

Xiangqin Cui

List of Publications by Year in descending order

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Version: 2024-02-01

69
papers

5,595
citations

156536

32
h-index

116156

66
g-index

77
all docs

77
docs citations

77
times ranked

10374
citing authors

#	ARTICLE	IF	CITATIONS
1	Pulmonary Hypertension. <i>Chest</i> , 2022, 161, 803-806.	0.4	1
2	Rapid Antiretroviral Therapy Program: Development and Evaluation at a Veterans Affairs Medical Center in the Southern United States. <i>AIDS Patient Care and STDs</i> , 2022, 36, 219-225.	1.1	8
3	Personalized Visual Mapping Assistive Technology to Improve Functional Ability in Persons With Dementia: Feasibility Cohort Study. <i>JMIR Aging</i> , 2021, 4, e28165.	1.4	10
4	Autosomal Dominant Polycystic Kidney Disease Does Not Significantly Alter Major COVID-19 Outcomes among Veterans. <i>Kidney360</i> , 2021, 2, 983-988.	0.9	2
5	Adverse Outcomes Associated With Inpatient Administration of Beers List Medications Following Total Knee Replacement. <i>Clinical Therapeutics</i> , 2020, 42, 592-604.e1.	1.1	6
6	JQ1 Induces DNA Damage and Apoptosis, and Inhibits Tumor Growth in a Patient-Derived Xenograft Model of Cholangiocarcinoma. <i>Molecular Cancer Therapeutics</i> , 2018, 17, 107-118.	1.9	27
7	Absorbance summation: A novel approach for analyzing high-throughput ELISA data in the absence of a standard. <i>PLoS ONE</i> , 2018, 13, e0198528.	1.1	27
8	Analysis of the tonsillar microbiome in young adults with sore throat reveals a high relative abundance of <i>Fusobacterium necrophorum</i> with low diversity. <i>PLoS ONE</i> , 2018, 13, e0189423.	1.1	18
9	Cross-Sectional Positive Association of Serum Lipids and Blood Pressure With Serum Sodium Within the Normal Reference Range of 135–145 mmol/L. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2017, 37, 598-606.	1.1	22
10	G protein-coupled estrogen receptor regulates embryonic heart rate in zebrafish. <i>PLoS Genetics</i> , 2017, 13, e1007069.	1.5	41
11	<i>Pdgfrb</i> is a direct regulatory target of TGF β ² signaling in atrioventricular cushion mesenchymal cells. <i>PLoS ONE</i> , 2017, 12, e0175791.	1.1	9
12	HIV-1 gp140 epitope recognition is influenced by immunoglobulin DH gene segment sequence. <i>Immunogenetics</i> , 2016, 68, 145-155.	1.2	18
13	Training in metabolomics research. I. Designing the experiment, collecting and extracting samples and generating metabolomics data. <i>Journal of Mass Spectrometry</i> , 2016, 51, 461-475.	0.7	64
14	Training in metabolomics research. II. Processing and statistical analysis of metabolomics data, metabolite identification, pathway analysis, applications of metabolomics and its future. <i>Journal of Mass Spectrometry</i> , 2016, 51, 535-548.	0.7	49
15	Multigroup Equivalence Analysis for High-Dimensional Expression Data. <i>Cancer Informatics</i> , 2015, 14s2, CIN.S17304.	0.9	0
16	Genetic and Informatic Analyses Implicate <i>Kif12</i> as a Candidate Gene within the <i>Mpkd2</i> Locus That Modulates Renal Cystic Disease Severity in the <i>Cys1cpk</i> Mouse. <i>PLoS ONE</i> , 2015, 10, e0135678.	1.1	13
17	Transforming Growth Factor Beta (TGF- β ²) Is a Muscle Biomarker of Disease Progression in ALS and Correlates with <i>Smad</i> Expression. <i>PLoS ONE</i> , 2015, 10, e0138425.	1.1	44
18	Predictor(s) of Abnormal Array Comparative Genomic Hybridization Results in Patients with Cleft Lip and/or Palate. <i>Cleft Palate-Craniofacial Journal</i> , 2015, 52, 724-731.	0.5	5

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19	A Sequence Kernel Association Test for Dichotomous Traits in Family Samples under a Generalized Linear Mixed Model. <i>Human Heredity</i> , 2015, 79, 60-68.	0.4	29
20	Simple regression for correcting $\hat{\Gamma}^{\text{Ct}}$ bias in RT-qPCR low-density array data normalization. <i>BMC Genomics</i> , 2015, 16, 82.	1.2	15
21	Brief Report: Expression of Interferon γ Receptor Genes in Peripheral Blood Mononuclear Cells Is Associated With Rheumatoid Arthritis and Its Radiographic Severity in African Americans. <i>Arthritis and Rheumatology</i> , 2015, 67, 1165-1170.	2.9	16
22	Alterations in Gene Expression and DNA Methylation during Murine and Human Lung Alveolar Septation. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2015, 53, 60-73.	1.4	49
23	Kernel-Machine Testing Coupled with a Rank-Truncation Method for Genetic Pathway Analysis. <i>Genetic Epidemiology</i> , 2014, 38, 447-456.	0.6	12
24	Altered microbiota associated with abnormal humoral immune responses to commensal organisms in enthesitis-related arthritis. <i>Arthritis Research and Therapy</i> , 2014, 16, 486.	1.6	176
25	Intragenic motifs regulate the transcriptional complexity of Pkhd1/PKHD1. <i>Journal of Molecular Medicine</i> , 2014, 92, 1045-1056.	1.7	32
26	Applying shrinkage variance estimators to the TOST test in high dimensional settings. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2014, 13, 323-41.	0.2	1
27	Critical roles of miRNA-mediated regulation of TGF β signalling during mouse cardiogenesis. <i>Cardiovascular Research</i> , 2014, 103, 258-267.	1.8	26
28	BCRgt: a Bayesian cluster regression-based genotyping algorithm for the samples with copy number alterations. <i>BMC Bioinformatics</i> , 2014, 15, 74.	1.2	1
29	Whole-genome profiling highlights the molecular complexity underlying eccentric cardiac hypertrophy. <i>Therapeutic Advances in Cardiovascular Disease</i> , 2014, 8, 97-118.	1.0	9
30	Portion sizes for children are predicted by parental characteristics and the amounts parents serve themselves. <i>American Journal of Clinical Nutrition</i> , 2014, 99, 763-770.	2.2	51
31	Gene expression patterns in peripheral blood cells associated with radiographic severity in African Americans with early rheumatoid arthritis. <i>Rheumatology International</i> , 2013, 33, 129-137.	1.5	12
32	Cluster analysis reveals differential transcript profiles associated with resistance training-induced human skeletal muscle hypertrophy. <i>Physiological Genomics</i> , 2013, 45, 499-507.	1.0	91
33	Innate Transcriptional Networks Activated in Bladder in Response to Uropathogenic <i>Escherichia coli</i> Drive Diverse Biological Pathways and Rapid Synthesis of IL-10 for Defense against Bacterial Urinary Tract Infection. <i>Journal of Immunology</i> , 2012, 188, 781-792.	0.4	87
34	Genome-Wide Mapping of Cystitis Due to <i>Streptococcus agalactiae</i> and <i>Escherichia coli</i> in Mice Identifies a Unique Bladder Transcriptome That Signifies Pathogen-Specific Antimicrobial Defense against Urinary Tract Infection. <i>Infection and Immunity</i> , 2012, 80, 3145-3160.	1.0	46
35	Kidney Injury Accelerates Cystogenesis via Pathways Modulated by Heme Oxygenase and Complement. <i>Journal of the American Society of Nephrology: JASN</i> , 2012, 23, 1161-1171.	3.0	40
36	Excretion of anti-angiogenic proteins in patients with chronic allograft dysfunction. <i>Nephrology Dialysis Transplantation</i> , 2012, 27, 494-497.	0.4	3

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37	Expression Signature of IFN/STAT1 Signaling Genes Predicts Poor Survival Outcome in Glioblastoma Multiforme in a Subtype-Specific Manner. PLoS ONE, 2012, 7, e29653.	1.1	118
38	Statistics for Next Generation Sequencing “ Meeting Report. Frontiers in Genetics, 2012, 3, 128.	1.1	0
39	Uniform Approximation Is More Appropriate for Wilcoxon Rank-Sum Test in Gene Set Analysis. PLoS ONE, 2012, 7, e31505.	1.1	11
40	Design and validation issues in RNA-seq experiments. Briefings in Bioinformatics, 2011, 12, 280-287.	3.2	184
41	Genes and biochemical pathways in human skeletal muscle affecting resting energy expenditure and fuel partitioning. Journal of Applied Physiology, 2011, 110, 746-755.	1.2	14
42	Dynamic molecular and histopathological changes in the extracellular matrix and inflammation in the transition to heart failure in isolated volume overload. American Journal of Physiology - Heart and Circulatory Physiology, 2011, 300, H2251-H2260.	1.5	64
43	Length bias correction for RNA-seq data in gene set analyses. Bioinformatics, 2011, 27, 662-669.	1.8	49
44	Experimental Designs and ANOVA for Microarray Data. , 2011, , 151-169.		2
45	Group B <i>Streptococcus</i> (GBS) Urinary Tract Infection Involves Binding of GBS to Bladder Uroepithelium and Potent but GBS-Specific Induction of Interleukin 11±. Journal of Infectious Diseases, 2010, 201, 866-870.	1.9	45
46	Evaluation of a Statistical Equivalence Test Applied to Microarray Data. Journal of Biopharmaceutical Statistics, 2010, 20, 240-266.	0.4	13
47	Renal CD14 expression correlates with the progression of cystic kidney disease. Kidney International, 2010, 78, 550-560.	2.6	41
48	Differential genomic responses in old vs. young humans despite similar levels of modest muscle damage after resistance loading. Physiological Genomics, 2010, 40, 141-149.	1.0	89
49	Validation of Endogenous Internal Real-Time PCR Controls in Renal Tissues. American Journal of Nephrology, 2009, 30, 413-417.	1.4	29
50	Repeatability of published microarray gene expression analyses. Nature Genetics, 2009, 41, 149-155.	9.4	477
51	Single nucleotide polymorphisms affect both cis- and trans-eQTLs. Genomics, 2009, 93, 501-508.	1.3	23
52	Arabidopsis Extra Large G-Protein 2 (XLG2) Interacts with the G β 2 Subunit of Heterotrimeric G Protein and Functions in Disease Resistance. Molecular Plant, 2009, 2, 513-525.	3.9	99
53	Consistency Analysis of Redundant Probe Sets on Affymetrix Three-Prime Expression Arrays and Applications to Differential mRNA Processing. PLoS ONE, 2009, 4, e4229.	1.1	20
54	Overexpression of innate immune response genes in a model of recessive polycystic kidney disease. Kidney International, 2008, 73, 63-76.	2.6	82

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55	Methods for Nutrigenomics and Longevity Studies in Drosophila. <i>Methods in Molecular Biology</i> , 2007, 371, 111-141.	0.4	14
56	The effect of insulin on expression of genes and biochemical pathways in human skeletal muscle. <i>Endocrine</i> , 2007, 31, 5-17.	2.2	66
57	Microarray data analysis: from disarray to consolidation and consensus. <i>Nature Reviews Genetics</i> , 2006, 7, 55-65.	7.7	1,186
58	Inheritance Patterns of Transcript Levels in F1 Hybrid Mice. <i>Genetics</i> , 2006, 174, 627-637.	1.2	35
59	Global correlation analysis between redundant probe sets using a large collection of Arabidopsis ath1 expression profiling data. <i>Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference</i> , 2006, , 223-6.	0.4	5
60	Evaluation of five ab initio gene prediction programs for the discovery of maize genes. <i>Plant Molecular Biology</i> , 2005, 57, 445-460.	2.0	45
61	Improved statistical tests for differential gene expression by shrinking variance components estimates. <i>Biostatistics</i> , 2005, 6, 59-75.	0.9	450
62	Kinesin Family Member 12 Is a Candidate Polycystic Kidney Disease Modifier in the cpk Mouse. <i>Journal of the American Society of Nephrology: JASN</i> , 2005, 16, 905-916.	3.0	55
63	How Many Mice and How Many Arrays? Replication in Mouse cDNA Microarray Experiments. , 2004, , 139-154.		6
64	Exploration of Low-Dose Estrogen Effects: Identification of No Observed Transcriptional Effect Level (NOTEL). <i>Toxicologic Pathology</i> , 2004, 32, 482-492.	0.9	53
65	Statistical tests for differential expression in cDNA microarray experiments. <i>Genome Biology</i> , 2003, 4, 210.	13.9	741
66	MAANOVA: A Software Package for the Analysis of Spotted cDNA Microarray Experiments. <i>Statistics in the Health Sciences</i> , 2003, , 313-341.	0.2	165
67	Alternative Transcription Initiation Sites and Polyadenylation Sites Are Recruited During μ Suppression at the $rf2a$ Locus of Maize. <i>Genetics</i> , 2003, 163, 685-698.	1.2	37
68	Characterization of the aldehyde dehydrogenase gene families of Zea mays and Arabidopsis. <i>Plant Molecular Biology</i> , 2002, 48, 751-764.	2.0	73
69	Mitochondrial Aldehyde Dehydrogenase Activity Is Required for Male Fertility in Maize. <i>Plant Cell</i> , 2001, 13, 1063-1078.	3.1	228