Baolin Wu

List of Publications by Year
in descending order

82	3,259	186265	155660
papers	citations	28	55
		h-index	g-index

86	86	86	5380
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Comparison of statistical methods for classification of ovarian cancer using mass spectrometry data. Bioinformatics, 2003, 19, 1636-1643.	4.1	421
2	Cerebral Malaria in Children Is Associated With Long-term Cognitive Impairment. Pediatrics, 2008, 122, e92-e99.	2.1	259
3	Malignant Transformation Initiated by Mll-AF9: Gene Dosage and Critical Target Cells. Cancer Cell, 2008, 13, 432-440.	16.8	186
4	A statistical method for identifying differential gene-gene co-expression patterns. Bioinformatics, 2004, 20, 3146-3155.	4.1	155
5	Network-based Survival Analysis Reveals Subnetwork Signatures for Predicting Outcomes of Ovarian Cancer Treatment. PLoS Computational Biology, 2013, 9, e1002975.	3.2	151
6	Mining the Structural Genomics Pipeline: Identification of Protein Properties that Affect High-throughput Experimental Analysis. Journal of Molecular Biology, 2004, 336, 115-130.	4.2	138
7	Information assessment on predicting protein-protein interactions. BMC Bioinformatics, 2004, 5, 154.	2.6	136
8	Racial/Ethnic Disparities in the Use of Nicotine Replacement Therapy and Quit Ratios in Lifetime Smokers Ages 25 to 44 Years. Cancer Epidemiology Biomarkers and Prevention, 2008, 17, 1640-1647.	2.5	120
9	Thoracoscopic Versus Thoracotomy Approaches to Lobectomy: Differential Impairment of Cellular Immunity. Annals of Thoracic Surgery, 2008, 86, 1735-1744.	1.3	109
10	Quantitative Proteomics Reveals Myosin and Actin as Promising Saliva Biomarkers for Distinguishing Pre-Malignant and Malignant Oral Lesions. PLoS ONE, 2010, 5, e11148.	2.5	93
11	Cancer outlier differential gene expression detection. Biostatistics, 2007, 8, 566-575.	1.5	91
12	A role for MEIS1 in MLL-fusion gene leukemia. Blood, 2009, 113, 1756-1758.	1.4	85
13	Multivariate relationships between peripheral inflammatory marker subtypes and cognitive and brain structural measures in psychosis. Molecular Psychiatry, 2021, 26, 3430-3443.	7.9	75
14	Differential gene expression detection and sample classification using penalized linear regression models. Bioinformatics, 2006, 22, 472-476.	4.1	73
15	Proteome of Human Calcium Kidney Stones. Urology, 2010, 76, 1017.e13-1017.e20.	1.0	63
16	Design and Implementation of the International Genetics and Translational Research in Transplantation Network. Transplantation, 2015, 99, 2401-2412.	1.0	60
17	Detection of DNA copy number alterations using penalized least squares regression. Bioinformatics, 2005, 21, 3811-3817.	4.1	57
18	Concept and design of a genome-wide association genotyping array tailored for transplantation-specific studies. Genome Medicine, 2015, 7, 90.	8.2	49

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19	Differential gene expression detection using penalized linear regression models: the improved SAM statistics. Bioinformatics, 2005, 21, 1565-1571.	4.1	47
20	Detecting and aligning peaks in mass spectrometry data with applications to MALDI. Computational Biology and Chemistry, 2006, 30, 27-38.	2.3	45
21	Sequence Kernel Association Test of Multiple Continuous Phenotypes. Genetic Epidemiology, 2016, 40, 91-100.	1.3	43
22	PSMIX: an R package for population structure inference via maximum likelihood method. BMC Bioinformatics, 2006, 7, 317.	2.6	42
23	Proteomic Profiles in Acute Respiratory Distress Syndrome Differentiates Survivors from Non-Survivors. PLoS ONE, 2014, 9, e109713.	2.5	40
24	Genome-wide association study identifies the common variants in CYP3A4 and CYP3A5 responsible for variation in tacrolimus trough concentration in Caucasian kidney transplant recipients. Pharmacogenomics Journal, 2018, 18, 501-505.	2.0	39
25	Robust and efficient identification of biomarkers by classifying features on graphs. Bioinformatics, 2008, 24, 2023-2029.	4.1	38
26	Tacrolimus troughs and genetic determinants of metabolism in kidney transplant recipients: A comparison of four ancestry groups. American Journal of Transplantation, 2019, 19, 2795-2804.	4.7	35
27	Proteomics and the Analysis of Proteomic Data: An Overview of Current Protein‐Profiling Technologies. Current Protocols in Bioinformatics, 2005, 10, Unit 13.1.	25.8	31
28	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. Clinical Transplantation, 2018, 32, e13424.	1.6	30
29	LTQ‐Quant: A freely available software pipeline for automated and accurate protein quantification of isobaric tagged peptide data from LTQ instruments. Proteomics, 2010, 10, 3533-3538.	2.2	26
30	Multiple Peak Alignment in Sequential Data Analysis: A Scale-Space-Based Approach. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2006, 3, 208-219.	3.0	24
31	Urinary microbiome associated with chronic allograft dysfunction in kidney transplant recipients. Clinical Transplantation, 2018, 32, e13436.	1.6	24
32	Integrate multiple traits to detect novel trait‐gene association using GWAS summary data with an adaptive test approach. Bioinformatics, 2019, 35, 2251-2257.	4.1	24
33	Attempted validation of 44 reported SNPs associated with tacrolimus troughs in a cohort of kidney allograft recipients. Pharmacogenomics, 2018, 19, 175-184.	1.3	23
34	On Efficient and Accurate Calculation of Significance P‐Values for Sequence Kernel Association Testing of Variant Set. Annals of Human Genetics, 2016, 80, 123-135.	0.8	22
35	Meis1 maintains stemness signature in MLL-AF9 leukemia. Blood, 2010, 115, 3642-3643.	1.4	21
36	Parametric and Nonparametric FDR Estimation Revisited. Biometrics, 2006, 62, 735-744.	1.4	20

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37	Differentially Expressed Gene Transcripts Using RNA Sequencing from the Blood of Immunosuppressed Kidney Allograft Recipients. PLoS ONE, 2015, 10, e0125045.	2.5	20
38	Statistical Methods for Association Tests of Multiple Continuous Traits in Genome‐Wide Association Studies. Annals of Human Genetics, 2015, 79, 282-293.	0.8	19
39	Proteome Profiling in Lung Injury after Hematopoietic Stem Cell Transplantation. Biology of Blood and Marrow Transplantation, 2016, 22, 1383-1390.	2.0	18
40	CRISPR/Cas9 Genetic Modification of <i>CYP3A5 *3</i> in HuH-7 Human Hepatocyte Cell Line Leads to Cell Lines with Increased Midazolam and Tacrolimus Metabolism. Drug Metabolism and Disposition, 2017, 45, 957-965.	3.3	18
41	Protein expression profile of rat type two alveolar epithelial cells during hyperoxic stress and recovery. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2013, 305, L604-L614.	2.9	17
42	Network-Based Isoform Quantification with RNA-Seq Data for Cancer Transcriptome Analysis. PLoS Computational Biology, 2015, 11, e1004465.	3.2	17
43	Tacrolimus Elimination in Four Patients With a <i><scp>CYP</scp>3A5*3/*3 <scp>CYP</scp>3A4*22/*22</i> Genotype Combination. Pharmacotherapy, 2018, 38, e46-e52.	2.6	17
44	Genetic Variants Associated With Immunosuppressant Pharmacokinetics and Adverse Effects in the DeKAF Genomics Genome-wide Association Studies. Transplantation, 2019, 103, 1131-1139.	1.0	17
45	Analysis of 75 Candidate SNPs Associated With Acute Rejection in Kidney Transplant Recipients: Validation of rs2910164 in MicroRNA MIR146A. Transplantation, 2019, 103, 1591-1602.	1.0	16
46	Sequence Kernel Association Analysis of Rare Variant Set Based on the Marginal Regression Model for Binary Traits. Genetic Epidemiology, 2015, 39, 399-405.	1.3	15
47	Statistical methods to detect novel genetic variants using publicly available GWAS summary data. Computational Biology and Chemistry, 2018, 74, 76-79.	2.3	15
48	Pleiotropy Informed Adaptive Association Test of Multiple Traits Using Genome-Wide Association Study Summary Data. Biometrics, 2019, 75, 1076-1085.	1.4	13
49	Powerful and efficient SNP-set association tests across multiple phenotypes using GWAS summary data. Bioinformatics, 2019, 35, 1366-1372.	4.1	13
50	Multi-group cancer outlier differential gene expression detection. Computational Biology and Chemistry, 2007, 31, 65-71.	2.3	12
51	Minimally invasive versus open Roux-en-Y gastric bypass: effect on immune effector cells. Surgery for Obesity and Related Diseases, 2009, 5, 181-193.	1.2	12
52	Signed network propagation for detecting differential gene expressions and DNA copy number variations. , 2012, , .		11
53	Identification of genetic variants associated with tacrolimus metabolism in kidney transplant recipients by extreme phenotype sampling and next generation sequencing. Pharmacogenomics Journal, 2019, 19, 375-389.	2.0	11
54	On Sample Size and Power Calculation for Variant Set‐Based Association Tests. Annals of Human Genetics, 2016, 80, 136-143.	0.8	10

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55	Powerful statistical method to detect disease‑associated genes using publicly available genome‑wide association studies summary data. Genetic Epidemiology, 2019, 43, 941-951.	1.3	9
56	Statistical Methods in Proteomics. , 2006, , 623-638.		9
57	Inflammation subtypes in psychosis and their relationships with genetic risk for psychiatric and cardiometabolic disorders. Brain, Behavior, & Immunity - Health, 2022, 22, 100459.	2.5	8
58	Ovarian Cancer Classification Based on Mass Spectrometry Analysis of Sera. Cancer Informatics, 2006, 2, 117693510600200.	1.9	5
59	Fast and Accurate Genome-Wide Association Test of Multiple Quantitative Traits. Computational and Mathematical Methods in Medicine, 2018, 2018, 1-9.	1.3	5
60	Penalized Fieller's confidence interval for the ratio of bivariate normal means. Biometrics, 2021, 77, 1355-1368.	1.4	5
61	Genome-wide association test of multiple continuous traits using imputed SNPs. Statistics and Its Interface, 2017, 10, 379-386.	0.3	5
62	MALDI-MS Data Analysis for Disease Biomarker Discovery. , 2006, 328, 199-216.		4
63	Sparse cluster analysis of large-scale discrete variables with application to single nucleotide polymorphism data. Journal of Applied Statistics, 2013, 40, 358-367.	1.3	4
64	Reader Reaction on the Generalized Kruskal–Wallis Test for Genetic Association Studies Incorporating Group Uncertainty. Biometrics, 2015, 71, 556-557.	1.4	4
65	T1ï·and T2 mapping detect acute ischemic injury in a piglet model of Legg–Calvé–Perthes disease. Journal of Orthopaedic Research, 2022, 40, 484-494.	2.3	4
66	Ovarian cancer classification based on mass spectrometry analysis of sera. Cancer Informatics, 2007, 2, 123-32.	1.9	4
67	A High Productivity/Low Maintenance Approach to High-performance Computation for Biomedicine: Four Case Studies. Journal of the American Medical Informatics Association: JAMIA, 2004, 12, 90-98.	4.4	3
68	A general statistic to test an optimally weighted combination of common and/or rare variants. Genetic Epidemiology, 2019, 43, 966-979.	1.3	3
69	Pharmacogenomics in kidney transplant recipients and potential for integration into practice. Journal of Clinical Pharmacy and Therapeutics, 2020, 45, 1457-1465.	1.5	3
70	Precision Dosing for Tacrolimus Using Genotypes and Clinical Factors in Kidney Transplant Recipients of European Ancestry. Journal of Clinical Pharmacology, 2021, 61, 1035-1044.	2.0	3
71	Impact of polygenic risk for coronary artery disease and cardiovascular medication burden on cognitive impairment in psychotic disorders. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2022, 113, 110464.	4.8	3
72	Network propagation models for gene selection. , 2010, , .		2

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73	On the geometric modeling approach to empirical null distribution estimation for empirical Bayes modeling of multiple hypothesis testing. Computational Biology and Chemistry, 2013, 43, 17-22.	2.3	2
74	Sparse regularized discriminant analysis with application to microarrays. Computational Biology and Chemistry, 2012, 39, 14-19.	2.3	1
75	A note on statistical method for genotype calling of high-throughput single-nucleotide polymorphism arrays. Journal of Applied Statistics, 2013, 40, 1372-1381.	1.3	1
76	Likelihood-Based Approach to Gene Set Enrichment Analysis with a Finite Mixture Model. Statistics in Biosciences, 2014, 6, 38-54.	1.2	1
77	Reader Reaction on the Fast Small-Sample Kernel Independence Test for Microbiome Community-Level Association Analysis. Biometrics, 2018, 74, 1120-1124.	1.4	1
78	A MEIS1 Dependent Genetic Program in Leukemia Associated with Cell Cycle Entry and â€˜Stemnessâ€™. Blood, 2008, 112, 746-746.	1.4	1
79	Bayesian Mass Spectra Peak Alignment from Mass Charge Ratios. Cancer Informatics, 2008, 6, 117693510800600.	1.9	0
80	A permutation test approach to the choice of size k for the nearest neighbors classifier. Journal of Applied Statistics, 2011, 38, 2289-2302.	1.3	0
81	Empirical null distribution-based modeling of multi-class differential gene expression detection. Journal of Applied Statistics, 2013, 40, 347-357.	1.3	0
82	Bayesian mass spectra peak alignment from mass charge ratios. Cancer Informatics, 2008, 6, 217-41.	1.9	0