

# Weihong Xu

## List of Publications by Year in descending order

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Version: 2024-02-01

32  
papers

7,895  
citations

304368

22  
h-index

414034

32  
g-index

32  
all docs

32  
docs citations

32  
times ranked

15121  
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	A genomic storm in critically injured humans. Journal of Experimental Medicine, 2011, 208, 2581-2590.	4.2	1,040
3	A comprehensive assessment of RNA-seq accuracy, reproducibility and information content by the Sequencing Quality Control Consortium. Nature Biotechnology, 2014, 32, 903-914.	9.4	883
4	IRE1 <sup>±</sup> Kinase Activation Modes Control Alternate Endoribonuclease Outputs to Determine Divergent Cell Fates. Cell, 2009, 138, 562-575.	13.5	717
5	A long noncoding RNA protects the heart from pathological hypertrophy. Nature, 2014, 514, 102-106.	13.7	672
6	Genome-wide inactivation of porcine endogenous retroviruses (PERVs). Science, 2015, 350, 1101-1104.	6.0	511
7	Comparison of RNA-seq and microarray-based models for clinical endpoint prediction. Genome Biology, 2015, 16, 133.	3.8	325
8	Clinical microfluidics for neutrophil genomics and proteomics. Nature Medicine, 2010, 16, 1042-1047.	15.2	168
9	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
10	Extensive germline genome engineering in pigs. Nature Biomedical Engineering, 2021, 5, 134-143.	11.6	117
11	Genome-wide mapping of ORC and Mcm2p binding sites on tiling arrays and identification of essential ARS consensus sequences in <i>S. cerevisiae</i> . BMC Genomics, 2006, 7, 276.	1.2	106
12	Mice are not men. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E345.	3.3	102
13	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
14	Rad53 regulates replication fork restart after DNA damage in <i>Saccharomyces cerevisiae</i> . Genes and Development, 2008, 22, 1906-1920.	2.7	81
15	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
16	Enrichment of short mutant cell-free DNA fragments enhanced detection of pancreatic cancer. EBioMedicine, 2019, 41, 345-356.	2.7	59
17	Identifiability of isoform deconvolution from junction arrays and RNA-Seq. Bioinformatics, 2009, 25, 3056-3059.	1.8	54
18	A method for high-throughput production of sequence-verified <i>scDNA</i> libraries and strain collections. Molecular Systems Biology, 2017, 13, 913.	3.2	41

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19	Quantitative analysis of protein interaction network dynamics in yeast. <i>Molecular Systems Biology</i> , 2017, 13, 934.	3.2	41
20	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.	1.0	35
21	A functional screen for copper homeostasis genes identifies a pharmacologically tractable cellular system. <i>BMC Genomics</i> , 2014, 15, 263.	1.2	30
22	Downregulation of glutathione S-transferase $\gamma$ 4 (hGSTA4) in the muscle of thermally injured patients is indicative of susceptibility to bacterial infection. <i>FASEB Journal</i> , 2012, 26, 730-737.	0.2	29
23	CaMV 35S Promoter Directs $\beta$ -Glucuronidase Expression in <i>Ganoderma lucidum</i> and <i>Pleurotus citrinopileatus</i> . <i>Molecular Biotechnology</i> , 2002, 20, 239-244.	1.3	20
24	JETTA: junction and exon toolkits for transcriptome analysis. <i>Bioinformatics</i> , 2012, 28, 1274-1275.	1.8	20
25	System-level metabolic modeling facilitates unveiling metabolic signature in exceptional longevity. <i>Aging Cell</i> , 2022, 21, e13595.	3.0	13
26	RASA: Robust Alternative Splicing Analysis for Human Transcriptome Arrays. <i>Scientific Reports</i> , 2015, 5, 11917.	1.6	10
27	Knowledge-Based Reconstruction of mRNA Transcripts with Short Sequencing Reads for Transcriptome Research. <i>PLoS ONE</i> , 2012, 7, e31440.	1.1	7
28	Targeted and Highly Multiplexed Detection of Microorganisms by Employing an Ensemble of Molecular Probes. <i>Applied and Environmental Microbiology</i> , 2014, 80, 4153-4161.	1.4	6
29	Systematic Mapping of Chemical-Genetic Interactions in <i>Saccharomyces cerevisiae</i> . <i>Cold Spring Harbor Protocols</i> , 2016, 2016, pdb.top077701.	0.2	5
30	Identification of Chemical-Genetic Interactions via Parallel Analysis of Barcoded Yeast Strains. <i>Cold Spring Harbor Protocols</i> , 2016, 2016, pdb.prot088054.	0.2	4
31	Community members in activated sludge as determined by molecular probe technology. <i>Water Research</i> , 2020, 168, 115104.	5.3	4
32	Coding SNPs as intrinsic markers for sample tracking in large-scale transcriptome studies. <i>BioTechniques</i> , 2012, 52, 386-8.	0.8	3