

Lue Ping Zhao

List of Publications by Year in descending order

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49
papers

4,305
citations

516710

16
h-index

223800

46
g-index

52
all docs

52
docs citations

52
times ranked

3778
citing authors

#	ARTICLE	IF	CITATIONS
1	Estimation of Regression Coefficients When Some Regressors are not Always Observed. Journal of the American Statistical Association, 1994, 89, 846-866.	3.1	1,811
2	Analysis of Semiparametric Regression Models for Repeated Outcomes in the Presence of Missing Data. Journal of the American Statistical Association, 1995, 90, 106-121.	3.1	1,183
3	Estimation of Regression Coefficients When Some Regressors Are Not Always Observed. Journal of the American Statistical Association, 1994, 89, 846.	3.1	229
4	Analysis of Semiparametric Regression Models for Repeated Outcomes in the Presence of Missing Data. Journal of the American Statistical Association, 1995, 90, 106.	3.1	175
5	A Method for the Assessment of Disease Associations with Single-Nucleotide Polymorphism Haplotypes and Environmental Variables in Case-Control Studies. American Journal of Human Genetics, 2003, 72, 1231-1250.	6.2	158
6	A Weighted Estimating Equation for Missing Covariate Data with Properties Similar to Maximum Likelihood. Journal of the American Statistical Association, 1999, 94, 1147-1160.	3.1	88
7	Tumor Evolution and Intratumor Heterogeneity of an Oropharyngeal Squamous Cell Carcinoma Revealed by Whole-Genome Sequencing. Neoplasia, 2013, 15, 1371-IN7.	5.3	78
8	Mapping of Complex Traits by Single-Nucleotide Polymorphisms. American Journal of Human Genetics, 1998, 63, 225-240.	6.2	67
9	Next-Generation Sequencing Reveals That <i>HLA-DRB3</i> , <i>DRB4</i> , and <i>DRB5</i> May Be Associated With Islet Autoantibodies and Risk for Childhood Type 1 Diabetes. Diabetes, 2016, 65, 710-718.	0.6	58
10	Big data visualization identifies the multidimensional molecular landscape of human gliomas. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 5394-5399.	7.1	45
11	Clinical and Genetic Determinants of Cardiomyopathy Risk among Hematopoietic Cell Transplantation Survivors. Biology of Blood and Marrow Transplantation, 2016, 22, 1094-1101.	2.0	33
12	Replication of associations between genetic polymorphisms and chronic graft-versus-host disease. Blood, 2016, 128, 2450-2456.	1.4	32
13	A hybrid solution for extracting structured medical information from unstructured data in medical records via a double-reading/entry system. BMC Medical Informatics and Decision Making, 2016, 16, 114.	3.0	30
14	Predicting multiallelic genes using unphased and flanking single nucleotide polymorphisms. Genetic Epidemiology, 2011, 35, 85-92.	1.3	24
15	Array rank order regression analysis for the detection of gene copy-number changes in human cancer. Genomics, 2003, 82, 122-129.	2.9	23
16	A Weighted Estimating Equation for Missing Covariate Data with Properties Similar to Maximum Likelihood. Journal of the American Statistical Association, 1999, 94, 1147.	3.1	23
17	Motifs of Three HLA-DQ Amino Acid Residues ($\hat{I}^{\pm 44}$, $\hat{I}^{\pm 57}$, $\hat{I}^{\pm 135}$) Capture Full Association With the Risk of Type 1 Diabetes in DQ2 and DQ8 Children. Diabetes, 2020, 69, 1573-1587.	0.6	17
18	A Degrees-Of-Freedom approximation in Multiple imputation. Journal of Statistical Computation and Simulation, 2002, 72, 309-318.	1.2	16

#	ARTICLE	IF	CITATIONS
19	Landscapes of binding antibody and T-cell responses to pox-protein HIV vaccines in Thais and South Africans. <i>PLoS ONE</i> , 2020, 15, e0226803.	2.5	16
20	Assessing changes in ages at onset over successive generation: An application to breast cancer. , 2000, 18, 17-32.		15
21	Object-oriented regression for building predictive models with high dimensional omics data from translational studies. <i>Journal of Biomedical Informatics</i> , 2016, 60, 431-445.	4.3	15
22	Evolving Healthcare Quality in Top Tertiary General Hospitals in China during the China Healthcare Reform (2010â€“2012) from the Perspective of Inpatient Mortality. <i>PLoS ONE</i> , 2015, 10, e0140568.	2.5	14
23	Empirical evaluations of analytical issues arising from predicting HLA alleles using multiple SNPs. <i>BMC Genetics</i> , 2011, 12, 39.	2.7	13
24	Eleven Amino Acids of HLA-DRB1 and Fifteen Amino Acids of HLA-DRB3, 4, and 5 Include Potentially Causal Residues Responsible for the Risk of Childhood Type 1 Diabetes. <i>Diabetes</i> , 2019, 68, 1692-1704.	0.6	11
25	On the Assessment of Statistical Significance in Disease-Gene Discovery. <i>American Journal of Human Genetics</i> , 1999, 64, 1739-1753.	6.2	10
26	An Objectâ€“Oriented Regression for Building Disease Predictive Models with Multiallelic HLA Genes. <i>Genetic Epidemiology</i> , 2016, 40, 315-332.	1.3	10
27	Tracking SARS-CoV-2 Spike Protein Mutations in the United States (January 2020â€“March 2021) Using a Statistical Learning Strategy. <i>Viruses</i> , 2022, 14, 9.	3.3	10
28	Efficient, robust, and unified method for mapping complex traits (I): Two-point linkage analysis. <i>American Journal of Medical Genetics Part A</i> , 1998, 77, 366-383.	2.4	9
29	Mapping alcoholism genes using linkage/linkage disequilibrium analysis. <i>Genetic Epidemiology</i> , 1999, 17, S43-8.	1.3	9
30	Allelic Heterogeneity at the CRP Locus Identified by Whole-Genome Sequencing in Multi-ancestry Cohorts. <i>American Journal of Human Genetics</i> , 2020, 106, 112-120.	6.2	9
31	Empirical vs Bayesian approach for estimating haplotypes from genotypes of unrelated individuals. <i>BMC Genetics</i> , 2007, 8, 2.	2.7	8
32	An efficient, robust and unified method for mapping complex traits (III): Combined linkage/linkage-disequilibrium analysis. <i>American Journal of Medical Genetics Part A</i> , 1999, 84, 433-453.	2.4	7
33	Next-Generation HLA Sequence Analysis Uncovers Seven HLA-DQ Amino Acid Residues and Six Motifs Resistant to Childhood Type 1 Diabetes. <i>Diabetes</i> , 2020, 69, 2523-2535.	0.6	7
34	Nine residues in HLA-DQ molecules determine with susceptibility and resistance to type 1 diabetes among young children in Sweden. <i>Scientific Reports</i> , 2021, 11, 8821.	3.3	6
35	The KAG motif of HLA-DRB1 (\hat{I}^271 , \hat{I}^274 , \hat{I}^286) predicts seroconversion and development of type 1 diabetes. <i>EBioMedicine</i> , 2021, 69, 103431.	6.1	6
36	An efficient, robust, and unified method for mapping complex traits (II): Multipoint linkage analysis. , 1998, 79, 48-61.		5

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37	A haplotype-linkage analysis method for estimating recombination rates using dense SNP trio data. <i>Genetic Epidemiology</i> , 2007, 31, 154-172.	1.3	5
38	Costs, Trends, and Related Factors in Treating Lung Cancer Patients in 67 Hospitals in Guangxi, China. <i>Cancer Investigation</i> , 2017, 35, 345-357.	1.3	5
39	Identifying Biomarkers for Acute GVHD.. <i>Blood</i> , 2006, 108, 38-38.	1.4	5
40	A steroid metabolizing gene variant in a polyfactorial model improves risk prediction in a high incidence breast cancer population. <i>BBA Clinical</i> , 2014, 2, 94-102.	4.1	4
41	Recursive organizer (ROR): an analytic framework for sequence-based association analysis. <i>Human Genetics</i> , 2013, 132, 745-759.	3.8	2
42	Deciphering Genome Environment Wide Interactions Using Exposed Subjects Only. <i>Genetic Epidemiology</i> , 2015, 39, 334-346.	1.3	2
43	Building and validating a prediction model for paediatric type 1 diabetes risk using next generation targeted sequencing of class II HLA genes. <i>Diabetes/Metabolism Research and Reviews</i> , 2017, 33, e2921.	4.0	2
44	Combined association, segregation and aggregation analysis on case-control family data. <i>Biostatistics</i> , 2002, 3, 315-329.	1.5	1
45	Building a Patient-Specific Risk Score with a Large Database of Discharge Summary Reports. <i>Medical Science Monitor</i> , 2016, 22, 2097-2104.	1.1	1
46	Prognostic Implications of the IDH1 synonymous SNP rs11554137 In Pediatric and Adult AML: a Children's Oncology Group and Southwest Oncology Group Study. <i>Blood</i> , 2010, 116, 2737-2737.	1.4	1
47	Association of HLA-DQ Heterodimer Residues $\hat{1}8\hat{1}^2$ and $\hat{1}^257$ With Progression From Islet Autoimmunity to Diabetes in the Diabetes Prevention Trialâ€™Type 1. <i>Diabetes Care</i> , 2022, 45, 1610-1620.	8.6	1
48	A genome-wide scan for a simulated data set using two newly developed methods. <i>Genetic Epidemiology</i> , 1999, 17, S621-S626.	1.3	0
49	Evaluation of Nine Strategies for Analyzing a cDNA Toxicology Microarray Data Set. <i>Journal of Biopharmaceutical Statistics</i> , 2005, 15, 403-418.	0.8	0