

Qing Lu

List of Publications by Year in descending order

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56
papers

660
citations

759233

12
h-index

642732

23
g-index

57
all docs

57
docs citations

57
times ranked

1490
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-Wide Association Studies of a Broad Spectrum of Antisocial Behavior. <i>JAMA Psychiatry</i> , 2017, 74, 1242.	11.0	174
2	Analysis pipeline for the epistasis search – statistical versus biological filtering. <i>Frontiers in Genetics</i> , 2014, 5, 106.	2.3	57
3	Using the Optimal Receiver Operating Characteristic Curve to Design a Predictive Genetic Test, Exemplified with Type 2 Diabetes. <i>American Journal of Human Genetics</i> , 2008, 82, 641-651.	6.2	52
4	Genetic association study of childhood aggression across raters, instruments, and age. <i>Translational Psychiatry</i> , 2021, 11, 413.	4.8	31
5	Genome-wide Association Meta-analysis of Childhood and Adolescent Internalizing Symptoms. <i>Journal of the American Academy of Child and Adolescent Psychiatry</i> , 2022, 61, 934-945.	0.5	26
6	Multi-kernel linear mixed model with adaptive lasso for prediction analysis on high-dimensional multi-omics data. <i>Bioinformatics</i> , 2020, 36, 1785-1794.	4.1	25
7	Functional Analysis of Variance for Association Studies. <i>PLoS ONE</i> , 2014, 9, e105074.	2.5	24
8	Detecting genetic interactions for quantitative traits with U-statistics. <i>Genetic Epidemiology</i> , 2011, 35, n/a-n/a.	1.3	22
9	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
10	The effect of multiple genetic variants in predicting the risk of type 2 diabetes. <i>BMC Proceedings</i> , 2009, 3, S49.	1.6	13
11	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
12	Modeling and testing for joint association using a genetic random field model. <i>Biometrics</i> , 2014, 70, 471-479.	1.4	13
13	Using the Optimal Robust Receiver Operating Characteristic (ROC) Curve for Predictive Genetic Tests. <i>Biometrics</i> , 2010, 66, 586-593.	1.4	12
14	A generalized association test based on U statistics. <i>Bioinformatics</i> , 2017, 33, 1963-1971.	4.1	11
15	Comparison of Frozen and Unfrozen Blood Spots for Gene Expression Studies. <i>Journal of Pediatrics</i> , 2014, 164, 189-191.e1.	1.8	10
16	A Weighted U -Statistic for Genetic Association Analyses of Sequencing Data. <i>Genetic Epidemiology</i> , 2014, 38, 699-708.	1.3	10
17	Uncovering Local Trends in Genetic Effects of Multiple Phenotypes via Functional Linear Models. <i>Genetic Epidemiology</i> , 2016, 40, 210-221.	1.3	10
18	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

#	ARTICLE	IF	CITATIONS
19	Multikernel linear mixed model with adaptive lasso for complex phenotype prediction. <i>Statistics in Medicine</i> , 2020, 39, 1311-1327.	1.6	9
20	Risk Prediction Modeling on Family-Based Sequencing Data Using a Random Field Method. <i>Genetics</i> , 2017, 207, 63-73.	2.9	8
21	GWGGI: software for genome-wide gene-gene interaction analysis. <i>BMC Genetics</i> , 2014, 15, 101.	2.7	7
22	Risk prediction models for oral clefts allowing for phenotypic heterogeneity. <i>Frontiers in Genetics</i> , 2015, 6, 264.	2.3	7
23	A weighted U statistic for association analyses considering genetic heterogeneity. <i>Statistics in Medicine</i> , 2016, 35, 2802-2814.	1.6	7
24	Risk Prediction Modeling of Sequencing Data Using a Forward Random Field Method. <i>Scientific Reports</i> , 2016, 6, 21120.	3.3	7
25	Sleep quality mediating the association of personality traits and quality of life among underground workers and surface workers of Chinese coal mine: A multi-group SEM with latent response variable mediation analysis. <i>Psychiatry Research</i> , 2019, 272, 196-205.	3.3	7
26	Explainable deep transfer learning model for disease risk prediction using high-dimensional genomic data. <i>PLoS Computational Biology</i> , 2022, 18, e1010328.	3.2	7
27	The postnatal presence of human chorionic gonadotropin in preterm infants and its potential inverse association with retinopathy of prematurity. <i>Pediatric Research</i> , 2020, 87, 558-563.	2.3	6
28	Bagging Optimal ROC Curve Method for Predictive Genetic Tests, with an Application for Rheumatoid Arthritis. <i>Journal of Biopharmaceutical Statistics</i> , 2010, 20, 401-414.	0.8	5
29	A functional U-statistic method for association analysis of sequencing data. <i>Genetic Epidemiology</i> , 2017, 41, 636-643.	1.3	5
30	Applying probability calibration to ensemble methods to predict 2-year mortality in patients with DLBCL. <i>BMC Medical Informatics and Decision Making</i> , 2021, 21, 14.	3.0	5
31	A goodness-of-fit test based on neural network sieve estimators. <i>Statistics and Probability Letters</i> , 2021, 174, 109100.	0.7	5
32	Testing Allele Transmission of an SNP Set Using a Family-Based Generalized Genetic Random Field Method. <i>Genetic Epidemiology</i> , 2016, 40, 341-351.	1.3	4
33	Detecting Rare Mutations with Heterogeneous Effects Using a Family-Based Genetic Random Field Method. <i>Genetics</i> , 2018, 210, 463-476.	2.9	4
34	Genetic risk prediction using a spatial autoregressive model with adaptive lasso. <i>Statistics in Medicine</i> , 2018, 37, 3764-3775.	1.6	4
35	Considering Genetic Heterogeneity in the Association Analysis Finds Genes Associated With Nicotine Dependence. <i>Frontiers in Genetics</i> , 2019, 10, 448.	2.3	4
36	Polygenic Risk for Insomnia in Adolescents of Diverse Ancestry. <i>Frontiers in Genetics</i> , 2021, 12, 654717.	2.3	4

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37	A non-parametric approach for detecting gene-gene interactions associated with age-at-onset outcomes. BMC Genetics, 2014, 15, 79.	2.7	3
38	A Clustered Multiclass Likelihood Ratio Ensemble Method for Family-Based Association Analysis Accounting for Phenotypic Heterogeneity. Genetic Epidemiology, 2016, 40, 512-519.	1.3	3
39	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
40	Probability calibration-based prediction of recurrence rate in patients with diffuse large B-cell lymphoma. BioData Mining, 2021, 14, 38.	4.0	3
41	A Powerful Nonparametric Statistical Framework for Family-Based Association Analyses. Genetics, 2015, 200, 69-78.	2.9	2
42	Detecting Gene-Gene Interactions Associated with Multiple Complex Traits with U-Statistics. Current Genomics, 2016, 17, 403-415.	1.6	2
43	An integrative U method for joint analysis of multi-level omic data. BMC Genetics, 2019, 20, 40.	2.7	2
44	Multiplier method estimates of the population of men who have sex with men: the effect of privacy protection. Journal of Public Health, 2020, 42, 429-434.	1.8	2
45	Set-based genetic association and interaction tests for survival outcomes based on weighted V statistics. Genetic Epidemiology, 2021, 45, 46-63.	1.3	2
46	Expectile Neural Networks for Genetic Data Analysis of Complex Diseases. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2023, 20, 352-359.	3.0	2
47	The impact of genetic structure on sequencing analysis. BMC Proceedings, 2016, 10, 171-174.	1.6	1
48	Joint analysis of genetic and epigenetic data using a conditional autoregressive model. BMC Genetics, 2018, 19, 71.	2.7	1
49	A clustered optimal ROC curve method for family-based genetic risk prediction. Statistics and Its Interface, 2011, 4, 373-380.	0.3	1
50	A conditional autoregressive model for genetic association analysis accounting for genetic heterogeneity. Statistics in Medicine, 2021, 41, 517.	1.6	1
51	Bridge: a GUI package for genetic risk prediction. BMC Genetics, 2013, 14, 122.	2.7	0
52	An ensemble-based likelihood ratio approach for family-based genomic risk prediction. Journal of Zhejiang University: Science B, 2018, 19, 935-947.	2.8	0
53	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
54	Multi-marker genetic association and interaction tests with interval-censored survival outcomes. Genetic Epidemiology, 2021, 45, 860-873.	1.3	0

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55	Statistical Methods and Software for Substance Use and Dependence Genetic Research. Current Genomics, 2019, 20, 172-183.	1.6	0
56	Neural network transformation models for counting processes. Statistical Analysis and Data Mining, 0, , .	2.8	0