Changshuai Wei

List of Publications by Year
in descending order

22 papers	182 citations	1040056 9 h-index	1199594 12 g-index
22 all docs	22 docs citations	22 times ranked	289 citing authors

#	Article	IF	Citations
1	Functional Analysis of Variance for Association Studies. PLoS ONE, 2014, 9, e105074.	2.5	24
2	Mixed linear model approach for mapping quantitative trait loci underlying crop seed traits. Heredity, 2014, 113, 224-232.	2.6	18
3	A Likelihood Ratio–Based Mann–Whitney Approach Finds Novel Replicable Joint Gene Action for Type 2 Diabetes. Genetic Epidemiology, 2012, 36, 583-593.	1.3	15
4	A Generalized Genetic Random Field Method for the Genetic Association Analysis of Sequencing Data. Genetic Epidemiology, 2014, 38, 242-253.	1.3	13
5	A Non-Parametric Method for Building Predictive Genetic Tests on High-Dimensional Data. Human Heredity, 2011, 71, 161-170.	0.8	12
6	A generalized association test based on U statistics. Bioinformatics, 2017, 33, 1963-1971.	4.1	11
7	Trees Assembling Mann–Whitney Approach for Detecting Genome–Wide Joint Association Among Low–Marginal–Effect Loci. Genetic Epidemiology, 2013, 37, 84-91.	1.3	10
8	Comparison of Frozen and Unfrozen Blood Spots for Gene Expression Studies. Journal of Pediatrics, 2014, 164, 189-191.e1.	1.8	10
9	A Weighted U-Statistic for Genetic Association Analyses of Sequencing Data. Genetic Epidemiology, 2014, 38, 699-708.	1.3	10
10	A Three-Way Interaction among Maternal and Fetal Variants Contributing to Congenital Heart Defects. Annals of Human Genetics, 2016, 80, 20-31.	0.8	9
11	A new mapping method for quantitative trait loci of silkworm. BMC Genetics, 2011, 12, 19.	2.7	7
12	GWGGI: software for genome-wide gene-gene interaction analysis. BMC Genetics, 2014, 15, 101.	2.7	7
13	A weighted U statistic for association analyses considering genetic heterogeneity. Statistics in Medicine, 2016, 35, 2802-2814.	1.6	7
14	Bagging Optimal ROC Curve Method for Predictive Genetic Tests, with an Application for Rheumatoid Arthritis. Journal of Biopharmaceutical Statistics, 2010, 20, 401-414.	0.8	5
15	Genome-Environmental Risk Assessment of Cocaine Dependence. Frontiers in Genetics, 2012, 3, 83.	2.3	5
16	Collapsing ROC approach for risk prediction research on both common and rare variants. BMC Proceedings, 2011, 5, S42.	1.6	4
17	High correlations in gene expression between paired umbilical cord blood and neonatal blood of healthy newborns on Guthrie cards. Journal of Maternal-Fetal and Neonatal Medicine, 2013, 26, 1765-1767.	1.5	4
18	An exploratory decision tree analysis to predict physical activity compliance rates in breast cancer survivors. Ethnicity and Health, 2019, 24, 754-766.	2.5	4

#	Article	IF	Citations
19	Genome-wide joint analysis of single-nucleotide variant sets and gene expression for hypertension and related phenotypes. BMC Proceedings, 2016, 10, 125-129.	1.6	3
20	A U-Statistic-based random forest approach for genetic interaction study. Frontiers in Bioscience - Elite, 2012, E4, 2607-2617.	1.8	2
21	Detecting Gene-Gene Interactions Associated with Multiple Complex Traits with U-Statistics. Current Genomics, 2016, 17, 403-415.	1.6	2
22	A multi-locus predictiveness curve and its summary assessment for genetic risk prediction. Statistical Methods in Medical Research, 2020, 29, 44-56.	1.5	0