecular Genetics and Genomics, 2022, 297, 591-600.	1.0	5
5	Transmission dynamics model and the coronavirus disease 2019 epidemic: applications and challenges. Medical Review, 2022, 2, 89-109.	0.3	3
6	APOLLO: An accurate and independently validated prediction model of lower-grade gliomas overall survival and a comparative study of model performance. EBioMedicine, 2022, 79, 104007.	2.7	10
7	A Large-Scale Genome-Wide Gene-Gene Interaction Study of Lung Cancer Susceptibility in Europeans With a Trans-Ethnic Validation in Asians. Journal of Thoracic Oncology, 2022, 17, 974-990.	0.5	18
8	Plasma Insulin-like Growth Factor Binding Protein 7 Contributes Causally to ARDS 28-Day Mortality. Chest, 2021, 159, 1007-1018.	0.4	9
9	Mendelian Randomization With Refined Instrumental Variables From Genetic Score Improves Accuracy and Reduces Bias. Frontiers in Genetics, 2021, 12, 618829.	1.1	7
10	Child marriage, maternal serum metal exposure, and risk of preterm birth in rural Bangladesh: evidence from mediation analysis. Journal of Exposure Science and Environmental Epidemiology, 2021, 31, 571-580.	1.8	12
11	Comprehensive analyses of m6A regulators and interactive coding and non-coding RNAs across 32 cancer types. Molecular Cancer, 2021, 20, 67.	7.9	65
12	A multi-omics study links TNS3 and SEPT7 to long-term former smoking NSCLC survival. Npj Precision Oncology, 2021, 5, 39.	2.3	9
13	A predictive paradigm for COVID-19 prognosis based on the longitudinal measure of biomarkers. Briefings in Bioinformatics, 2021, 22, .	3.2	9
14	Genome-wide gene‐smoking interaction study identified novel susceptibility loci for non-small cell lung cancer in Chinese populations. Carcinogenesis, 2021, 42, 1154-1161.	1.3	1
15	Cord serum elementomics profiling of 56 elements depicts risk of preterm birth: Evidence from a prospective birth cohort in rural Bangladesh. Environment International, 2021, 156, 106731.	4.8	17
16	Association between aspirin use and lung cancer incidence depends on high-frequency use, bodyweight, and age in U.S. adults. Translational Lung Cancer Research, 2021, 10, 392-401.	1.3	2
17	Epigenetic‐smoking interaction reveals histologically heterogeneous effects of TRIM27 DNA methylation on overall survival among early‐stage NSCLC patients. Molecular Oncology, 2020, 14, 2759-2774.	2.1	13
18	Protein-altering germline mutations implicate novel genes related to lung cancer development. Nature Communications, 2020, 11, 2220.	5.8	31

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19	Independent Validation of Early-Stage Non-Small Cell Lung Cancer Prognostic Scores Incorporating Epigenetic and Transcriptional Biomarkers With Gene-Gene Interactions and Main Effects. Chest, 2020, 158, 808-819.	0.4	26
20	Identification of genetic features associated with fine particulate matter (PM2.5) modulated DNA damage using improved random forest analysis. Gene, 2020, 740, 144570.	1.0	2
21	Epigenome-wide gene–age interaction analysis reveals reversed effects of *PRODH* DNA methylation on survival between young and elderly early-stage NSCLC patients. Aging, 2020, 12, 10642-10662.	1.4	8
22	Biomass fuel as a risk factor for esophageal squamous cell carcinoma: a systematic review and meta-analysis. Environmental Health, 2019, 18, 60.	1.7	35
23	*EGLN2* DNA methylation and expression interact with *HIF1A* to affect survival of early-stage NSCLC. Epigenetics, 2019, 14, 118-129.	1.3	28
24	Elevated Platelet Count Appears to Be Causally Associated with Increased Risk of Lung Cancer: A Mendelian Randomization Analysis. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 935-942.	1.1	21
25	*SIPA1L3* methylation modifies the benefit of smoking cessation on lung adenocarcinoma survival: an epigenomic–smoking interaction analysis. Molecular Oncology, 2019, 13, 1235-1248.	2.1	19
26	shinyBN: an online application for interactive Bayesian network inference and visualization. BMC Bioinformatics, 2019, 20, 711.	1.2	10
27	TOBMI: trans-omics block missing data imputation using a k-nearest neighbor weighted approach. Bioinformatics, 2019, 35, 1278-1283.	1.8	32
28	Development and validation of an immune gene-set based Prognostic signature in ovarian cancer. EBioMedicine, 2019, 40, 318-326.	2.7	209
29	Trans-omics biomarker model improves prognostic prediction accuracy for early-stage lung adenocarcinoma. Aging, 2019, 11, 6312-6335.	1.4	13
30	Epigenome-wide association study for 28-day survival of acute respiratory distress syndrome. Intensive Care Medicine, 2018, 44, 1182-1184.	3.9	3
31	A multi–omic study reveals *BTG2* as a reliable prognostic marker for early–stage non–small cell lung cancer. Molecular Oncology, 2018, 12, 913-924.	2.1	31
32	Epigenetic modifications in KDM lysine demethylases associate with survival of early-stage NSCLC. Clinical Epigenetics, 2018, 10, 41.	1.8	12
33	Bayesian variable selection for parametric survival model with applications to cancer omics data. Human Genomics, 2018, 12, 49.	1.4	11
34	DNA Methylation of *LRRC3B*: A Biomarker for Survival of Early-Stage Non–Small Cell Lung Cancer Patients. Cancer Epidemiology Biomarkers and Prevention, 2018, 27, 1527-1535.	1.1	10
35	Genetic variant of IRAK2 in the toll–like receptor signaling pathway and survival of non–small cell lung cancer. International Journal of Cancer, 2018, 143, 2400-2408.	2.3	14
36	Welding fume exposure is associated with inflammation: a global metabolomics profiling study. Environmental Health, 2018, 17, 68.	1.7	24

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37	Identification of susceptibility pathways for the role of chromosome 15q25.1 in modifying lung cancer risk. Nature Communications, 2018, 9, 3221.	5.8	60
38	Multi-Omics Analysis Reveals a HIF Network and Hub Gene EPAS1 Associated with Lung Adenocarcinoma. EBioMedicine, 2018, 32, 93-101.	2.7	35
39	Large-scale association analysis identifies new lung cancer susceptibility loci and heterogeneity in genetic susceptibility across histological subtypes. Nature Genetics, 2017, 49, 1126-1132.	9.4	472
40	Late-onset moderate to severe acute respiratory distress syndrome is associated with shorter survival and higher mortality: a two-stage association study. Intensive Care Medicine, 2017, 43, 399-407.	3.9	27
41	Maternal/fetal metabolomes appear to mediate the impact of arsenic exposure on birth weight: A pilot study. Journal of Exposure Science and Environmental Epidemiology, 2017, 27, 313-319.	1.8	13
42	Common *TDP1* Polymorphisms in Relation to Survival among Small Cell Lung Cancer Patients: A Multicenter Study from the International Lung Cancer Consortium. Clinical Cancer Research, 2017, 23, 7550-7557.	3.2	6
43	A seven-gene prognostic signature for rapid determination of head and neck squamous cell carcinoma survival. Oncology Reports, 2017, 38, 3403-3411.	1.2	29
44	Whole blood microRNA markers are associated with acute respiratory distress syndrome. Intensive Care Medicine Experimental, 2017, 5, 38.	0.9	44
45	Mutant‐allele fraction heterogeneity is associated with non‐small cell lung cancer patient survival. Oncology Letters, 2017, 15, 795-802.	0.8	11
46	Seven-CpG-based prognostic signature coupled with gene expression predicts survival of oral squamous cell carcinoma. Clinical Epigenetics, 2017, 9, 88.	1.8	65
47	A Comparative Study of Five Association Tests Based on CpG Set for Epigenome-Wide Association Studies. PLoS ONE, 2016, 11, e0156895.	1.1	15
48	Interaction between β-hexachlorocyclohexane and ADIPOQ genotypes contributes to the risk of type 2 diabetes mellitus in East Chinese adults. Scientific Reports, 2016, 6, 37769.	1.6	8
49	Whole blood microRNAs as a prognostic classifier for acute respiratory distress syndrome 28-day mortality. Intensive Care Medicine, 2016, 42, 1824-1825.	3.9	7
50	Gene control of tyrosine kinase *TIE2* and vascular manifestations of infections. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 2472-2477.	3.3	85
51	Pathway analysis for a genome-wide association study of pneumoconiosis. Toxicology Letters, 2015, 232, 284-292.	0.4	8
52	Statistical analysis for genome-wide association study. Journal of Biomedical Research, 2015, 29, 285.	0.7	73
53	A genome-wide gene‐gene interaction analysis identifies an epistatic gene pair for lung cancer susceptibility in Han Chinese. Carcinogenesis, 2014, 35, 572-577.	1.3	29
54	Variable selection approach for zero-inflated count data via adaptive lasso. Journal of Applied Statistics, 2014, 41, 879-894.	0.6	19

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55	A genome-wide gene-environment interaction analysis for tobacco smoke and lung cancer susceptibility. Carcinogenesis, 2014, 35, 1528-1535.	1.3	47
56	Gene copy number alterations in the azoospermia-associated AZFc region and their effect on spermatogenic impairment. Molecular Human Reproduction, 2014, 20, 836-843.	1.3	27
57	Pathway Analysis for Genome-Wide Association Study of Lung Cancer in Han Chinese Population. PLoS ONE, 2013, 8, e57763.	1.1	9
58	A Large Scale Gene-Centric Association Study of Lung Function in Newly-Hired Female Cotton Textile Workers with Endotoxin Exposure. PLoS ONE, 2013, 8, e59035.	1.1	4