

Changshuai Wei

List of Publications by Year in descending order

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22
papers

182
citations

1040056

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289
citing authors

#	ARTICLE	IF	CITATIONS
1	A multi-locus predictiveness curve and its summary assessment for genetic risk prediction. <i>Statistical Methods in Medical Research</i> , 2020, 29, 44-56.	1.5	0
2	An exploratory decision tree analysis to predict physical activity compliance rates in breast cancer survivors. <i>Ethnicity and Health</i> , 2019, 24, 754-766.	2.5	4
3	A generalized association test based on U statistics. <i>Bioinformatics</i> , 2017, 33, 1963-1971.	4.1	11
4	Detecting Gene-Gene Interactions Associated with Multiple Complex Traits with U -Statistics. <i>Current Genomics</i> , 2016, 17, 403-415.	1.6	2
5	A weighted U statistic for association analyses considering genetic heterogeneity. <i>Statistics in Medicine</i> , 2016, 35, 2802-2814.	1.6	7
6	A Three-Way Interaction among Maternal and Fetal Variants Contributing to Congenital Heart Defects. <i>Annals of Human Genetics</i> , 2016, 80, 20-31.	0.8	9
7	Genome-wide joint analysis of single-nucleotide variant sets and gene expression for hypertension and related phenotypes. <i>BMC Proceedings</i> , 2016, 10, 125-129.	1.6	3
8	GWGGI: software for genome-wide gene-gene interaction analysis. <i>BMC Genetics</i> , 2014, 15, 101.	2.7	7
9	Mixed linear model approach for mapping quantitative trait loci underlying crop seed traits. <i>Heredity</i> , 2014, 113, 224-232.	2.6	18
10	A Generalized Genetic Random Field Method for the Genetic Association Analysis of Sequencing Data. <i>Genetic Epidemiology</i> , 2014, 38, 242-253.	1.3	13
11	Comparison of Frozen and Unfrozen Blood Spots for Gene Expression Studies. <i>Journal of Pediatrics</i> , 2014, 164, 189-191.e1.	1.8	10
12	A Weighted U -Statistic for Genetic Association Analyses of Sequencing Data. <i>Genetic Epidemiology</i> , 2014, 38, 699-708.	1.3	10
13	Functional Analysis of Variance for Association Studies. <i>PLoS ONE</i> , 2014, 9, e105074.	2.5	24
14	High correlations in gene expression between paired umbilical cord blood and neonatal blood of healthy newborns on Guthrie cards. <i>Journal of Maternal-Fetal and Neonatal Medicine</i> , 2013, 26, 1765-1767.	1.5	4
15	Trees Assembling Mann-Whitney Approach for Detecting Genome-Wide Joint Association Among Low-Marginal Effect Loci. <i>Genetic Epidemiology</i> , 2013, 37, 84-91.	1.3	10
16	Genome-Environmental Risk Assessment of Cocaine Dependence. <i>Frontiers in Genetics</i> , 2012, 3, 83.	2.3	5
17	A U -Statistic-based random forest approach for genetic interaction study. <i>Frontiers in Bioscience - Elite</i> , 2012, E4, 2607-2617.	1.8	2
18	A Likelihood Ratio-Based Mann-Whitney Approach Finds Novel Replicable Joint Gene Action for Type 2 Diabetes. <i>Genetic Epidemiology</i> , 2012, 36, 583-593.	1.3	15

#	ARTICLE	IF	CITATIONS
19	A Non-Parametric Method for Building Predictive Genetic Tests on High-Dimensional Data. Human Heredity, 2011, 71, 161-170.	0.8	12
20	Collapsing ROC approach for risk prediction research on both common and rare variants. BMC Proceedings, 2011, 5, S42.	1.6	4
21	A new mapping method for quantitative trait loci of silkworm. BMC Genetics, 2011, 12, 19.	2.7	7
22	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