Zuoheng Wang

List of Publications by Year
in descending order

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	Single-cell multi-omics reveals dyssynchrony of the innate and adaptive immune system in progressive COVID-19. Nature Communications, 2022, 13, 440.	12.8	100
2	tRFtarget: a database for transfer RNA-derived fragment targets. Nucleic Acids Research, 2021, 49, D254-D260.	14.5	37
3	Regulation and characterization of tumor-infiltrating immune cells in breast cancer. International Immunopharmacology, 2021, 90, 107167.	3.8	13
4	Immune dysregulation and autoreactivity correlate with disease severity in SARS-CoV-2-associated multisystem inflammatory syndrome in children. Immunity, 2021, 54, 1083-1095.e7.	14.3	164
5	G2S3: A gene graph-based imputation method for single-cell RNA sequencing data. PLoS Computational Biology, 2021, 17, e1009029.	3.2	6
6	Impact of Neoantigen Expression and T-Cell Activation on Breast Cancer Survival. Cancers, 2021, 13, 2879.	3.7	8
7	Testing gene–environment interactions in the presence of confounders and mismeasured environmental exposures. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	0
8	A novel transcriptional risk score for risk prediction of complex human diseases. Genetic Epidemiology, 2021, 45, 811-820.	1.3	3
9	Interplay of tRNA-Derived Fragments and T Cell Activation in Breast Cancer Patient Survival. Cancers, 2020, 12, 2230.	3.7	21
10	DNA methylation mediates the effect of cocaine use on HIV severity. Clinical Epigenetics, 2020, 12, 140.	4.1	14
11	Defining the learning curve in robot-assisted thoracoscopic lobectomy. Surgery, 2019, 165, 450-454.	1.9	28
12	An omnidirectional visualization model of personalized gene regulatory networks. Npj Systems Biology and Applications, 2019, 5, 38.	3.0	20
13	Maximum likelihood estimation of nonlinear mixed-effects models with crossed random effects by combining first-order conditional linearization and sequential quadratic programming. International Journal of Biomathematics, 2019, 12, 1950040.	2.9	2
14	BRCA1 mRNA expression modifies the effect of T cell activation score on patient survival in breast cancer. BMC Cancer, 2019, 19, 387.	2.6	17
15	Identification of trans-eQTLs using mediation analysis with multiple mediators. BMC Bioinformatics, 2019, 20, 126.	2.6	34
16	Retrospective Association Analysis of Longitudinal Binary Traits Identifies Important Loci and Pathways in Cocaine Use. Genetics, 2019, 213, 1225-1236.	2.9	13
17	Biological and practical implications of genome-wide association study of schizophrenia using Bayesian variable selection. NPJ Schizophrenia, 2019, 5, 19.	3.6	0
18	Epigenome-wide association analysis revealed that SOCS3 methylation influences the effect of cumulative stress on obesity. Biological Psychology, 2018, 131, 63-71.	2.2	49

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19	Statistical Analysis of Multiple Phenotypes in Genetic Epidemiologic Studies: From Cross-Phenotype Associations to Pleiotropy. American Journal of Epidemiology, 2018, 187, 855-863.	3.4	20
20	fGWAS: An R package for genome-wide association analysis with longitudinal phenotypes. Journal of Genetics and Genomics, 2018, 45, 411-413.	3.9	5
21	Integrating evolutionary game theory into epigenetic study of embryonic development. Physics of Life Reviews, 2017, 20, 164-165.	2.8	1
22	Elevated T cell activation score is associated with improved survival of breast cancer. Breast Cancer Research and Treatment, 2017, 164, 689-696.	2.5	49
23	Association of Delayed Adjuvant Chemotherapy With Survival After Lung Cancer Surgery. JAMA Oncology, 2017, 3, 610.	7.1	142
24	The differential impact of preoperative comorbidity on perioperative outcomes following thoracoscopic and open lobectomies. European Journal of Cardio-thoracic Surgery, 2017, 51, 169-174.	1.4	28
25	Longitudinal SNPâ€set association analysis of quantitative phenotypes. Genetic Epidemiology, 2017, 41, 81-93.	1.3	13
26	DNA methylation signatures of illicit drug injection and hepatitis C are associated with HIV frailty. Nature Communications, 2017, 8, 2243.	12.8	32
27	Targeted drug delivery to ischemic stroke via chlorotoxin-anchored, lexiscan-loaded nanoparticles. Nanomedicine: Nanotechnology, Biology, and Medicine, 2016, 12, 1833-1842.	3.3	79
28	Lobectomy versus stereotactic body radiotherapy in healthy patients with stage I lung cancer. Journal of Thoracic and Cardiovascular Surgery, 2016, 152, 44-54.e9.	0.8	105
29	Estimating the Annual Incremental Cost of Several Complications Following Pulmonary Lobectomy. Seminars in Thoracic and Cardiovascular Surgery, 2016, 28, 531-540.	0.6	10
30	A model for predicting prolonged length of stay in patients undergoing anatomical lung resection: a National Surgical Quality Improvement Program (NSQIP) database study. Interactive Cardiovascular and Thoracic Surgery, 2016, 23, 208-215.	1.1	13
31	Evaluating the fate of patients who undergo resections of very large, node-negative lung cancers using the National Cancer DataBase. European Journal of Cardio-thoracic Surgery, 2016, 49, 596-601.	1.4	2
32	Isolation and characterization of a poplar d-type cyclin gene associated with the SHORT-ROOT/SCARECROW network. Trees - Structure and Function, 2016, 30, 255-263.	1.9	10
33	Resection of oligometastatic lung cancer to the pancreas may yield a survival benefit in select patients â€" A systematic review. Pancreatology, 2015, 15, 456-462.	1.1	13
34	Preliminary analysis of positive and negative syndrome scale in ketamine-associated psychosis in comparison with schizophrenia. Journal of Psychiatric Research, 2015, 61, 64-72.	3.1	50
35	MODELING PHENOTYPIC PLASTICITY IN GROWTH TRAJECTORIES: A STATISTICAL FRAMEWORK. Evolution; International Journal of Organic Evolution, 2014, 68, 81-91.	2.3	22
36	Treating Locally Advanced Disease: An Analysis of Very Large, Hilar Lymph Node Positive Non-Small Cell Lung Cancer Using the National Cancer Data Base. Annals of Thoracic Surgery, 2014, 97, 1149-1155.	1.3	9

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37	Stochastic modeling of systems mapping in pharmacogenomics. Advanced Drug Delivery Reviews, 2013, 65, 912-917.	13.7	8
38	Mathematical modeling of systems pharmacogenomics towards personalized drug delivery. Advanced Drug Delivery Reviews, 2013, 65, 903-904.	13.7	6
39	The Role and Challenges of Exome Sequencing in Studies of Human Diseases. Frontiers in Genetics, 2013, 4, 160.	2.3	79
40	Systems mapping of HIV-1 infection. BMC Genetics, 2012, 13, 91.	2.7	1
41	Influence of extracapsular extension on lymph node staging for patients with squamous cell carcinoma of the head and neck.. Journal of Clinical Oncology, 2012, 30, 5532-5532.	1.6	0
42	Prognostic significance of the AJCC staging in patients with squamous cell carcinoma of the oropharynx.. Journal of Clinical Oncology, 2012, 30, 5529-5529.	1.6	0
43	A Comparison of Association Methods Correcting for Population Stratification in Case–Control Studies. Annals of Human Genetics, 2011, 75, 418-427.	0.8	83
44	Direct assessment of multiple testing correction in case-control association studies with related individuals. Genetic Epidemiology, 2011, 35, 70-79.	1.3	5
45	ATRIUM: Testing Untyped SNPs in Case-Control Association Studies with Related Individuals. American Journal of Human Genetics, 2009, 85, 667-678.	6.2	6
46	A statistical model to analyse quantitative trait locus interactions for HIV dynamics from the virus and human genomes. Statistics in Medicine, 2006, 25, 495-511.	1.6	14
47	A statistical model for high-resolution mapping of quantitative trait loci determining HIV dynamics. Statistics in Medicine, 2004, 23, 3033-3051.	1.6	41