

# Xiangqin Cui

## List of Publications by Year in descending order

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69  
papers

5,595  
citations

136950

32  
h-index

102487

66  
g-index

77  
all docs

77  
docs citations

77  
times ranked

9286  
citing authors

#	ARTICLE	IF	CITATIONS
1	Microarray data analysis: from disarray to consolidation and consensus. Nature Reviews Genetics, 2006, 7, 55-65.	16.3	1,186
2	Statistical tests for differential expression in cDNA microarray experiments. Genome Biology, 2003, 4, 210.	9.6	741
3	Repeatability of published microarray gene expression analyses. Nature Genetics, 2009, 41, 149-155.	21.4	477
4	Improved statistical tests for differential gene expression by shrinking variance components estimates. Biostatistics, 2005, 6, 59-75.	1.5	450
5	Mitochondrial Aldehyde Dehydrogenase Activity Is Required for Male Fertility in Maize. Plant Cell, 2001, 13, 1063-1078.	6.6	228
6	Design and validation issues in RNA-seq experiments. Briefings in Bioinformatics, 2011, 12, 280-287.	6.5	184
7	Altered microbiota associated with abnormal humoral immune responses to commensal organisms in enthesitis-related arthritis. Arthritis Research and Therapy, 2014, 16, 486.	3.5	176
8	MAANOVA: A Software Package for the Analysis of Spotted cDNA Microarray Experiments. Statistics in the Health Sciences, 2003, , 313-341.	0.2	165
9	Expression Signature of IFN/STAT1 Signaling Genes Predicts Poor Survival Outcome in Glioblastoma Multiforme in a Subtype-Specific Manner. PLoS ONE, 2012, 7, e29653.	2.5	118
10	Arabidopsis Extra Large G-Protein 2 (XLG2) Interacts with the G $\beta$ 2 Subunit of Heterotrimeric G Protein and Functions in Disease Resistance. Molecular Plant, 2009, 2, 513-525.	8.3	99
11	Cluster analysis reveals differential transcript profiles associated with resistance training-induced human skeletal muscle hypertrophy. Physiological Genomics, 2013, 45, 499-507.	2.3	91
12	Differential genomic responses in old vs. young humans despite similar levels of modest muscle damage after resistance loading. Physiological Genomics, 2010, 40, 141-149.	2.3	89
13	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. Journal of Immunology, 2012, 188, 781-792.	0.8	87
14	Overexpression of innate immune response genes in a model of recessive polycystic kidney disease. Kidney International, 2008, 73, 63-76.	5.2	82
15	Characterization of the aldehyde dehydrogenase gene families of Zea mays and Arabidopsis. Plant Molecular Biology, 2002, 48, 751-764.	3.9	73
16	The effect of insulin on expression of genes and biochemical pathways in human skeletal muscle. Endocrine, 2007, 31, 5-17.	2.2	66
17	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.	3.2	64
18	Training in metabolomics research. I. Designing the experiment, collecting and extracting samples and generating metabolomics data. Journal of Mass Spectrometry, 2016, 51, 461-475.	1.6	64

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19	Kinesin Family Member 12 Is a Candidate Polycystic Kidney Disease Modifier in the cpk Mouse. Journal of the American Society of Nephrology: JASN, 2005, 16, 905-916.	6.1	55
20	Exploration of Low-Dose Estrogen Effects: Identification of No Observed Transcriptional Effect Level (NOTEL). Toxicologic Pathology, 2004, 32, 482-492.	1.8	53
21	Portion sizes for children are predicted by parental characteristics and the amounts parents serve themselves. American Journal of Clinical Nutrition, 2014, 99, 763-770.	4.7	51
22	Length bias correction for RNA-seq data in gene set analyses. Bioinformatics, 2011, 27, 662-669.	4.1	49
23	Alterations in Gene Expression and DNA Methylation during Murine and Human Lung Alveolar Septation. American Journal of Respiratory Cell and Molecular Biology, 2015, 53, 60-73.	2.9	49
24	Training in metabolomics research. II. Processing and statistical analysis of metabolomics data, metabolite identification, pathway analysis, applications of metabolomics and its future. Journal of Mass Spectrometry, 2016, 51, 535-548.	1.6	49
25	Genome-Wide Mapping of Cystitis Due to Streptococcus agalactiae and Escherichia coli in Mice Identifies a Unique Bladder Transcriptome That Signifies Pathogen-Specific Antimicrobial Defense against Urinary Tract Infection. Infection and Immunity, 2012, 80, 3145-3160.	2.2	46
26	Evaluation of five ab initio gene prediction programs for the discovery of maize genes. Plant Molecular Biology, 2005, 57, 445-460.	3.9	45
27	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.	4.0	45
28	Transforming Growth Factor Beta (TGF-β <sup>2</sup> ) Is a Muscle Biomarker of Disease Progression in ALS and Correlates with Smad Expression. PLoS ONE, 2015, 10, e0138425.	2.5	44
29	Renal CD14 expression correlates with the progression of cystic kidney disease. Kidney International, 2010, 78, 550-560.	5.2	41
30	G protein-coupled estrogen receptor regulates embryonic heart rate in zebrafish. PLoS Genetics, 2017, 13, e1007069.	3.5	41
31	Kidney Injury Accelerates Cystogenesis via Pathways Modulated by Heme Oxygenase and Complement. Journal of the American Society of Nephrology: JASN, 2012, 23, 1161-1171.	6.1	40
32	Alternative Transcription Initiation Sites and Polyadenylation Sites Are Recruited During <i>Mu</i> Suppression at the <i>rf2a</i> Locus of Maize. Genetics, 2003, 163, 685-698.	2.9	37
33	Inheritance Patterns of Transcript Levels in F1 Hybrid Mice. Genetics, 2006, 174, 627-637.	2.9	35
34	Intragenic motifs regulate the transcriptional complexity of Pkhd1/PKHD1. Journal of Molecular Medicine, 2014, 92, 1045-1056.	3.9	32
35	Validation of Endogenous Internal Real-Time PCR Controls in Renal Tissues. American Journal of Nephrology, 2009, 30, 413-417.	3.1	29
36	A Sequence Kernel Association Test for Dichotomous Traits in Family Samples under a Generalized Linear Mixed Model. Human Heredity, 2015, 79, 60-68.	0.8	29

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37	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.	4.1	27
38	Absorbance summation: A novel approach for analyzing high-throughput ELISA data in the absence of a standard. <i>PLoS ONE</i> , 2018, 13, e0198528.	2.5	27
39	Critical roles of miRNA-mediated regulation of TGF $\beta$ signalling during mouse cardiogenesis. <i>Cardiovascular Research</i> , 2014, 103, 258-267.	3.8	26
40	Single nucleotide polymorphisms affect both cis- and trans-eQTLs. <i>Genomics</i> , 2009, 93, 501-508.	2.9	23
41	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.	2.4	22
42	Consistency Analysis of Redundant Probe Sets on Affymetrix Three-Prime Expression Arrays and Applications to Differential mRNA Processing. <i>PLoS ONE</i> , 2009, 4, e4229.	2.5	20
43	HIV-1 gp140 epitope recognition is influenced by immunoglobulin DH gene segment sequence. <i>Immunogenetics</i> , 2016, 68, 145-155.	2.4	18
44	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.	2.5	18
45	Brief Report: Expression of Interferon $\gamma$ 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.	5.6	16
46	Simple regression for correcting $\Delta$ Ct bias in RT-qPCR low-density array data normalization. <i>BMC Genomics</i> , 2015, 16, 82.	2.8	15
47	Methods for Nutrigenomics and Longevity Studies in <i>Drosophila</i> . <i>Methods in Molecular Biology</i> , 2007, 371, 111-141.	0.9	14
48	Genes and biochemical pathways in human skeletal muscle affecting resting energy expenditure and fuel partitioning. <i>Journal of Applied Physiology</i> , 2011, 110, 746-755.	2.5	14
49	Evaluation of a Statistical Equivalence Test Applied to Microarray Data. <i>Journal of Biopharmaceutical Statistics</i> , 2010, 20, 240-266.	0.8	13
50	Genetic and Informatic Analyses Implicate Kif12 as a Candidate Gene within the Mpkd2 Locus That Modulates Renal Cystic Disease Severity in the Cys1cpk Mouse. <i>PLoS ONE</i> , 2015, 10, e0135678.	2.5	13
51	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.	3.0	12
52	Kernel-Machine Testing Coupled with a Rank-Truncation Method for Genetic Pathway Analysis. <i>Genetic Epidemiology</i> , 2014, 38, 447-456.	1.3	12
53	Uniform Approximation Is More Appropriate for Wilcoxon Rank-Sum Test in Gene Set Analysis. <i>PLoS ONE</i> , 2012, 7, e31505.	2.5	11
54	Personalized Visual Mapping Assistive Technology to Improve Functional Ability in Persons With Dementia: Feasibility Cohort Study. <i>JMIR Aging</i> , 2021, 4, e28165.	3.0	10

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55	Whole-genome profiling highlights the molecular complexity underlying eccentric cardiac hypertrophy. <i>Therapeutic Advances in Cardiovascular Disease</i> , 2014, 8, 97-118.	2.1	9
56	Pdgfrb is a direct regulatory target of TGF $\beta$ <sup>2</sup> signaling in atrioventricular cushion mesenchymal cells. <i>PLoS ONE</i> , 2017, 12, e0175791.	2.5	9
57	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.	2.5	8
58	Adverse Outcomes Associated With Inpatient Administration of Beers List Medications Following Total Knee Replacement. <i>Clinical Therapeutics</i> , 2020, 42, 592-604.e1.	2.5	6
59	How Many Mice and How Many Arrays? Replication in Mouse cDNA Microarray Experiments. , 2004, , 139-154.		6
60	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.	0.9	5
61	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
62	Excretion of anti-angiogenic proteins in patients with chronic allograft dysfunction. <i>Nephrology Dialysis Transplantation</i> , 2012, 27, 494-497.	0.7	3
63	Autosomal Dominant Polycystic Kidney Disease Does Not Significantly Alter Major COVID-19 Outcomes among Veterans. <i>Kidney360</i> , 2021, 2, 983-988.	2.1	2
64	Experimental Designs and ANOVA for Microarray Data. , 2011, , 151-169.		2
65	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.	0.6	1
66	BCRgt: a Bayesian cluster regression-based genotyping algorithm for the samples with copy number alterations. <i>BMC Bioinformatics</i> , 2014, 15, 74.	2.6	1
67	Pulmonary Hypertension. <i>Chest</i> , 2022, 161, 803-806.	0.8	1
68	Statistics for Next Generation Sequencing “ Meeting Report. <i>Frontiers in Genetics</i> , 2012, 3, 128.	2.3	0
69	Multigroup Equivalence Analysis for High-Dimensional Expression Data. <i>Cancer Informatics</i> , 2015, 14s2, CIN.S17304.	1.9	0