Kai Wang

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Systematic review of human biomonitoring studies of ethylenethiourea, a urinary biomarker for exposure to dithiocarbamate fungicides. Environmental Pollution, 2022, 292, 118419.	7.5	11
2	Estimation of Causal Effect of Age at Menarche on Pubertal Height Growth Using Mendelian Randomization. Genes, 2022, 13, 710.	2.4	4
3	Misdiagnosis of fungal infections of the orbit. Canadian Journal of Ophthalmology, 2022, , .	0.7	0
4	Effect of selection bias on two sample summary data based Mendelian randomization. Scientific Reports, 2021, 11, 7585.	3.3	10
5	A mouse model of Bardet-Biedl Syndrome has impaired fear memory, which is rescued by lithium treatment. PLoS Genetics, 2021, 17, e1009484.	3.5	8
6	Evaluation of occupational pesticide exposure on Egyptian male adolescent cognitive and motor functioning. Environmental Research, 2021, 197, 111137.	7.5	5
7	Direct effect and indirect effect on an outcome under nonlinear modeling. International Journal of Biostatistics, 2020, 16, .	0.7	2
8	A genetic association test through combining two independent tests. Genomics, 2019, 111, 1152-1159.	2.9	6
9	A novel gene-set association test based on variance-gamma distribution. Statistical Methods in Medical Research, 2019, 28, 2868-2875.	1.5	4
10	Geneâ€based sequential burden association test. Statistics in Medicine, 2019, 38, 2353-2363.	1.6	13
11	Maximum Likelihood Analysis of Linear Mediation Models with Treatment–Mediator Interaction. Psychometrika, 2019, 84, 719-748.	2.1	4
12	Occupational pesticide exposure and symptoms of attention deficit hyperactivity disorder in adolescent pesticide applicators in Egypt. NeuroToxicology, 2019, 74, 1-6.	3.0	31
13	Absence of BBSome function leads to astrocyte reactivity in the brain. Molecular Brain, 2019, 12, 48.	2.6	14
14	Geneâ€based genetic association test with adaptive optimal weights. Genetic Epidemiology, 2018, 42, 95-103.	1.3	10
15	Understanding Power Anomalies in Mediation Analysis. Psychometrika, 2018, 83, 387-406.	2.1	8
16	The impact of repeated organophosphorus pesticide exposure on biomarkers and neurobehavioral outcomes among adolescent pesticide applicators. Journal of Toxicology and Environmental Health - Part A: Current Issues, 2017, 80, 542-555.	2.3	42
17	A gene-based test of association through an orthogonal decomposition of genotype scores. Human Genetics, 2017, 136, 1385-1394.	3.8	8
18	Genetic association test based on principal component analysis. Statistical Applications in Genetics and Molecular Biology, 2017, 16, 189-198.	0.6	10

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19	A Powerful Variant-Set Association Test Based on Chi-Square Distribution. Genetics, 2017, 207, 903-910.	2.9	15
20	Comparison of neurological health outcomes between two adolescent cohorts exposed to pesticides in Egypt. PLoS ONE, 2017, 12, e0172696.	2.5	29
21	Boosting the Power of the Sequence Kernel Association Test by Properly Estimating Its Null Distribution. American Journal of Human Genetics, 2016, 99, 104-114.	6.2	23
22	Quantitative measurement of retinal ganglion cell populations via histology-based random forest classification. Experimental Eye Research, 2016, 146, 370-385.	2.6	23
23	A 10-month prospective study of organophosphorus pesticide exposure and neurobehavioral performance among adolescents in Egypt. Cortex, 2016, 74, 383-395.	2.4	48
24	RetFM-J, an ImageJ-based module for automated counting andÂquantifying features of nuclei in retinal whole-mounts. Experimental Eye Research, 2016, 146, 386-392.	2.6	24
25	Testing Genetic Association by Regressing Genotype over Multiple Phenotypes. PLoS ONE, 2014, 9, e106918.	2.5	13
26	An Analytical Comparison of the Principal Component Method and the Mixed Effects Model for Association Studies in the Presence of Cryptic Relatedness and Population Stratification. Human Heredity, 2013, 76, 1-9.	0.8	20
27	A Genome-Wide Association Study for Primary Open Angle Glaucoma and Macular Degeneration Reveals Novel Loci. PLoS ONE, 2013, 8, e58657.	2.5	35
28	Statistical tests of genetic association for case-control study designs. Biostatistics, 2012, 13, 724-733.	1.5	11
29	Statistical Tests for Detecting Rare Variants Using Variance‣tabilising Transformations. Annals of Human Genetics, 2012, 76, 402-409.	0.8	7
30	Gene-based interaction analysis by incorporating external linkage disequilibrium information. European Journal of Human Genetics, 2011, 19, 164-172.	2.8	18
31	Treating phenotype as given: a simple resampling method for genome-wide association studies. BMC Proceedings, 2011, 5, S60.	1.6	2
32	Multiple testing in highâ€ŧhroughput sequence data: experiences from Group 8 of Genetic Analysis Workshop 17. Genetic Epidemiology, 2011, 35, S61-6.	1.3	2
33	Analysing biological pathways in genome-wide association studies. Nature Reviews Genetics, 2010, 11, 843-854.	16.3	722
34	ATOM: a powerful gene-based association test by combining optimally weighted markers. Bioinformatics, 2009, 25, 497-503.	4.1	45
35	Association of KCNB1 to rheumatoid arthritis via interaction with HLA-DRB1. BMC Proceedings, 2009, 3, S134.	1.6	4
36	Testing for genetic association in the presence of population stratification in genomeâ€wide association studies. Genetic Epidemiology, 2009, 33, 637-645.	1.3	27

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37	An Analytic Study of the Power of Popular Quantitative-Trait-Locus Mapping Methods. Behavior Genetics, 2008, 38, 554-559.	2.1	2
38	A principal components regression approach to multilocus genetic association studies. Genetic Epidemiology, 2008, 32, 108-118.	1.3	124
39	Genetic association tests in the presence of epistasis or geneâ€environment interaction. Genetic Epidemiology, 2008, 32, 606-614.	1.3	10
40	A Constrained-Likelihood Approach to Marker-Trait Association Studies. American Journal of Human Genetics, 2005, 77, 768-780.	6.2	51
41	Score tests for epistasis models on quantitative traits using general pedigree data. Genetic Epidemiology, 2003, 25, 314-326.	1.3	6
42	Bivariate linkage analysis of cholesterol and triglyceride levels in the Framingham Heart Study. BMC Genetics, 2003, 4, S62.	2.7	5
43	Linkage analysis of systolic blood pressure: a score statistic and computer implementation. BMC Genetics, 2003, 4, S77.	2.7	1
44	Genome-wide linkage analysis of blood pressure under locus heterogeneity. BMC Genetics, 2003, 4, S78.	2.7	6
45	Mapping Quantitative Trait Loci Using Multiple Phenotypes in General Pedigrees. Human Heredity, 2003, 55, 1-15.	0.8	19
46	Efficient Score Statistics for Mapping Quantitative Trait Loci with Extended Pedigrees. Human Heredity, 2002, 54, 57-68.	0.8	9
47	Score test for mapping quantitative-trait loci with sibships of arbitrary size when the dominance effect is not negligible. Genetic Epidemiology, 2002, 23, 398-412.	1.3	9