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	Tracking SARS-CoV-2 Spike Protein Mutations in the United States (January 2020â€"March 2021) Using a Statistical Learning Strategy. Viruses, 2022, 14, 9.	3.3	10
2	Association of HLA-DQ Heterodimer Residues â^'18Î² and Î²57 With Progression From Islet Autoimmunity to Diabetes in the Diabetes Prevention Trialâ€"Type 1. Diabetes Care, 2022, 45, 1610-1620.	8.6	1
3	Nine residues in HLA-DQ molecules determine with susceptibility and resistance to type 1 diabetes among young children in Sweden. Scientific Reports, 2021, 11, 8821.	3.3	6
4	The KAG motif of HLA-DRB1 (Î²71, Î²74, Î²86) predicts seroconversion and development of type 1 diabetes. EBioMedicine, 2021, 69, 103431.	6.1	6
5	Next-Generation HLA Sequence Analysis Uncovers Seven HLA-DQ Amino Acid Residues and Six Motifs Resistant to Childhood Type 1 Diabetes. Diabetes, 2020, 69, 2523-2535.	0.6	7
6	Allelic Heterogeneity at the CRP Locus Identified by Whole-Genome Sequencing in Multi-ancestry Cohorts. American Journal of Human Genetics, 2020, 106, 112-120.	6.2	9
7	Motifs of Three HLA-DQ Amino Acid Residues (Î±44, Î²57, Î²135) Capture Full Association With the Risk of Type 1 Diabetes in DQ2 and DQ8 Children. Diabetes, 2020, 69, 1573-1587.	0.6	17
8	Landscapes of binding antibody and T-cell responses to pox-protein HIV vaccines in Thais and South Africans. PLoS ONE, 2020, 15, e0226803.	2.5	16
9	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. Diabetes, 2019, 68, 1692-1704.	0.6	11
10	Costs, Trends, and Related Factors in Treating Lung Cancer Patients in 67 Hospitals in Guangxi, China. Cancer Investigation, 2017, 35, 345-357.	1.3	5
11	Building and validating a prediction model for paediatric type 1 diabetes risk using next generation targeted sequencing of class II HLA genes. Diabetes/Metabolism Research and Reviews, 2017, 33, e2921.	4.0	2
12	Replication of associations between genetic polymorphisms and chronic graft-versus-host disease. Blood, 2016, 128, 2450-2456.	1.4	32
13	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
14	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
15	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
16	An Objectâ€Oriented Regression for Building Disease Predictive Models with Multiallelic HLA Genes. Genetic Epidemiology, 2016, 40, 315-332.	1.3	10
17	Object-oriented regression for building predictive models with high dimensional omics data from translational studies. Journal of Biomedical Informatics, 2016, 60, 431-445.	4.3	15
18	Next-Generation Sequencing Reveals That HLA-DRB3, -DRB4, and -DRB5 May Be Associated With Islet Autoantibodies and Risk for Childhood Type 1 Diabetes. Diabetes, 2016, 65, 710-718.	0.6	58

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19	Building a Patient-Specific Risk Score with a Large Database of Discharge Summary Reports. Medical Science Monitor, 2016, 22, 2097-2104.	1.1	1
20	Deciphering Genome Environment Wide Interactions Using Exposed Subjects Only. Genetic Epidemiology, 2015, 39, 334-346.	1.3	2
21	Evolving Healthcare Quality in Top Tertiary General Hospitals in China during the China Healthcare Reform (2010â€“2012) from the Perspective of Inpatient Mortality. PLoS ONE, 2015, 10, e0140568.	2.5	14
22	A steroid metabolizing gene variant in a polyfactorial model improves risk prediction in a high incidence breast cancer population. BBA Clinical, 2014, 2, 94-102.	4.1	4
23	Recursive organizer (ROR): an analytic framework for sequence-based association analysis. Human Genetics, 2013, 132, 745-759.	3.8	2
24	Tumor Evolution and Intratumor Heterogeneity of an Oropharyngeal Squamous Cell Carcinoma Revealed by Whole-Genome Sequencing. Neoplasia, 2013, 15, 1371-IN7.	5.3	78
25	Empirical evaluations of analytical issues arising from predicting HLA alleles using multiple SNPs. BMC Genetics, 2011, 12, 39.	2.7	13
26	Predicting multiallelic genes using unphased and flanking single nucleotide polymorphisms. Genetic Epidemiology, 2011, 35, 85-92.	1.3	24
27	Prognostic Implications of the IDH1 synonymous SNP rs11554137 In Pediatric and Adult AML: a Children's Oncology Group and Southwest Oncology Group Study. Blood, 2010, 116, 2737-2737.	1.4	1
28	A haplotype-linkage analysis method for estimating recombination rates using dense SNP trio data. Genetic Epidemiology, 2007, 31, 154-172.	1.3	5
29	Empirical vs Bayesian approach for estimating haplotypes from genotypes of unrelated individuals. BMC Genetics, 2007, 8, 2.	2.7	8
30	Identifying Biomarkers for Acute GVHD.. Blood, 2006, 108, 38-38.	1.4	5
31	Evaluation of Nine Strategies for Analyzing a cDNA Toxicology Microarray Data Set. Journal of Biopharmaceutical Statistics, 2005, 15, 403-418.	0.8	0
32	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
33	Array rank order regression analysis for the detection of gene copy-number changes in human cancer. Genomics, 2003, 82, 122-129.	2.9	23
34	Combined association, segregation and aggregation analysis on case-control family data. Biostatistics, 2002, 3, 315-329.	1.5	1
35	A Degrees-Of-Freedom approximation in Multiple imputation. Journal of Statistical Computation and Simulation, 2002, 72, 309-318.	1.2	16
36	Assessing changes in ages at onset over successive generation: An application to breast cancer. , 2000, 18, 17-32.		15

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37	A genome-wide scan for a simulated data set using two newly developed methods. Genetic Epidemiology, 1999, 17, S621-S626.	1.3	0
38	Mapping alcoholism genes using linkage/linkage disequilibrium analysis. Genetic Epidemiology, 1999, 17, S43-8.	1.3	9
39	An efficient, robust and unified method for mapping complex traits (III): Combined linkage/linkage-disequilibrium analysis. American Journal of Medical Genetics Part A, 1999, 84, 433-453.	2.4	7
40	On the Assessment of Statistical Significance in Disease-Gene Discovery. American Journal of Human Genetics, 1999, 64, 1739-1753.	6.2	10
41	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
42	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
43	Efficient, robust, and unified method for mapping complex traits (I): Two-point linkage analysis. American Journal of Medical Genetics Part A, 1998, 77, 366-383.	2.4	9
44	An efficient, robust, and unified method for mapping complex traits (II): Multipoint linkage analysis. , 1998, 79, 48-61.		5
45	Mapping of Complex Traits by Single-Nucleotide Polymorphisms. American Journal of Human Genetics, 1998, 63, 225-240.	6.2	67
46	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
47	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
48	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
49	Estimation of Regression Coefficients When Some Regressors Are Not Always Observed. Journal of the American Statistical Association, 1994, 89, 846.	3.1	229