

# Ying Zhou

## List of Publications by Year in descending order

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15  
papers

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1937685  
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#	ARTICLE	IF	CITATIONS
1	A two-stage testing strategy for detecting genes—environment interactions in association studies. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	0
2	Quantitative trait locus mapping analysis of multiple traits when using genotype data with potential errors. <i>PeerJ</i> , 2021, 9, e12187.	2.0	0
3	Gene association detection via local linear regression method. <i>Journal of Human Genetics</i> , 2020, 65, 115-123.	2.3	0
4	Bayesian interval mapping of count trait loci based on zero-inflated generalized Poisson regression model. <i>Biometrical Journal</i> , 2020, 62, 1428-1442.	1.0	0
5	A modified association test for rare and common variants based on affected sib-pair design. <i>Journal of Theoretical Biology</i> , 2019, 467, 1-6.	1.7	3
6	Association detection between ordinal trait and rare variants based on adaptive combination of P values. <i>Journal of Human Genetics</i> , 2018, 63, 37-45.	2.3	10
7	Simultaneous estimation of QTL parameters for mapping multiple traits. <i>Journal of Genetics</i> , 2018, 97, 267-274.	0.7	2
8	Simultaneous estimation of QTL parameters for mapping multiple traits. <i>Journal of Genetics</i> , 2018, 97, 267-274.	0.7	1
9	Joint parameter estimation in the QTL mapping of ordinal traits. <i>Journal of Theoretical Biology</i> , 2017, 432, 100-108.	1.7	1
10	A nonparametric method to test for associations between rare variants and multiple traits. <i>Genetical Research</i> , 2016, 98, e1.	0.9	5
11	Simultaneous estimation of QTL effects and positions when using genotype data with errors. <i>Journal of Genetics</i> , 2015, 94, 27-34.	0.7	5
12	A modified two-stage approach for family-based genome-wide association studies. <i>European Journal of Human Genetics</i> , 2014, 22, 148-151.	2.8	2
13	An estimating function approach to linkage heterogeneity. <i>Journal of Genetics</i> , 2013, 92, 413-421.	0.7	1
14	A two-step method for estimating QTL effects and positions in multi-marker analysis. <i>Genetical Research</i> , 2011, 93, 115-124.	0.9	4
15	Multiple Interval Mapping for Quantitative Trait Loci via EM Algorithm in the Presence of Crossover Interference. <i>Communications in Statistics - Theory and Methods</i> , 2010, 39, 3041-3057.	1.0	5