

# Ji-Yuan Zhou

## List of Publications by Year in descending order

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Version: 2024-02-01

43  
papers

300  
citations

840776

11  
h-index

996975

15  
g-index

48  
all docs

48  
docs citations

48  
times ranked

495  
citing authors

#	ARTICLE	IF	CITATIONS
1	Incidence, clinical course and risk factor for recurrent PCR positivity in discharged COVID-19 patients in Guangzhou, China: A prospective cohort study. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008648.	3.0	42
2	Effect of the 2008 cold spell on preterm births in two subtropical cities of Guangdong Province, Southern China. <i>Science of the Total Environment</i> , 2018, 642, 307-313.	8.0	26
3	Detection of Parent-of-Origin Effects Based on Complete and Incomplete Nuclear Families with Multiple Affected Children. <i>Human Heredity</i> , 2009, 67, 1-12.	0.8	20
4	HLA Polymorphism and Susceptibility to End-Stage Renal Disease in Cantonese Patients Awaiting Kidney Transplantation. <i>PLoS ONE</i> , 2014, 9, e90869.	2.5	19
5	Migrant population is more vulnerable to the effect of air pollution on preterm birth: Results from a birth cohort study in seven Chinese cities. <i>International Journal of Hygiene and Environmental Health</i> , 2019, 222, 1047-1053.	4.3	19
6	A statistical measure for the skewness of X chromosome inactivation based on case-control design. <i>BMC Bioinformatics</i> , 2019, 20, 11.	2.6	16
7	The transmission disequilibrium test and imprinting effects test based on case-parent pairs. <i>Genetic Epidemiology</i> , 2007, 31, 273-287.	1.3	13
8	Detection of parent-of-origin effects using general pedigree data. <i>Genetic Epidemiology</i> , 2010, 34, 151-158.	1.3	13
9	An Extension of the Transmission Disequilibrium Test Incorporating Imprinting. <i>Genetics</i> , 2007, 175, 1489-1504.	2.9	12
10	Detection of Parent-of-Origin Effects for Quantitative Traits in Complete and Incomplete Nuclear Families With Multiple Children. <i>American Journal of Epidemiology</i> , 2011, 174, 226-233.	3.4	12
11	A robust and powerful test for case-control genetic association study on X chromosome. <i>Statistical Methods in Medical Research</i> , 2019, 28, 3260-3272.	1.5	12
12	A powerful approach for association analysis incorporating imprinting effects. <i>Bioinformatics</i> , 2011, 27, 2571-2577.	4.1	11
13	Fluorescent wood sponge toward selective detection and efficient removal of Cr(VI). <i>Environmental Science: Nano</i> , 2021, 8, 3331-3342.	4.3	9
14	A powerful parent-of-origin effects test for qualitative traits incorporating control children in nuclear families. <i>Journal of Human Genetics</i> , 2012, 57, 500-507.	2.3	8
15	Likelihood Ratio Test for Excess Homozygosity at Marker Loci on X Chromosome. <i>PLoS ONE</i> , 2015, 10, e0145032.	2.5	7
16	A powerful parent-of-origin effects test for qualitative traits on X chromosome in general pedigrees. <i>BMC Bioinformatics</i> , 2018, 19, 8.	2.6	7
17	Detection of Parent-of-Origin Effects in Complete and Incomplete Nuclear Families with Multiple Affected Children Using Multiple Tightly Linked Markers. <i>Human Heredity</i> , 2009, 67, 116-127.	0.8	6
18	A statistical measure for the skewness of X chromosome inactivation based on family trios. <i>BMC Genetics</i> , 2018, 19, 109.	2.7	6

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19	Repetitive transcranial magnetic stimulation for depression after basal ganglia ischaemic stroke: protocol for a multicentre randomised double-blind placebo-controlled trial. <i>BMJ Open</i> , 2018, 8, e018011.	1.9	5
20	Detection of imprinting effects for qualitative traits on X chromosome based on nuclear families. <i>Statistical Methods in Medical Research</i> , 2018, 27, 2329-2343.	1.5	5
21	A statistical measure for the skewness of X chromosome inactivation for quantitative traits and its application to the MCTFR data. <i>BMC Genomic Data</i> , 2021, 22, 24.	1.7	5
22	A robust test for X-chromosome genetic association accounting for X-chromosome inactivation and imprinting. <i>Genetical Research</i> , 2020, 102, e2.	0.9	4
23	Powerful Haplotype-Based Hardy-Weinberg Equilibrium Tests for Tightly Linked Loci. <i>PLoS ONE</i> , 2013, 8, e77399.	2.5	4
24	X-chromosome genetic association test incorporating X-chromosome inactivation and imprinting effects. <i>Journal of Genetics</i> , 2019, 98, 1.	0.7	3
25	Inferring Haplotype/Disease Association by Joint Use of Case-Parents Trios and Case-Parent Pairs. <i>Annals of Human Genetics</i> , 2010, 74, 263-274.	0.8	2
26	Powerful tests for association on quantitative trait loci incorporating imprinting effects. <i>Journal of Human Genetics</i> , 2013, 58, 384-390.	2.3	2
27	Detection of parent-of-origin effects for quantitative traits using general pedigree data. <i>Journal of Genetics</i> , 2014, 93, 339-347.	0.7	2
28	Detection of Imprinting Effects for Quantitative Traits on X Chromosome Using Nuclear Families with Multiple Daughters. <i>Annals of Human Genetics</i> , 2017, 81, 147-160.	0.8	2
29	Simple-to-use nomogram for predicting the risk of syphilis among MSM in Guangdong Province: results from a serial cross-sectional study. <i>BMC Infectious Diseases</i> , 2021, 21, 1199.	2.9	2
30	BEXCIS: Bayesian methods for estimating the degree of the skewness of X chromosome inactivation. <i>BMC Bioinformatics</i> , 2022, 23, .	2.6	2
31	A powerful association test for qualitative traits incorporating imprinting effects using general pedigree data. <i>Journal of Human Genetics</i> , 2015, 60, 77-83.	2.3	1
32	Photodynamic therapy for synovial hyperplasia in patients with refractory rheumatoid arthritis: a study protocol for a randomized, double-blind, blank-controlled prospective trial. <i>Trials</i> , 2021, 22, 685.	1.6	1
33	X-chromosome genetic association test incorporating X-chromosome inactivation and imprinting effects. <i>Journal of Genetics</i> , 2019, 98, .	0.7	1
34	Robust Joint Analysis with Data Fusion in Two-Stage Quantitative Trait Genome-Wide Association Studies. <i>Computational and Mathematical Methods in Medicine</i> , 2013, 2013, 1-12.	1.3	0
35	Generalized disequilibrium test for association in qualitative traits incorporating imprinting effects based on extended pedigrees. <i>BMC Genetics</i> , 2017, 18, 90.	2.7	0
36	Efficient Monte Carlo evaluation of resampling-based hypothesis tests with applications to genetic epidemiology. <i>Statistical Methods in Medical Research</i> , 2018, 27, 1437-1450.	1.5	0

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37	Two Powerful Tests for Parent-of-Origin Effects at Quantitative Trait Loci on the X Chromosome. <i>Human Heredity</i> , 2018, 83, 250-273.	0.8	0
38	Title is missing!., 2020, 14, e0008648.		0
39	Title is missing!., 2020, 14, e0008648.		0
40	Title is missing!., 2020, 14, e0008648.		0
41	Title is missing!., 2020, 14, e0008648.		0
42	Detection of Parent-of-Origin Effects for the Variants Associated With Behavioral Disinhibition in the MCTFR Data. <i>Frontiers in Genetics</i> , 2022, 13, 831685.	2.3	0
43	Gene-Based Methods for Estimating the Degree of the Skewness of X Chromosome Inactivation. <i>Genes</i> , 2022, 13, 827.	2.4	0