

Wenzhong Xiao

List of Articles by Year in descending order

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79

PR articles

8,864

PR citations

88531

37

PR h-index

74299

75

g-index

88

documents

12135

doc citations

69917

43

h-index

23874

citing authors

#	ARTICLE	IF	CITATIONS
1	Systems Modeling Reveals Shared Metabolic Dysregulation and Potential Treatments in ME/CFS and Long COVID. <i>International Journal of Molecular Sciences</i> , 2025, 26, 6082.	4.4	3
2	Targeted DNA-seq and RNA-seq of Reference Samples with Short-read and Long-read Sequencing. <i>Scientific Data</i> , 2024, 11, .	5.7	6
3	Molecular profiles of blood from numerous species that differ in sensitivity to acute inflammation. <i>Molecular Medicine</i> , 2024, 30, .	5.6	6
4	A systematic comparison of hepatobiliary adverse drug reactions in FDA and EMA drug labeling reveals discrepancies. <i>Drug Discovery Today</i> , 2022, 27, 337-346.	6.6	11
5	Assessing reproducibility of inherited variants detected with short-read whole genome sequencing. <i>Genome Biology</i> , 2022, 23, .	8.1	39
6	System-level metabolic modeling facilitates unveiling metabolic signature in exceptional longevity. <i>Aging Cell</i> , 2022, 21, .	6.8	27
7	Neurovascular Dysregulation and Acute Exercise Intolerance in Myalgic Encephalomyelitis/Chronic Fatigue Syndrome. <i>Chest</i> , 2022, 162, 1116-1126.	1.0	35
8	Deep oncopanel sequencing reveals within block position-dependent quality degradation in FFPE processed samples. <i>Genome Biology</i> , 2022, 23, .	8.1	12
9	Evaluating the analytical validity of circulating tumor DNA sequencing assays for precision oncology. <i>Nature Biotechnology</i> , 2021, 39, 1115-1128.	29.8	225
10	Cross-oncopanel study reveals high sensitivity and accuracy with overall analytical performance depending on genomic regions. <i>Genome Biology</i> , 2021, 22, .	8.1	32
11	A verified genomic reference sample for assessing performance of cancer panels detecting small variants of low allele frequency. <i>Genome Biology</i> , 2021, 22, .	8.1	49
12	Case-control study evaluating risk factors for SARS-CoV-2 outbreak amongst healthcare personnel at a tertiary care center. <i>American Journal of Infection Control</i> , 2021, 49, 1457-1463.	1.9	13
13	A Comprehensive Examination of Severely Ill ME/CFS Patients. <i>Healthcare (Switzerland)</i> , 2021, 9, 1290.	2.2	32
14	A comprehensive rat transcriptome built from large scale RNA-seq-based annotation. <i>Nucleic Acids Research</i> , 2020, 48, 8320-8331.	15.5	27
15	Genomic Analysis of Circulating Tumor Cells at the Single-Cell Level. <i>Journal of Molecular Diagnostics</i> , 2020, 22, 770-781.	2.5	30
16	Sequencing XMET genes to promote genotype-guided risk assessment and precision medicine. <i>Science China Life Sciences</i> , 2019, 62, 895-904.	6.7	5
17	Collection and storage of HLA NGS genotyping data for the 17th International HLA and Immunogenetics Workshop. <i>Human Immunology</i> , 2018, 79, 77-86.	1.0	17
18	Strategic Targeting of Multiple BMP Receptors Prevents Trauma-Induced Heterotopic Ossification. <i>Molecular Therapy</i> , 2017, 25, 1974-1987.	10.2	70

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19	KERIS: kaleidoscope of gene responses to inflammation between species. <i>Nucleic Acids Research</i> , 2017, 45, D908-D914.	15.5	11
20	Inhibition of Hif1 α prevents both trauma-induced and genetic heterotopic ossification. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, .	7.5	215
21	A Hybrid Approach of Gene Sets and Single Genes for the Prediction of Survival Risks with Gene Expression Data. <i>PLoS ONE</i> , 2015, 10, e0122103.	2.3	4
22	Comparison of RNA-seq and microarray-based models for clinical endpoint prediction. <i>Genome Biology</i> , 2015, 16, .	12.2	378
23	RASA: Robust Alternative Splicing Analysis for Human Transcriptome Arrays. <i>Scientific Reports</i> , 2015, 5, .	3.4	10
24	Mice are not men. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, .	7.5	111
25	Detecting differential protein expression in large-scale population proteomics. <i>Bioinformatics</i> , 2014, 30, 2741-2746.	4.7	18
26	Beyond the proteome: Mass Spectrometry Special Interest Group (MS-SIG) at ISMB/ECCB 2013. <i>Bioinformatics</i> , 2014, 30, 2089-2090.	4.7	0
27	Treatment of heterotopic ossification through remote ATP hydrolysis. <i>Science Translational Medicine</i> , 2014, 6, .	12.5	127
28	Inference for longitudinal data with nonignorable nonmonotone missing responses. <i>Computational Statistics and Data Analysis</i> , 2014, 72, 77-91.	1.4	3
29	Molecular indexing enables quantitative targeted RNA sequencing and reveals poor efficiencies in standard library preparations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 1891-1896.	7.5	97
30	The Identification of Novel Potential Injury Mechanisms and Candidate Biomarkers in Renal Allograft Rejection by Quantitative Proteomics. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 621-631.	3.0	85
31	Trauma-associated human neutrophil alterations revealed by comparative proteomics profiling. <i>Proteomics - Clinical Applications</i> , 2013, 7, 571-583.	2.3	16
32	Genomic responses in mouse models poorly mimic human inflammatory diseases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 3507-3512.	7.5	2,814
33	Determination of Burn Patient Outcome by Large-Scale Quantitative Discovery Proteomics. <i>Critical Care Medicine</i> , 2013, 41, 1421-1434.	0.5	61
34	Reply to Osterburg et al.: To study human inflammatory diseases in humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E3371-E3371.	7.5	6
35	Reply to Cauwels et al.: Of men, not mice, and inflammation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E3151-E3151.	7.5	8
36	Down-regulation of glutathione S-transferase γ 4 (hGSTA4) in the muscle of thermally injured patients is indicative of susceptibility to bacterial infection. <i>FASEB Journal</i> , 2012, 26, 730-737.	0.6	30

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37	Benchmarking Outcomes in the Critically Injured Trauma Patient and the Effect of Implementing Standard Operating Procedures. <i>Annals of Surgery</i> , 2012, 255, 993-999.	4.6	98
38	JETTA: junction and exon toolkits for transcriptome analysis. <i>Bioinformatics</i> , 2012, 28, 1274-1275.	4.7	22
39	Knowledge-Based Reconstruction of mRNA Transcripts with Short Sequencing Reads for Transcriptome Research. <i>PLoS ONE</i> , 2012, 7, e31440.	2.3	7
40	High-throughput VDJ sequencing for quantification of minimal residual disease in chronic lymphocytic leukemia and immune reconstitution assessment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 21194-21199.	7.5	169
41	Distinctive Responsiveness to Stromal Signaling Accompanies Histologic Grade Programming of Cancer Cells. <i>PLoS ONE</i> , 2011, 6, e20016.	2.3	13
42	Human transcriptome array for high-throughput clinical studies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 3707-3712.	7.5	135
43	Knowledge-based analysis of microarrays for the discovery of transcriptional regulation relationships. <i>BMC Bioinformatics</i> , 2010, 11, .	3.0	13
44	Shotgun proteomics identifies proteins specific for acute renal transplant rejection. <i>Proteomics - Clinical Applications</i> , 2010, 4, 32-47.	2.3	108
45	Analysis of factorial time-course microarrays with application to a clinical study of burn injury. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 9923-9928.	7.5	64
46	Changes in DnaA-Dependent Gene Expression Contribute to the Transcriptional and Developmental Response of <i>Bacillus subtilis</i> to Manganese Limitation in Luria-Bertani Medium. <i>Journal of Bacteriology</i> , 2010, 192, 3915-3924.	2.9	38
47	Plasma Proteome Response to Severe Burn Injury Revealed by ¹⁸ O-Labeled "Universal" Reference-Based Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2010, 9, 4779-4789.	3.4	55
48	Isolating highly enriched populations of circulating epithelial cells and other rare cells from blood using a magnetic sweeper device. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 3970-3975.	7.5	466
49	A dynamic network of transcription in LPS-treated human subjects. <i>BMC Systems Biology</i> , 2009, 3, .	3.1	36
50	Large-Scale Multiplexed Quantitative Discovery Proteomics Enabled by the Use of an ¹⁸ O-Labeled "Universal" Reference Sample. <i>Journal of Proteome Research</i> , 2009, 8, 290-299.	3.4	59
51	Genome-wide transcriptome analysis of 150 cell samples. <i>Integrative Biology (United Kingdom)</i> , 2009, 1, 99-107.	1.3	15
52	Comparison of longitudinal leukocyte gene expression after burn injury or trauma-hemorrhage in mice. <i>Physiological Genomics</i> , 2008, 32, 299-310.	2.5	32
53	Interference of globin genes with biomarker discovery for allograft rejection in peripheral blood samples. <i>Physiological Genomics</i> , 2008, 32, 190-197.	2.5	43
54	Involvement of Skeletal Muscle Gene Regulatory Network in Susceptibility to Wound Infection Following Trauma. <i>PLoS ONE</i> , 2007, 2, e1356.	2.3	33

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55	Commonality and differences in leukocyte gene expression patterns among three models of inflammation and injury. <i>Physiological Genomics</i> , 2006, 24, 298-309.	2.5	41
56	PROLONGED CATABOLIC, INFLAMMATORY AND GENOMIC CHANGES IN PEDIATRIC BURN PATIENTS.. <i>Critical Care Medicine</i> , 2006, 34, A9.	0.5	0
57	High Dynamic Range Characterization of the Trauma Patient Plasma Proteome. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 1899-1913.	3.0	145
58	Cell-specific expression and pathway analyses reveal alterations in trauma-related human T cell and monocyte pathways. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 15564-15569.	7.5	109
59	A network-based analysis of systemic inflammation in humans. <i>Nature</i> , 2005, 437, 1032-1037.	37.9	1,462
60	Comparative proteome analyses of human plasma following <i>in vivo</i> lipopolysaccharide administration using multidimensional separations coupled with tandem mass spectrometry. <i>Proteomics</i> , 2005, 5, 572-584.	3.1	127
61	Application of genome-wide expression analysis to human health and disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 4801-4806.	7.5	239
62	Significance analysis of time course microarray experiments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 12837-12842.	7.5	544
63	Quantitative Proteome Analysis of Human Plasma following <i>In Vivo</i> Lipopolysaccharide Administration Using ¹⁶ O/ ¹⁸ O Labeling and the Accurate Mass and Time Tag Approach. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 700-709.	3.0	156
64	Profiling early infection responses: <i>Pseudomonas aeruginosa</i> eludes host defenses by suppressing antimicrobial peptide gene expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 2573-2578.	7.5	161
65	Genomic and Proteomic Determinants of Outcome in Patients Undergoing Thoracoabdominal Aortic Aneurysm Repair. <i>Journal of Immunology</i> , 2004, 172, 7103-7109.	0.6	62
66	Whole blood and leukocyte RNA isolation for gene expression analyses. <i>Physiological Genomics</i> , 2004, 19, 247-254.	2.5	187
67	A Transcriptional Profile of Aging in the Human Kidney. <i>PLoS Biology</i> , 2004, 2, e427.	5.0	299
68	Integrative Analysis of the Mitochondrial Proteome in Yeast. <i>PLoS Biology</i> , 2004, 2, e160.	5.0	184
69	Global Analysis of the Membrane Subproteome of <i>Pseudomonas aeruginosa</i> Using Liquid Chromatography-Tandem Mass Spectrometry. <i>Journal of Proteome Research</i> , 2004, 3, 434-444.	3.4	55
70	Ultra-High-Efficiency Strong Cation Exchange LC/RPLC/MS/MS for High Dynamic Range Characterization of the Human Plasma Proteome. <i>Analytical Chemistry</i> , 2004, 76, 1134-1144.	6.5	296
71	The <i>Drosophila melanogaster</i> Toll Pathway Participates in Resistance to Infection by the Gram-Negative Human Pathogen <i>Pseudomonas aeruginosa</i> . <i>Infection and Immunity</i> , 2003, 71, 4059-4066.	2.7	168
72	Yeast tRNA as Carrier in the Isolation of Microscale RNA for Global Amplification and Expression Profiling. <i>BioTechniques</i> , 2002, 33, 788-796.	6.2	22

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73	Temperature-Modulated Array High-Performance Liquid Chromatography. <i>Genome Research</i> , 2001, 11, 1944-1951.	4.6	23
74	Denaturing high-performance liquid chromatography: A review. <i>Human Mutation</i> , 2001, 17, 439-474.	4.5	685
75	Title is missing!. <i>Nature Structural Biology</i> , 2001, 8, 308-311.	11.0	108
76	Light-induced Rotation of a Transmembrane α -Helix in Bacteriorhodopsin. <i>Journal of Molecular Biology</i> , 2000, 304, 715-721.	4.1	67
77	Design and Characterization of A Synthetic Electron-Transfer Protein. <i>Journal of the American Chemical Society</i> , 2000, 122, 7999-8006.	15.0	52
78	The synaptic SNARE complex is a parallel four-stranded helical bundle. <i>Nature Structural Biology</i> , 1998, 5, 765-769.	11.0	472
79	Patient-reported treatment outcomes in ME/CFS and long COVID. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 0, 122, .	7.5	8