

Baolin Wu

List of Publications by Year in descending order

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82
papers

3,259
citations

186265

28
h-index

155660

55
g-index

86
all docs

86
docs citations

86
times ranked

5380
citing authors

#	ARTICLE	IF	CITATIONS
1	T1 and T2 mapping detect acute ischemic injury in a piglet model of Legg-Calvé-Perthes disease. <i>Journal of Orthopaedic Research</i> , 2022, 40, 484-494.	2.3	4
2	Impact of polygenic risk for coronary artery disease and cardiovascular medication burden on cognitive impairment in psychotic disorders. <i>Progress in Neuro-Psychopharmacology and Biological Psychiatry</i> , 2022, 113, 110464.	4.8	3
3	Inflammation subtypes in psychosis and their relationships with genetic risk for psychiatric and cardiometabolic disorders. <i>Brain, Behavior, & Immunity - Health</i> , 2022, 22, 100459.	2.5	8
4	Multivariate relationships between peripheral inflammatory marker subtypes and cognitive and brain structural measures in psychosis. <i>Molecular Psychiatry</i> , 2021, 26, 3430-3443.	7.9	75
5	Penalized Fieller's confidence interval for the ratio of bivariate normal means. <i>Biometrics</i> , 2021, 77, 1355-1368.	1.4	5
6	Precision Dosing for Tacrolimus Using Genotypes and Clinical Factors in Kidney Transplant Recipients of European Ancestry. <i>Journal of Clinical Pharmacology</i> , 2021, 61, 1035-1044.	2.0	3
7	Pharmacogenomics in kidney transplant recipients and potential for integration into practice. <i>Journal of Clinical Pharmacy and Therapeutics</i> , 2020, 45, 1457-1465.	1.5	3
8	Powerful statistical method to detect disease-associated genes using publicly available genome-wide association studies summary data. <i>Genetic Epidemiology</i> , 2019, 43, 941-951.	1.3	9
9	A general statistic to test an optimally weighted combination of common and/or rare variants. <i>Genetic Epidemiology</i> , 2019, 43, 966-979.	1.3	3
10	Pleiotropy Informed Adaptive Association Test of Multiple Traits Using Genome-Wide Association Study Summary Data. <i>Biometrics</i> , 2019, 75, 1076-1085.	1.4	13
11	Tacrolimus troughs and genetic determinants of metabolism in kidney transplant recipients: A comparison of four ancestry groups. <i>American Journal of Transplantation</i> , 2019, 19, 2795-2804.	4.7	35
12	Genetic Variants Associated With Immunosuppressant Pharmacokinetics and Adverse Effects in the DeKAF Genomics Genome-wide Association Studies. <i>Transplantation</i> , 2019, 103, 1131-1139.	1.0	17
13	Analysis of 75 Candidate SNPs Associated With Acute Rejection in Kidney Transplant Recipients: Validation of rs2910164 in MicroRNA MIR146A. <i>Transplantation</i> , 2019, 103, 1591-1602.	1.0	16
14	Powerful and efficient SNP-set association tests across multiple phenotypes using GWAS summary data. <i>Bioinformatics</i> , 2019, 35, 1366-1372.	4.1	13
15	Integrate multiple traits to detect novel trait gene association using GWAS summary data with an adaptive test approach. <i>Bioinformatics</i> , 2019, 35, 2251-2257.	4.1	24
16	Identification of genetic variants associated with tacrolimus metabolism in kidney transplant recipients by extreme phenotype sampling and next generation sequencing. <i>Pharmacogenomics Journal</i> , 2019, 19, 375-389.	2.0	11
17	Reader Reaction on the Fast Small-Sample Kernel Independence Test for Microbiome Community-Level Association Analysis. <i>Biometrics</i> , 2018, 74, 1120-1124.	1.4	1
18	Attempted validation of 44 reported SNPs associated with tacrolimus troughs in a cohort of kidney allograft recipients. <i>Pharmacogenomics</i> , 2018, 19, 175-184.	1.3	23

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19	Statistical methods to detect novel genetic variants using publicly available GWAS summary data. <i>Computational Biology and Chemistry</i> , 2018, 74, 76-79.	2.3	15
20	Genome-wide association study identifies the common variants in CYP3A4 and CYP3A5 responsible for variation in tacrolimus trough concentration in Caucasian kidney transplant recipients. <i>Pharmacogenomics Journal</i> , 2018, 18, 501-505.	2.0	39
21	Tacrolimus trough and dose intra-patient variability and CYP3A5 genotype: Effects on acute rejection and graft failure in European American and African American kidney transplant recipients. <i>Clinical Transplantation</i> , 2018, 32, e13424.	1.6	30
22	Urinary microbiome associated with chronic allograft dysfunction in kidney transplant recipients. <i>Clinical Transplantation</i> , 2018, 32, e13436.	1.6	24
23	Tacrolimus Elimination in Four Patients With a CYP3A5*3/*3 CYP3A4*22/*22 Genotype Combination. <i>Pharmacotherapy</i> , 2018, 38, e46-e52.	2.6	17
24	Fast and Accurate Genome-Wide Association Test of Multiple Quantitative Traits. <i>Computational and Mathematical Methods in Medicine</i> , 2018, 2018, 1-9.	1.3	5
25	CRISPR/Cas9 Genetic Modification of CYP3A5*3 in HuH-7 Human Hepatocyte Cell Line Leads to Cell Lines with Increased Midazolam and Tacrolimus Metabolism. <i>Drug Metabolism and Disposition</i> , 2017, 45, 957-965.	3.3	18
26	Genome-wide association test of multiple continuous traits using imputed SNPs. <i>Statistics and Its Interface</i> , 2017, 10, 379-386.	0.3	5
27	Sequence Kernel Association Test of Multiple Continuous Phenotypes. <i>Genetic Epidemiology</i> , 2016, 40, 91-100.	1.3	43
28	Proteome Profiling in Lung Injury after Hematopoietic Stem Cell Transplantation. <i>Biology of Blood and Marrow Transplantation</i> , 2016, 22, 1383-1390.	2.0	18
29	On Efficient and Accurate Calculation of Significance P-Values for Sequence Kernel Association Testing of Variant Set. <i>Annals of Human Genetics</i> , 2016, 80, 123-135.	0.8	22
30	On Sample Size and Power Calculation for Variant Set-Based Association Tests. <i>Annals of Human Genetics</i> , 2016, 80, 136-143.	0.8	10
31	Sequence Kernel Association Analysis of Rare Variant Set Based on the Marginal Regression Model for Binary Traits. <i>Genetic Epidemiology</i> , 2015, 39, 399-405.	1.3	15
32	Concept and design of a genome-wide association genotyping array tailored for transplantation-specific studies. <i>Genome Medicine</i> , 2015, 7, 90.	8.2	49
33	Design and Implementation of the International Genetics and Translational Research in Transplantation Network. <i>Transplantation</i> , 2015, 99, 2401-2412.	1.0	60
34	Differentially Expressed Gene Transcripts Using RNA Sequencing from the Blood of Immunosuppressed Kidney Allograft Recipients. <i>PLoS ONE</i> , 2015, 10, e0125045.	2.5	20
35	Network-Based Isoform Quantification with RNA-Seq Data for Cancer Transcriptome Analysis. <i>PLoS Computational Biology</i> , 2015, 11, e1004465.	3.2	17
36	Statistical Methods for Association Tests of Multiple Continuous Traits in Genome-Wide Association Studies. <i>Annals of Human Genetics</i> , 2015, 79, 282-293.	0.8	19

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37	Reader Reaction on the Generalized Kruskal-Wallis Test for Genetic Association Studies Incorporating Group Uncertainty. <i>Biometrics</i> , 2015, 71, 556-557.	1.4	4
38	Likelihood-Based Approach to Gene Set Enrichment Analysis with a Finite Mixture Model. <i>Statistics in Biosciences</i> , 2014, 6, 38-54.	1.2	1
39	Proteomic Profiles in Acute Respiratory Distress Syndrome Differentiates Survivors from Non-Survivors. <i>PLoS ONE</i> , 2014, 9, e109713.	2.5	40
40	On the geometric modeling approach to empirical null distribution estimation for empirical Bayes modeling of multiple hypothesis testing. <i>Computational Biology and Chemistry</i> , 2013, 43, 17-22.	2.3	2
41	Protein expression profile of rat type two alveolar epithelial cells during hyperoxic stress and recovery. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2013, 305, L604-L614.	2.9	17
42	Network-based Survival Analysis Reveals Subnetwork Signatures for Predicting Outcomes of Ovarian Cancer Treatment. <i>PLoS Computational Biology</i> , 2013, 9, e1002975.	3.2	151
43	Sparse cluster analysis of large-scale discrete variables with application to single nucleotide polymorphism data. <i>Journal of Applied Statistics</i> , 2013, 40, 358-367.	1.3	4
44	A note on statistical method for genotype calling of high-throughput single-nucleotide polymorphism arrays. <i>Journal of Applied Statistics</i> , 2013, 40, 1372-1381.	1.3	1
45	Empirical null distribution-based modeling of multi-class differential gene expression detection. <i>Journal of Applied Statistics</i> , 2013, 40, 347-357.	1.3	0
46	Signed network propagation for detecting differential gene expressions and DNA copy number variations. , 2012, , .		11
47	Sparse regularized discriminant analysis with application to microarrays. <i>Computational Biology and Chemistry</i> , 2012, 39, 14-19.	2.3	1
48	A permutation test approach to the choice of size k for the nearest neighbors classifier. <i>Journal of Applied Statistics</i> , 2011, 38, 2289-2302.	1.3	0
49	Meis1 maintains stemness signature in MLL-AF9 leukemia. <i>Blood</i> , 2010, 115, 3642-3643.	1.4	21
50	LTDQuant: A freely available software pipeline for automated and accurate protein quantification of isobaric tagged peptide data from LTQ instruments. <i>Proteomics</i> , 2010, 10, 3533-3538.	2.2	26
51	Quantitative Proteomics Reveals Myosin and Actin as Promising Saliva Biomarkers for Distinguishing Pre-Malignant and Malignant Oral Lesions. <i>PLoS ONE</i> , 2010, 5, e11148.	2.5	93
52	Proteome of Human Calcium Kidney Stones. <i>Urology</i> , 2010, 76, 1017.e13-1017.e20.	1.0	63
53	Network propagation models for gene selection. , 2010, , .		2
54	Minimally invasive versus open Roux-en-Y gastric bypass: effect on immune effector cells. <i>Surgery for Obesity and Related Diseases</i> , 2009, 5, 181-193.	1.2	12

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55	A role for MEIS1 in MLL-fusion gene leukemia. <i>Blood</i> , 2009, 113, 1756-1758.	1.4	85
56	Malignant Transformation Initiated by Mll-AF9: Gene Dosage and Critical Target Cells. <i>Cancer Cell</i> , 2008, 13, 432-440.	16.8	186
57	Thoracoscopic Versus Thoracotomy Approaches to Lobectomy: Differential Impairment of Cellular Immunity. <i>Annals of Thoracic Surgery</i> , 2008, 86, 1735-1744.	1.3	109
58	Cerebral Malaria in Children Is Associated With Long-term Cognitive Impairment. <i>Pediatrics</i> , 2008, 122, e92-e99.	2.1	259
59	Racial/Ethnic Disparities in the Use of Nicotine Replacement Therapy and Quit Ratios in Lifetime Smokers Ages 25 to 44 Years. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2008, 17, 1640-1647.	2.5	120
60	Robust and efficient identification of biomarkers by classifying features on graphs. <i>Bioinformatics</i> , 2008, 24, 2023-2029.	4.1	38
61	Bayesian Mass Spectra Peak Alignment from Mass Charge Ratios. <i>Cancer Informatics</i> , 2008, 6, 117693510800600.	1.9	0
62	A MEIS1 Dependent Genetic Program in Leukemia Associated with Cell Cycle Entry and "Stemness". <i>Blood</i> , 2008, 112, 746-746.	1.4	1
63	Bayesian mass spectra peak alignment from mass charge ratios. <i>Cancer Informatics</i> , 2008, 6, 217-41.	1.9	0
64	Cancer outlier differential gene expression detection. <i>Biostatistics</i> , 2007, 8, 566-575.	1.5	91
65	Multi-group cancer outlier differential gene expression detection. <i>Computational Biology and Chemistry</i> , 2007, 31, 65-71.	2.3	12
66	Ovarian cancer classification based on mass spectrometry analysis of sera. <i>Cancer Informatics</i> , 2007, 2, 123-32.	1.9	4
67	Multiple Peak Alignment in Sequential Data Analysis: A Scale-Space-Based Approach. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2006, 3, 208-219.	3.0	24
68	Ovarian Cancer Classification Based on Mass Spectrometry Analysis of Sera. <i>Cancer Informatics</i> , 2006, 2, 117693510600200.	1.9	5
69	Parametric and Nonparametric FDR Estimation Revisited. <i>Biometrics</i> , 2006, 62, 735-744.	1.4	20
70	Detecting and aligning peaks in mass spectrometry data with applications to MALDI. <i>Computational Biology and Chemistry</i> , 2006, 30, 27-38.	2.3	45
71	PSMIX: an R package for population structure inference via maximum likelihood method. <i>BMC Bioinformatics</i> , 2006, 7, 317.	2.6	42
72	MALDI-MS Data Analysis for Disease Biomarker Discovery. , 2006, 328, 199-216.		4

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73	Differential gene expression detection and sample classification using penalized linear regression models. <i>Bioinformatics</i> , 2006, 22, 472-476.	4.1	73
74	Statistical Methods in Proteomics. , 2006, , 623-638.		9
75	Detection of DNA copy number alterations using penalized least squares regression. <i>Bioinformatics</i> , 2005, 21, 3811-3817.	4.1	57
76	Differential gene expression detection using penalized linear regression models: the improved SAM statistics. <i>Bioinformatics</i> , 2005, 21, 1565-1571.	4.1	47
77	Proteomics and the Analysis of Proteomic Data: An Overview of Current Protein Profiling Technologies. <i>Current Protocols in Bioinformatics</i> , 2005, 10, Unit 13.1.	25.8	31
78	A statistical method for identifying differential gene-gene co-expression patterns. <i>Bioinformatics</i> , 2004, 20, 3146-3155.	4.1	155
79	Information assessment on predicting protein-protein interactions. <i>BMC Bioinformatics</i> , 2004, 5, 154.	2.6	136
80	A High Productivity/Low Maintenance Approach to High-performance Computation for Biomedicine: Four Case Studies. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2004, 12, 90-98.	4.4	3
81	Mining the Structural Genomics Pipeline: Identification of Protein Properties that Affect High-throughput Experimental Analysis. <i>Journal of Molecular Biology</i> , 2004, 336, 115-130.	4.2	138
82	Comparison of statistical methods for classification of ovarian cancer using mass spectrometry data. <i>Bioinformatics</i> , 2003, 19, 1636-1643.	4.1	421