

# Zuoheng Wang

## List of Publications by Year in descending order

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Version: 2024-02-01

47  
papers

1,375  
citations

430874

18  
h-index

361022

35  
g-index

48  
all docs

48  
docs citations

48  
times ranked

2868  
citing authors

#	ARTICLE	IF	CITATIONS
1	Immune dysregulation and autoreactivity correlate with disease severity in SARS-CoV-2-associated multisystem inflammatory syndrome in children. <i>Immunity</i> , 2021, 54, 1083-1095.e7.	14.3	164
2	Association of Delayed Adjuvant Chemotherapy With Survival After Lung Cancer Surgery. <i>JAMA Oncology</i> , 2017, 3, 610.	7.1	142
3	Lobectomy versus stereotactic body radiotherapy in healthy patients with stage I lung cancer. <i>Journal of Thoracic and Cardiovascular Surgery</i> , 2016, 152, 44-54.e9.	0.8	105
4	Single-cell multi-omics reveals dyssynchrony of the innate and adaptive immune system in progressive COVID-19. <i>Nature Communications</i> , 2022, 13, 440.	12.8	100
5	A Comparison of Association Methods Correcting for Population Stratification in Case-€“Control Studies. <i>Annals of Human Genetics</i> , 2011, 75, 418-427.	0.8	83
6	The Role and Challenges of Exome Sequencing in Studies of Human Diseases. <i>Frontiers in Genetics</i> , 2013, 4, 160.	2.3	79
7	Targeted drug delivery to ischemic stroke via chlorotoxin-anchored, lexican-loaded nanoparticles. <i>Nanomedicine: Nanotechnology, Biology, and Medicine</i> , 2016, 12, 1833-1842.	3.3	79
8	Preliminary analysis of positive and negative syndrome scale in ketamine-associated psychosis in comparison with schizophrenia. <i>Journal of Psychiatric Research</i> , 2015, 61, 64-72.	3.1	50
9	Elevated T cell activation score is associated with improved survival of breast cancer. <i>Breast Cancer Research and Treatment</i> , 2017, 164, 689-696.	2.5	49
10	Epigenome-wide association analysis revealed that SOCS3 methylation influences the effect of cumulative stress on obesity. <i>Biological Psychology</i> , 2018, 131, 63-71.	2.2	49
11	A statistical model for high-resolution mapping of quantitative trait loci determining HIV dynamics. <i>Statistics in Medicine</i> , 2004, 23, 3033-3051.	1.6	41
12	tRFtarget: a database for transfer RNA-derived fragment targets. <i>Nucleic Acids Research</i> , 2021, 49, D254-D260.	14.5	37
13	Identification of trans-eQTLs using mediation analysis with multiple mediators. <i>BMC Bioinformatics</i> , 2019, 20, 126.	2.6	34
14	DNA methylation signatures of illicit drug injection and hepatitis C are associated with HIV frailty. <i>Nature Communications</i> , 2017, 8, 2243.	12.8	32
15	The differential impact of preoperative comorbidity on perioperative outcomes following thoroscopic and open lobectomies. <i>European Journal of Cardio-thoracic Surgery</i> , 2017, 51, 169-174.	1.4	28
16	Defining the learning curve in robot-assisted thoroscopic lobectomy. <i>Surgery</i> , 2019, 165, 450-454.	1.9	28
17	MODELING PHENOTYPIC PLASTICITY IN GROWTH TRAJECTORIES: A STATISTICAL FRAMEWORK. <i>Evolution; International Journal of Organic Evolution</i> , 2014, 68, 81-91.	2.3	22
18	Interplay of tRNA-Derived Fragments and T Cell Activation in Breast Cancer Patient Survival. <i>Cancers</i> , 2020, 12, 2230.	3.7	21

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19	Statistical Analysis of Multiple Phenotypes in Genetic Epidemiologic Studies: From Cross-Phenotype Associations to Pleiotropy. <i>American Journal of Epidemiology</i> , 2018, 187, 855-863.	3.4	20
20	An omnidirectional visualization model of personalized gene regulatory networks. <i>Npj Systems Biology and Applications</i> , 2019, 5, 38.	3.0	20
21	BRCA1 mRNA expression modifies the effect of T cell activation score on patient survival in breast cancer. <i>BMC Cancer</i> , 2019, 19, 387.	2.6	17
22	A statistical model to analyse quantitative trait locus interactions for HIV dynamics from the virus and human genomes. <i>Statistics in Medicine</i> , 2006, 25, 495-511.	1.6	14
23	DNA methylation mediates the effect of cocaine use on HIV severity. <i>Clinical Epigenetics</i> , 2020, 12, 140.	4.1	14
24	Resection of oligometastatic lung cancer to the pancreas may yield a survival benefit in select patients – A systematic review. <i>Pancreatology</i> , 2015, 15, 456-462.	1.1	13
25	A model for predicting prolonged length of stay in patients undergoing anatomical lung resection: a National Surgical Quality Improvement Program (NSQIP) database study. <i>Interactive Cardiovascular and Thoracic Surgery</i> , 2016, 23, 208-215.	1.1	13
26	Longitudinal SNP-set association analysis of quantitative phenotypes. <i>Genetic Epidemiology</i> , 2017, 41, 81-93.	1.3	13
27	Retrospective Association Analysis of Longitudinal Binary Traits Identifies Important Loci and Pathways in Cocaine Use. <i>Genetics</i> , 2019, 213, 1225-1236.	2.9	13
28	Regulation and characterization of tumor-infiltrating immune cells in breast cancer. <i>International Immunopharmacology</i> , 2021, 90, 107167.	3.8	13
29	Estimating the Annual Incremental Cost of Several Complications Following Pulmonary Lobectomy. <i>Seminars in Thoracic and Cardiovascular Surgery</i> , 2016, 28, 531-540.	0.6	10
30	Isolation and characterization of a poplar d-type cyclin gene associated with the SHORT-ROOT/SCARECROW network. <i>Trees - Structure and Function</i> , 2016, 30, 255-263.	1.9	10
31	Treating Locally Advanced Disease: An Analysis of Very Large, Hilar Lymph Node Positive Non-Small Cell Lung Cancer Using the National Cancer Data Base. <i>Annals of Thoracic Surgery</i> , 2014, 97, 1149-1155.	1.3	9
32	Stochastic modeling of systems mapping in pharmacogenomics. <i>Advanced Drug Delivery Reviews</i> , 2013, 65, 912-917.	13.7	8
33	Impact of Neoantigen Expression and T-Cell Activation on Breast Cancer Survival. <i>Cancers</i> , 2021, 13, 2879.	3.7	8
34	ATRIUM: Testing Untyped SNPs in Case-Control Association Studies with Related Individuals. <i>American Journal of Human Genetics</i> , 2009, 85, 667-678.	6.2	6
35	Mathematical modeling of systems pharmacogenomics towards personalized drug delivery. <i>Advanced Drug Delivery Reviews</i> , 2013, 65, 903-904.	13.7	6
36	G2S3: A gene graph-based imputation method for single-cell RNA sequencing data. <i>PLoS Computational Biology</i> , 2021, 17, e1009029.	3.2	6

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37	Direct assessment of multiple testing correction in case-control association studies with related individuals. <i>Genetic Epidemiology</i> , 2011, 35, 70-79.	1.3	5
38	fGWAS: An R package for genome-wide association analysis with longitudinal phenotypes. <i>Journal of Genetics and Genomics</i> , 2018, 45, 411-413.	3.9	5
39	A novel transcriptional risk score for risk prediction of complex human diseases. <i>Genetic Epidemiology</i> , 2021, 45, 811-820.	1.3	3
40	Evaluating the fate of patients who undergo resections of very large, node-negative lung cancers using the National Cancer DataBase. <i>European Journal of Cardio-thoracic Surgery</i> , 2016, 49, 596-601.	1.4	2
41	Maximum likelihood estimation of nonlinear mixed-effects models with crossed random effects by combining first-order conditional linearization and sequential quadratic programming. <i>International Journal of Biomathematics</i> , 2019, 12, 1950040.	2.9	2
42	Systems mapping of HIV-1 infection. <i>BMC Genetics</i> , 2012, 13, 91.	2.7	1
43	Integrating evolutionary game theory into epigenetic study of embryonic development. <i>Physics of Life Reviews</i> , 2017, 20, 164-165.	2.8	1
44	Biological and practical implications of genome-wide association study of schizophrenia using Bayesian variable selection. <i>NPJ Schizophrenia</i> , 2019, 5, 19.	3.6	0
45	Testing gene-environment interactions in the presence of confounders and mismeasured environmental exposures. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	0
46	Influence of extracapsular extension on lymph node staging for patients with squamous cell carcinoma of the head and neck.. <i>Journal of Clinical Oncology</i> , 2012, 30, 5532-5532.	1.6	0
47	Prognostic significance of the AJCC staging in patients with squamous cell carcinoma of the oropharynx.. <i>Journal of Clinical Oncology</i> , 2012, 30, 5529-5529.	1.6	0