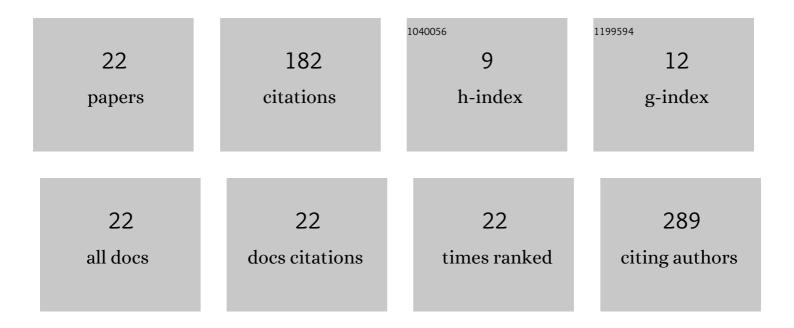
Changshuai Wei

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7251872/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	A multi-locus predictiveness curve and its summary assessment for genetic risk prediction. Statistical Methods in Medical Research, 2020, 29, 44-56.	1.5	Ο
2	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
3	A generalized association test based on <i>U</i> statistics. Bioinformatics, 2017, 33, 1963-1971.	4.1	11
4	Detecting Gene-Gene Interactions Associated with Multiple Complex Traits with U-Statistics. Current Genomics, 2016, 17, 403-415.	1.6	2
5	A weighted U statistic for association analyses considering genetic heterogeneity. Statistics in Medicine, 2016, 35, 2802-2814.	1.6	7
6	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
7	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
8	GWGGI: software for genome-wide gene-gene interaction analysis. BMC Genetics, 2014, 15, 101.	2.7	7
9	Mixed linear model approach for mapping quantitative trait loci underlying crop seed traits. Heredity, 2014, 113, 224-232.	2.6	18
10	A Generalized Genetic Random Field Method for the Genetic Association Analysis of Sequencing Data. Genetic Epidemiology, 2014, 38, 242-253.	1.3	13
11	Comparison of Frozen and Unfrozen Blood Spots for Gene Expression Studies. Journal of Pediatrics, 2014, 164, 189-191.e1.	1.8	10
12	A Weighted <i>U</i> -Statistic for Genetic Association Analyses of Sequencing Data. Genetic Epidemiology, 2014, 38, 699-708.	1.3	10
13	Functional Analysis of Variance for Association Studies. PLoS ONE, 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. Journal of Maternal-Fetal and Neonatal Medicine, 2013, 26, 1765-1767.	1.5	4
15	Trees Assembling Mannâ€Whitney Approach for Detecting Genomeâ€Wide Joint Association Among Lowâ€Marginalâ€Effect Loci. Genetic Epidemiology, 2013, 37, 84-91.	1.3	10
16	Genome-Environmental Risk Assessment of Cocaine Dependence. Frontiers in Genetics, 2012, 3, 83.	2.3	5
17	A U-Statistic-based random forest approach for genetic interaction study. Frontiers in Bioscience - Elite, 2012, E4, 2607-2617.	1.8	2
18	A Likelihood Ratioâ€Based Mannâ€Whitney Approach Finds Novel Replicable Joint Gene Action for Type 2 Diabetes. Genetic Epidemiology, 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