Qiuying Sha

List of Publications by Year
in descending order

40 papers	532 citations	687363 13 h-index	752698 20 g-index
47 all docs	47 docs citations	47 times ranked	447 citing authors

#	Article	IF	Citations
1	Gene-based association tests using GWAS summary statistics and incorporating eQTL. Scientific Reports, 2022, 12, 3553.	3.3	1
2	A computationally efficient clustering linear combination approach to jointly analyze multiple phenotypes for GWAS. PLoS ONE, 2022, 17, e0260911.	2.5	3
3	MF–TOWmuT: Testing an optimally weighted combination of common and rare variants with multiple traits using family data. Genetic Epidemiology, 2021, 45, 64-81.	1.3	0
4	Joint analysis of multiple phenotypes using a clustering linear combination method based on hierarchical clustering. Genetic Epidemiology, 2020, 44, 67-78.	1.3	7
5	Testing gene-environment interactions for rare and/or common variants in sequencing association studies. PLoS ONE, 2020, 15, e0229217.	2.5	4
6	A gene based approach to test genetic association based on an optimally weighted combination of multiple traits. PLoS ONE, 2019, 14, e0220914.	2.5	1
7	A general statistic to test an optimally weighted combination of common and/or rare variants. Genetic Epidemiology, 2019, 43, 966-979.	1.3	3
8	Joint Analysis of Multiple Phenotypes in Association Studies based on Cross-Validation Prediction Error. Scientific Reports, 2019, 9, 1073.	3.3	7
9	Test Gene-Environment Interactions for Multiple Traits in Sequencing Association Studies. Human Heredity, 2019, 84, 170-196.	0.8	4
10	A clustering linear combination approach to jointly analyze multiple phenotypes for GWAS. Bioinformatics, 2019, 35, 1373-1379.	4.1	14
11	Testing an optimally weighted combination of common and/or rare variants with multiple traits. PLoS ONE, 2018, 13, e0201186.	2.5	7
12	A hierarchical clustering method for dimension reduction in joint analysis of multiple phenotypes. Genetic Epidemiology, 2018, 42, 344-353.	1.3	13
13	A novel method to test associations between a weighted combination of phenotypes and genetic variants. PLoS ONE, 2018, 13, e0190788.	2.5	12
14	Detecting association of rare and common variants based on cross-validation prediction error. Genetic Epidemiology, 2017, 41, 233-243.	1.3	9
15	Joint Analysis of Multiple Traits Using "Optimal" Maximum Heritability Test. PLoS ONE, 2016, 11, e0150975.	2.5	25
16	An Adaptive Fisher's Combination Method for Joint Analysis of Multiple Phenotypes in Association Studies. Scientific Reports, 2016, 6, 34323.	3.3	25
17	Joint Analysis of Multiple Traits in Rare Variant Association Studies. Annals of Human Genetics, 2016, 80, 162-171.	0.8	17
18	Power Comparisons of Methods for Joint Association Analysis of Multiple Phenotypes. Human Heredity, 2015, 80, 144-152.	0.8	13

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19	A Powerful Approach to Test an Optimally Weighted Combination of Rare Variants in Admixed Populations. Genetic Epidemiology, 2015, 39, 294-305.	1.3	2
20	A Novel Test for Testing the Optimally Weighted Combination of Rare and Common Variants Based on Data of Parents and Affected Children. Genetic Epidemiology, 2014, 38, 135-143.	1.3	5
21	A Rare Variant Association Test Based on Combinations of Single-Variant Tests. Genetic Epidemiology, 2014, 38, 494-501.	1.3	7
22	Adaptive clustering and adaptive weighting methods to detect disease associated rare variants. European Journal of Human Genetics, 2013, 21, 332-337.	2.8	13
23	Detecting Association of Rare Variants by Testing an Optimally Weighted Combination of Variants for Quantitative Traits in General Families. Annals of Human Genetics, 2013, 77, 524-534.	0.8	7
24	Two Adaptive Weighting Methods to Test for Rare Variant Associations in Family‐Based Designs. Genetic Epidemiology, 2012, 36, 499-507.	1.3	24
25	Detecting Association of Rare and Common Variants by Testing an Optimally Weighted Combination of Variants. Genetic Epidemiology, 2012, 36, 561-571.	1.3	74
26	A Novel Method to Detect Gene-Gene Interactions in Structured Populations: MDR-SP. Annals of Human Genetics, 2011, 75, 742-754.	0.8	15
27	An improved score test for genetic association studies. Genetic Epidemiology, 2011, 35, 350-359.	1.3	19
28	Joint Analysis for Genome-Wide Association Studies in Family-Based Designs. PLoS ONE, 2011, 6, e21957.	2.5	11
29	Identification of Interacting Genes in Genome‐Wide Association Studies Using a Model‐Based Two‐Stage Approach. Annals of Human Genetics, 2010, 74, 406-415.	0.8	1
30	Incorporating multiple-marker information to detect risk loci for rheumatoid arthritis. BMC Proceedings, 2009, 3, S28.	1.6	6
31	Detecting susceptibility genes for rheumatoid arthritis based on a novel sliding-window approach. BMC Proceedings, 2009, 3, S14.	1.6	5
32	A new association test to test multiple‐marker association. Genetic Epidemiology, 2009, 33, 164-171.	1.3	8
33	Genome-wide association reveals three SNPs associated with sporadic amyotrophic lateral sclerosis through a two-locus analysis. BMC Medical Genetics, 2009, 10, 86.	2.1	19
34	An ensemble learning approach jointly modeling main and interaction effects in genetic association studies. Genetic Epidemiology, 2008, 32, 285-300.	1.3	15
35	A new association test using haplotype similarity. Genetic Epidemiology, 2007, 31, 577-593.	1.3	21
36	A Combinatorial Searching Method for Detecting a Set of Interacting Loci Associated with Complex Traits. Annals of Human Genetics, 2006, 70, 677-692.	0.8	14

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37	Tests of Association Between Quantitative Traits and Haplotypes In A Reduced‐Dimensional Space. Annals of Human Genetics, 2005, 69, 715-732.	0.8	15
38	Haplotype sharing transmission/disequilibrium tests that allow for genotyping errors. Genetic Epidemiology, 2005, 28, 341-351.	1.3	11
39	Transmission/Disequilibrium Test Based on Haplotype Sharing for Tightly Linked Markers. American Journal of Human Genetics, 2003, 73, 566-579.	6.2	73
40	Control for population stratification in genetic association studies based on GWAS summary statistics. Genetic Epidemiology, 0, , .	1.3	0