

# Ruyang Zhang

## List of Publications by Year in descending order

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Version: 2024-02-01

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  | Large-scale association analysis identifies new lung cancer susceptibility loci and heterogeneity in genetic susceptibility across histological subtypes. <i>Nature Genetics</i> , 2017, 49, 1126-1132. | 9.4 | 472       |
| 2  | Development and validation of an immune gene-set based Prognostic signature in ovarian cancer. <i>EBioMedicine</i> , 2019, 40, 318-326.   | 2.7 | 209       |
| 3  | Gene control of tyrosine kinase <i>TIE2</i> and vascular manifestations of infections. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 2472-2477.   | 3.3 | 85        |
| 4  | Statistical analysis for genome-wide association study. <i>Journal of Biomedical Research</i> , 2015, 29, 285.  | 0.7 | 73        |
| 5  | Seven-CpG-based prognostic signature coupled with gene expression predicts survival of oral squamous cell carcinoma. <i>Clinical Epigenetics</i> , 2017, 9, 88.   | 1.8 | 65        |
| 6  | Comprehensive analyses of m6A regulators and interactive coding and non-coding RNAs across 32 cancer types. <i>Molecular Cancer</i> , 2021, 20, 67.   | 7.9 | 65        |
| 7  | Identification of susceptibility pathways for the role of chromosome 15q25.1 in modifying lung cancer risk. <i>Nature Communications</i> , 2018, 9, 3221.   | 5.8 | 60        |
| 8  | A genome-wide gene-environment interaction analysis for tobacco smoke and lung cancer susceptibility. <i>Carcinogenesis</i> , 2014, 35, 1528-1535.  | 1.3 | 47        |
| 9  | Whole blood microRNA markers are associated with acute respiratory distress syndrome. <i>Intensive Care Medicine Experimental</i> , 2017, 5, 38.  | 0.9 | 44        |
| 10 | Multi-Omics Analysis Reveals a HIF Network and Hub Gene EPAS1 Associated with Lung Adenocarcinoma. <i>EBioMedicine</i> , 2018, 32, 93-101.  | 2.7 | 35        |
| 11 | Biomass fuel as a risk factor for esophageal squamous cell carcinoma: a systematic review and meta-analysis. <i>Environmental Health</i> , 2019, 18, 60.  | 1.7 | 35        |
| 12 | TOBMI: trans-omics block missing data imputation using a k-nearest neighbor weighted approach. <i>Bioinformatics</i> , 2019, 35, 1278-1283.   | 1.8 | 32        |
| 13 | A multi-omic study reveals <i>BTG2</i> as a reliable prognostic marker for early-stage non-small cell lung cancer. <i>Molecular Oncology</i> , 2018, 12, 913-924.                                       | 2.1 | 31        |
| 14 | Protein-altering germline mutations implicate novel genes related to lung cancer development. <i>Nature Communications</i> , 2020, 11, 2220.  | 5.8 | 31        |
| 15 | A genome-wide gene-gene interaction analysis identifies an epistatic gene pair for lung cancer susceptibility in Han Chinese. <i>Carcinogenesis</i> , 2014, 35, 572-577.                                | 1.3 | 29        |
| 16 | A seven-gene prognostic signature for rapid determination of head and neck squamous cell carcinoma survival. <i>Oncology Reports</i> , 2017, 38, 3403-3411.   | 1.2 | 29        |
| 17 | <i>EGLN2</i> DNA methylation and expression interact with <i>HIF1A</i> to affect survival of early-stage NSCLC. <i>Epigenetics</i> , 2019, 14, 118-129.   | 1.3 | 28        |
| 18 | Gene copy number alterations in the azoospermia-associated AZFc region and their effect on spermatogenic impairment. <i>Molecular Human Reproduction</i> , 2014, 20, 836-843.                           | 1.3 | 27        |

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| 19 | Late-onset moderate to severe acute respiratory distress syndrome is associated with shorter survival and higher mortality: a two-stage association study. <i>Intensive Care Medicine</i> , 2017, 43, 399-407.              | 3.9 | 27        |
| 20 | Independent Validation of Early-Stage Non-Small Cell Lung Cancer Prognostic Scores Incorporating Epigenetic and Transcriptional Biomarkers With Gene-Gene Interactions and Main Effects. <i>Chest</i> , 2020, 158, 808-819. | 0.4 | 26        |
| 21 | Welding fume exposure is associated with inflammation: a global metabolomics profiling study. <i>Environmental Health</i> , 2018, 17, 68.   | 1.7 | 24        |
| 22 | Elevated Platelet Count Appears to Be Causally Associated with Increased Risk of Lung Cancer: A Mendelian Randomization Analysis. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019, 28, 935-942.                 | 1.1 | 21        |
| 23 | Variable selection approach for zero-inflated count data via adaptive lasso. <i>Journal of Applied Statistics</i> , 2014, 41, 879-894.  | 0.6 | 19        |
| 24 | <i>SIPA1L3</i> methylation modifies the benefit of smoking cessation on lung adenocarcinoma survival: an epigenetic-smoking interaction analysis. <i>Molecular Oncology</i> , 2019, 13, 1235-1248.                          | 2.1 | 19        |
| 25 | 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        |
| 26 | Cord serum elementomics profiling of 56 elements depicts risk of preterm birth: Evidence from a prospective birth cohort in rural Bangladesh. <i>Environment International</i> , 2021, 156, 106731.                         | 4.8 | 17        |
| 27 | A Comparative Study of Five Association Tests Based on CpG Set for Epigenome-Wide Association Studies. <i>PLoS ONE</i> , 2016, 11, e0156895.  | 1.1 | 15        |
| 28 | Genetic variant of <i>IRAK2</i> in the toll-like receptor signaling pathway and survival of non-small cell lung cancer. <i>International Journal of Cancer</i> , 2018, 143, 2400-2408.                                      | 2.3 | 14        |
| 29 | Maternal/fetal metabolomes appear to mediate the impact of arsenic exposure on birth weight: A pilot study. <i>Journal of Exposure Science and Environmental Epidemiology</i> , 2017, 27, 313-319.                          | 1.8 | 13        |
| 30 | Epigenetic-smoking interaction reveals histologically heterogeneous effects of <i>TRIM27</i> DNA methylation on overall survival among early-stage NSCLC patients. <i>Molecular Oncology</i> , 2020, 14, 2759-2774.         | 2.1 | 13        |
| 31 | Trans-omics biomarker model improves prognostic prediction accuracy for early-stage lung adenocarcinoma. <i>Aging</i> , 2019, 11, 6312-6335.  | 1.4 | 13        |
| 32 | Epigenetic modifications in KDM lysine demethylases associate with survival of early-stage NSCLC. <i>Clinical Epigenetics</i> , 2018, 10, 41.   | 1.8 | 12        |
| 33 | Child marriage, maternal serum metal exposure, and risk of preterm birth in rural Bangladesh: evidence from mediation analysis. <i>Journal of Exposure Science and Environmental Epidemiology</i> , 2021, 31, 571-580.      | 1.8 | 12        |
| 34 | Comprehensive estimation for the length and dispersion of COVID-19 incubation period: a systematic review and meta-analysis. <i>Infection</i> , 2022, 50, 803-813.  | 2.3 | 12        |
| 35 | Mutant-allele fraction heterogeneity is associated with non-small cell lung cancer patient survival. <i>Oncology Letters</i> , 2017, 15, 795-802.   | 0.8 | 11        |
| 36 | Bayesian variable selection for parametric survival model with applications to cancer omics data. <i>Human Genomics</i> , 2018, 12, 49.   | 1.4 | 11        |

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|----|---|-----|-----------|
| 37 | DNA Methylation of <i>LRRC3B</i> : A Biomarker for Survival of Early-Stage Non-Small Cell Lung Cancer Patients. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2018, 27, 1527-1535.   | 1.1 | 10        |
| 38 | shinyBN: an online application for interactive Bayesian network inference and visualization. <i>BMC Bioinformatics</i> , 2019, 20, 711.   | 1.2 | 10        |
| 39 | Global COVID-19 Pandemic Waves: Limited Lessons Learned Worldwide over the Past Year. <i>Engineering</i> , 2022, 13, 91-98.   | 3.2 | 10        |
| 40 | APOLLO: An accurate and independently validated prediction model of lower-grade gliomas overall survival and a comparative study of model performance. <i>EBioMedicine</i> , 2022, 79, 104007.                                      | 2.7 | 10        |
| 41 | Pathway Analysis for Genome-Wide Association Study of Lung Cancer in Han Chinese Population. <i>PLoS ONE</i> , 2013, 8, e57763.   | 1.1 | 9         |
| 42 | Plasma Insulin-like Growth Factor Binding Protein 7 Contributes Causally to ARDS 28-Day Mortality. <i>Chest</i> , 2021, 159, 1007-1018.   | 0.4 | 9         |
| 43 | A multi-omics study links TNS3 and SEPT7 to long-term former smoking NSCLC survival. <i>Npj Precision Oncology</i> , 2021, 5, 39.   | 2.3 | 9         |
| 44 | A predictive paradigm for COVID-19 prognosis based on the longitudinal measure of biomarkers. <i>Briefings in Bioinformatics</i> , 2021, 22, .  | 3.2 | 9         |
| 45 | Pathway analysis for a genome-wide association study of pneumoconiosis. <i>Toxicology Letters</i> , 2015, 232, 284-292.   | 0.4 | 8         |
| 46 | Interaction between $\hat{I}^2$ -hexachlorocyclohexane and ADIPOQ genotypes contributes to the risk of type 2 diabetes mellitus in East Chinese adults. <i>Scientific Reports</i> , 2016, 6, 37769.                                 | 1.6 | 8         |
| 47 | Epigenome-wide gene-age interaction analysis reveals reversed effects of <i>PRODH</i> DNA methylation on survival between young and elderly early-stage NSCLC patients. <i>Aging</i> , 2020, 12, 10642-10662.                       | 1.4 | 8         |
| 48 | Whole blood microRNAs as a prognostic classifier for acute respiratory distress syndrome 28-day mortality. <i>Intensive Care Medicine</i> , 2016, 42, 1824-1825.  | 3.9 | 7         |
| 49 | Mendelian Randomization With Refined Instrumental Variables From Genetic Score Improves Accuracy and Reduces Bias. <i>Frontiers in Genetics</i> , 2021, 12, 618829.   | 1.1 | 7         |
| 50 | Common <i>TDP1</i> Polymorphisms in Relation to Survival among Small Cell Lung Cancer Patients: A Multicenter Study from the International Lung Cancer Consortium. <i>Clinical Cancer Research</i> , 2017, 23, 7550-7557.           | 3.2 | 6         |
| 51 | A two-phase comprehensive NSCLC prognostic study identifies lncRNAs with significant main effect and interaction. <i>Molecular Genetics and Genomics</i> , 2022, 297, 591-600.  | 1.0 | 5         |
| 52 | A Large Scale Gene-Centric Association Study of Lung Function in Newly-Hired Female Cotton Textile Workers with Endotoxin Exposure. <i>PLoS ONE</i> , 2013, 8, e59035.  | 1.1 | 4         |
| 53 | Epigenome-wide three-way interaction study identifies a complex pattern between <i>TRIM27</i> , <i>KIAA0226</i> , and smoking associated with overall survival of early-stage NSCLC. <i>Molecular Oncology</i> , 2022, 16, 717-731. | 2.1 | 4         |
| 54 | Epigenome-wide association study for 28-day survival of acute respiratory distress syndrome. <i>Intensive Care Medicine</i> , 2018, 44, 1182-1184.  | 3.9 | 3         |

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|----|---|-----|-----------|
| 55 | Transmission dynamics model and the coronavirus disease 2019 epidemic: applications and challenges. <i>Medical Review</i> , 2022, 2, 89-109.  | 0.3 | 3         |
| 56 | Identification of genetic features associated with fine particulate matter (PM2.5) modulated DNA damage using improved random forest analysis. <i>Gene</i> , 2020, 740, 144570.             | 1.0 | 2         |
| 57 | Association between aspirin use and lung cancer incidence depends on high-frequency use, bodyweight, and age in U.S. adults. <i>Translational Lung Cancer Research</i> , 2021, 10, 392-401. | 1.3 | 2         |
| 58 | 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         |