

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	System-level metabolic modeling facilitates unveiling metabolic signature in exceptional longevity. <i>Aging Cell</i> , 2022, 21, e13595.	3.0	13
2	Extensive germline genome engineering in pigs. <i>Nature Biomedical Engineering</i> , 2021, 5, 134-143.	11.6	117
3	Community members in activated sludge as determined by molecular probe technology. <i>Water Research</i> , 2020, 168, 115104.	5.3	4
4	Enrichment of short mutant cell-free DNA fragments enhanced detection of pancreatic cancer. <i>EBioMedicine</i> , 2019, 41, 345-356.	2.7	59
5	A method for high-throughput production of sequence-verified <sc>DNA</sc> libraries and strain collections. <i>Molecular Systems Biology</i> , 2017, 13, 913.	3.2	41
6	Quantitative analysis of protein interaction network dynamics in yeast. <i>Molecular Systems Biology</i> , 2017, 13, 934.	3.2	41
7	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
8	Systematic Mapping of Chemical-Genetic Interactions in <i>Saccharomyces cerevisiae</i> . <i>Cold Spring Harbor Protocols</i> , 2016, 2016, pdb.top077701.	0.2	5
9	Comparison of RNA-seq and microarray-based models for clinical endpoint prediction. <i>Genome Biology</i> , 2015, 16, 133.	3.8	325
10	RASA: Robust Alternative Splicing Analysis for Human Transcriptome Arrays. <i>Scientific Reports</i> , 2015, 5, 11917.	1.6	10
11	Genome-wide inactivation of porcine endogenous retroviruses (PERVs). <i>Science</i> , 2015, 350, 1101-1104.	6.0	511
12	Mice are not men. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E345.	3.3	102
13	A long noncoding RNA protects the heart from pathological hypertrophy. <i>Nature</i> , 2014, 514, 102-106.	13.7	672
14	A comprehensive assessment of RNA-seq accuracy, reproducibility and information content by the Sequencing Quality Control Consortium. <i>Nature Biotechnology</i> , 2014, 32, 903-914.	9.4	883
15	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.	3.3	90
16	A functional screen for copper homeostasis genes identifies a pharmacologically tractable cellular system. <i>BMC Genomics</i> , 2014, 15, 263.	1.2	30
17	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
18	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.	3.3	2,518

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19	Downregulation 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.	0.2	29
20	Coding SNPs as intrinsic markers for sample tracking in large-scale transcriptome studies. <i>BioTechniques</i> , 2012, 52, 386-8.	0.8	3
21	JETTA: junction and exon toolkits for transcriptome analysis. <i>Bioinformatics</i> , 2012, 28, 1274-1275.	1.8	20
22	Knowledge-Based Reconstruction of mRNA Transcripts with Short Sequencing Reads for Transcriptome Research. <i>PLoS ONE</i> , 2012, 7, e31440.	1.1	7
23	A genomic storm in critically injured humans. <i>Journal of Experimental Medicine</i> , 2011, 208, 2581-2590.	4.2	1,040
24	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.	3.3	122
25	Clinical microfluidics for neutrophil genomics and proteomics. <i>Nature Medicine</i> , 2010, 16, 1042-1047.	15.2	168
26	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.	3.3	62
27	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
28	Identifiability of isoform deconvolution from junction arrays and RNA-Seq. <i>Bioinformatics</i> , 2009, 25, 3056-3059.	1.8	54
29	IRE1 Kinase Activation Modes Control Alternate Endoribonuclease Outputs to Determine Divergent Cell Fates. <i>Cell</i> , 2009, 138, 562-575.	13.5	717
30	Rad53 regulates replication fork restart after DNA damage in <i>Saccharomyces cerevisiae</i> . <i>Genes and Development</i> , 2008, 22, 1906-1920.	2.7	81
31	Genome-wide mapping of ORC and Mcm2p binding sites on tiling arrays and identification of essential ARS consensus sequences in <i>S. cerevisiae</i> . <i>BMC Genomics</i> , 2006, 7, 276.	1.2	106
32	CaMV 35S Promoter Directs β -Glucuronidase Expression in <i>Ganoderma lucidum</i> and <i>Pleurotus citrinopileatus</i> . <i>Molecular Biotechnology</i> , 2002, 20, 239-244.	1.3	20