Wenzhong Xiao

List of Publications by Year
in descending order

91 papers	12,707 citations	53660 45 h-index	45213 90 g-index
97 all docs	97 docs citations	97 times ranked	19278 citing authors

#	Article	IF	Citations
1	A systematic comparison of hepatobiliary adverse drug reactions in FDA and EMA drug labeling reveals discrepancies. Drug Discovery Today, 2022, 27, 337-346.	3.2	5
2	Assessing reproducibility of inherited variants detected with short-read whole genome sequencing. Genome Biology, 2022, 23, 2.	3.8	18
3	System-level metabolic modeling facilitates unveiling metabolic signature in exceptional longevity. Aging Cell, 2022, 21, e13595.	3.0	13
4	Neurovascular Dysregulation and Acute Exercise Intolerance in Myalgic Encephalomyelitis/Chronic Fatigue Syndrome. Chest, 2022, 162, 1116-1126.	0.4	10
5	Evaluating the analytical validity of circulating tumor DNA sequencing assays for precision oncology. Nature Biotechnology, 2021, 39, 1115-1128.	9.4	126
6	Cross-oncopanel study reveals high sensitivity and accuracy with overall analytical performance depending on genomic regions. Genome Biology, 2021, 22, 109.	3.8	20
7	A verified genomic reference sample for assessing performance of cancer panels detecting small variants of low allele frequency. Genome Biology, 2021, 22, 111.	3.8	29
8	Case-control study evaluating risk factors for SARS-CoV-2 outbreak amongst healthcare personnel at a tertiary care center. American Journal of Infection Control, 2021, 49, 1457-1463.	1.1	8
9	A Comprehensive Examination of Severely Ill ME/CFS Patients. Healthcare (Switzerland), 2021, 9, 1290.	1.0	12
10	Prospective Validation of a Transcriptomic Metric in Severe Trauma. Annals of Surgery, 2020, 271, 802-810.	2.1	26
11	A comprehensive rat transcriptome built from large scale RNA-seq-based annotation. Nucleic Acids Research, 2020, 48, 8320-8331.	6.5	19
12	FastMM: an efficient toolbox for personalized constraint-based metabolic modeling. BMC Bioinformatics, 2020, 21, 67.	1.2	6
13	Genomic Analysis of Circulating Tumor Cells at the Single-Cell Level. Journal of Molecular Diagnostics, 2020, 22, 770-781.	1.2	20
14	Sequencing XMET genes to promote genotype-guided risk assessment and precision medicine. Science China Life Sciences, 2019, 62, 895-904.	2.3	5
15	Collection and storage of HLA NGS genotyping data for the 17th International HLA and Immunogenetics Workshop. Human Immunology, 2018, 79, 77-86.	1.2	16
16	Strategic Targeting of Multiple BMP Receptors Prevents Trauma-Induced Heterotopic Ossification. Molecular Therapy, 2017, 25, 1974-1987.	3.7	57
17	KERIS: kaleidoscope of gene responses to inflammation between species. Nucleic Acids Research, 2017, 45, D908-D914.	6.5	11
18	Detecting common genomic mechanism between diseases using paired sparse canonical correlation analysis. , 2016, , .		0

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19	Inhibition of Hif1α prevents both trauma-induced and genetic heterotopic ossification. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E338-47.	3.3	178
20	A Hybrid Approach of Gene Sets and Single Genes for the Prediction of Survival Risks with Gene Expression Data. PLoS ONE, 2015, 10, e0122103.	1.1	3
21	Comparison of RNA-seq and microarray-based models for clinical endpoint prediction. Genome Biology, 2015, 16, 133.	3.8	325
22	RASA: Robust Alternative Splicing Analysis for Human Transcriptome Arrays. Scientific Reports, 2015, 5, 11917.	1.6	10
23	Mice are not men. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E345.	3.3	102
24	Detecting differential protein expression in large-scale population proteomics. Bioinformatics, 2014, 30, 2741-2746.	1.8	17
25	Benchmarking Outcomes in the Critically Injured Burn Patient. Annals of Surgery, 2014, 259, 833-841.	2.1	76
26	Treatment of heterotopic ossification through remote ATP hydrolysis. Science Translational Medicine, 2014, 6, 255ra132.	5.8	119
27	Inference for longitudinal data with nonignorable nonmonotone missing responses. Computational Statistics and Data Analysis, 2014, 72, 77-91.	0.7	3
28	Molecular indexing enables quantitative targeted RNA sequencing and reveals poor efficiencies in standard library preparations. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 1891-1896.	3.3	90
29	The Identification of Novel Potential Injury Mechanisms and Candidate Biomarkers in Renal Allograft Rejection by Quantitative Proteomics. Molecular and Cellular Proteomics, 2014, 13, 621-631.	2.5	73
30	Trauma‐associated human neutrophil alterations revealed by comparative proteomics profiling. Proteomics - Clinical Applications, 2013, 7, 571-583.	0.8	17
31	Genomic responses in mouse models poorly mimic human inflammatory diseases. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 3507-3512.	3.3	2,518
32	Development of a Genomic Metric That Can Be Rapidly Used to Predict Clinical Outcome in Severely Injured Trauma Patients*. Critical Care Medicine, 2013, 41, 1175-1185.	0.4	88
33	Determination of Burn Patient Outcome by Large-Scale Quantitative Discovery Proteomics. Critical Care Medicine, 2013, 41, 1421-1434.	0.4	55
34	Reply to Osterburg et al.: To study human inflammatory diseases in humans. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E3371-E3371.	3.3	6
35	Reply to Cauwels et al.: Of men, not mice, and inflammation. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E3151-E3151.	3.3	8
36	Down‐regulation of glutathione S‐transferase α 4 (hGSTA4) in the muscle of thermally injured patients is indicative of susceptibility to bacterial infection. FASEB Journal, 2012, 26, 730-737.	0.2	29

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37	Benchmarking Outcomes in the Critically Injured Trauma Patient and the Effect of Implementing Standard Operating Procedures. Annals of Surgery, 2012, 255, 993-999.	2.1	92
38	A Peripheral Blood Diagnostic Test for Acute Rejection in Renal Transplantation. American Journal of Transplantation, 2012, 12, 2710-2718.	2.6	124
39	Coding SNPs as intrinsic markers for sample tracking in large-scale transcriptome studies. BioTechniques, 2012, 52, 386-8.	0.8	3
40	JETTA: junction and exon toolkits for transcriptome analysis. Bioinformatics, 2012, 28, 1274-1275.	1.8	20
41	Knowledge-Based Reconstruction of mRNA Transcripts with Short Sequencing Reads for Transcriptome Research. PLoS ONE, 2012, 7, e31440.	1.1	7
42	4.11 High-Throughput VDJ Sequencing for Chronic Lymphocytic Leukemia: Minimal Residual Disease Quantification and Immunoglobulin Repertoire Assessment Following Hematopoietic Cell Transplantation. Clinical Lymphoma, Myeloma and Leukemia, 2011, 11, S224.	0.2	0
43	High-throughput VDJ sequencing for quantification of minimal residual disease in chronic lymphocytic leukemia and immune reconstitution assessment. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 21194-21199.	3.3	160
44	Distinctive Responsiveness to Stromal Signaling Accompanies Histologic Grade Programming of Cancer Cells. PLoS ONE, 2011, 6, e20016.	1.1	10
45	A genomic storm in critically injured humans. Journal of Experimental Medicine, 2011, 208, 2581-2590.	4.2	1,040
46	Human transcriptome array for high-throughput clinical studies. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 3707-3712.	3.3	122
47	Knowledge-based analysis of microarrays for the discovery of transcriptional regulation relationships. BMC Bioinformatics, 2010, 11, S8.	1.2	12
48	Shotgun proteomics identifies proteins specific for acute renal transplant rejection. Proteomics - Clinical Applications, 2010, 4, 32-47.	0.8	105
49	Analysis of factorial time-course microarrays with application to a clinical study of burn injury. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 9923-9928.	3.3	62
50	Changes in DnaA-Dependent Gene Expression Contribute to the Transcriptional and Developmental Response of *Bacillus subtilis* to Manganese Limitation in Luria-Bertani Medium. Journal of Bacteriology, 2010, 192, 3915-3924.	1.0	35
51	Plasma Proteome Response to Severe Burn Injury Revealed by ^{18}O-Labeled "Universal" Reference-Based Quantitative Proteomics. Journal of Proteome Research, 2010, 9, 4779-4789.	1.8	54
52	Isolating highly enriched populations of circulating epithelial cells and other rare cells from blood using a magnetic sweeper device. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 3970-3975.	3.3	448
53	A dynamic network of transcription in LPS-treated human subjects. BMC Systems Biology, 2009, 3, 78.	3.0	36
54	Analysis of the relationship between longitudinal gene expressions and ordered categorical event data. Statistics in Medicine, 2009, 28, 2817-2832.	0.8	5

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55	Large-Scale Multiplexed Quantitative Discovery Proteomics Enabled by the Use of an 18O-Labeled "Universal" Reference Sample. Journal of Proteome Research, 2009, 8, 290-299.	1.8	59
56	Genome-wide transcriptome analysis of 150 cell samples. Integrative Biology (United Kingdom), 2009, 1, 99-107.	0.6	15
57	Inflammation and the Host Response to Injury, a Large-Scale Collaborative Project: Patient-Oriented Research Core Standard Operating Procedures for Clinical Care IX. Definitions for Complications of Clinical Care of Critically Injured Patients. Journal of Trauma, 2009, 67, 384-388.	2.3	27
58	Shotgun Proteomics Identifies Protein Biomarkers Specific for Acute Renal Transplant Rejection. FASEB Journal, 2009, 23, LB239.	0.2	0
59	Bisphenol A Induces a Profile of Tumor Aggressiveness in High-Risk Cells from Breast Cancer Patients. Cancer Research, 2008, 68, 2076-2080.	0.4	101
60	Microfluidic Leukocyte Isolation for Gene Expression Analysis in Critically Ill Hospitalized Patients. Clinical Chemistry, 2008, 54, 891-900.	1.5	26
61	Comparison of longitudinal leukocyte gene expression after burn injury or trauma-hemorrhage in mice. Physiological Genomics, 2008, 32, 299-310.	1.0	28
62	Interference of globin genes with biomarker discovery for allograft rejection in peripheral blood samples. Physiological Genomics, 2008, 32, 190-197.	1.0	43
63	V. Guidelines for Sedation and Analgesia During Mechanical Ventilation General Overview. Journal of Trauma, 2007, 63, 945-950.	2.3	20
64	Involvement of Skeletal Muscle Gene Regulatory Network in Susceptibility to Wound Infection Following Trauma. PLoS ONE, 2007, 2, e1356.	1.1	32
65	Commonality and differences in leukocyte gene expression patterns among three models of inflammation and injury. Physiological Genomics, 2006, 24, 298-309.	1.0	39
66	PROLONGED CATABOLIC, INFLAMMATORY AND GENOMIC CHANGES IN PEDIATRIC BURN PATIENTS.. Critical Care Medicine, 2006, 34, A9.	0.4	0
67	High Dynamic Range Characterization of the Trauma Patient Plasma Proteome. Molecular and Cellular Proteomics, 2006, 5, 1899-1913.	2.5	142
68	Cell-specific expression and pathway analyses reveal alterations in trauma-related human T cell and monocyte pathways. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 15564-15569.	3.3	106
69	A network-based analysis of systemic inflammation in humans. Nature, 2005, 437, 1032-1037.	13.7	1,419
70	Comparative proteome analyses of human plasma followingin vivo lipopolysaccharide administration using multidimensional separations coupled with tandem mass spectrometry. Proteomics, 2005, 5, 572-584.	1.3	125
71	Application of genome-wide expression analysis to human health and disease. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 4801-4806.	3.3	238
72	Significance analysis of time course microarray experiments. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 12837-12842.	3.3	534

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73	Quantitative Proteome Analysis of Human Plasma following in Vivo Lipopolysaccharide Administration Using 16O/18O Labeling and the Accurate Mass and Time Tag Approach. Molecular and Cellular Proteomics, 2005, 4, 700-709.	2.5	156
74	Profiling early infection responses: Pseudomonas aeruginosa eludes host defenses by suppressing antimicrobial peptide gene expression. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 2573-2578.	3.3	149
75	Genomic and Proteomic Determinants of Outcome in Patients Undergoing Thoracoabdominal Aortic Aneurysm Repair. Journal of Immunology, 2004, 172, 7103-7109.	0.4	61
76	Whole blood and leukocyte RNA isolation for gene expression analyses. Physiological Genomics, 2004, 19, 247-254.	1.0	186
77	A Transcriptional Profile of Aging in the Human Kidney. PLoS Biology, 2004, 2, e427.	2.6	281
78	Integrative Analysis of the Mitochondrial Proteome in Yeast. PLoS Biology, 2004, 2, e160.	2.6	181
79	Global Analysis of the Membrane Subproteome ofPseudomonas aeruginosaUsing Liquid Chromatography-Tandem Mass Spectrometry. Journal of Proteome Research, 2004, 3, 434-444.	1.8	55
80	Ultra-High-Efficiency Strong Cation Exchange LC/RPLC/MS/MS for High Dynamic Range Characterization of the Human Plasma Proteome. Analytical Chemistry, 2004, 76, 1134-1144.	3.2	290
81	The Drosophila melanogaster Toll Pathway Participates in Resistance to Infection by the Gram-Negative Human Pathogen Pseudomonas aeruginosa. Infection and Immunity, 2003, 71, 4059-4066.	1.0	162
82	EPR Spectroscopic Ruler: the Method and its Applications. Biological Magnetic Resonance, 2002, , 249-276.	0.4	5
83	Yeast tRNA as Carrier in the Isolation of Microscale RNA for Global Amplification and Expression Profiling. BioTechniques, 2002, 33, 788-796.	0.8	21
84	Temperature-Modulated Array High-Performance Liquid Chromatography. Genome Research, 2001, 11, 1944-1951.	2.4	23
85	Denaturing high-performance liquid chromatography: A review. Human Mutation, 2001, 17, 439-474.	1.1	674
86	The neuronal t-SNARE complex is a parallel four-helix bundle. Nature Structural Biology, 2001, 8, 308-311.	9.7	101
87	Light-induced Rotation of a Transmembrane Î±-Helix in Bacteriorhodopsin. Journal of Molecular Biology, 2000, 304, 715-721.	2.0	67
88	Design and Characterization of A Synthetic Electron-Transfer Protein. Journal of the American Chemical Society, 2000, 122, 7999-8006.	6.6	51
89	A Piston Model for Transmembrane Signaling of the Aspartate Receptor. Science, 1999, 285, 1751-1754.	6.0	259
90	The synaptic SNARE complex is a parallel four-stranded helical bundle. Nature Structural Biology, 1998, 5, 765-769.	9.7	450

#	ARTICLE	IF	CITATIONS
91	Transient channel-opening in bacteriorhodopsin: an EPR study 1 1Edited by D. Ress. Journal of Molecular Biology, 1997, 273, 951-957.	2.0	119