Xiu-Jie Wang

List of Publications by Year in descending order

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101384 118652 12,374 66 36 62 citations h-index g-index papers 69 69 69 15120 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	ALKBH5 Is a Mammalian RNA Demethylase that Impacts RNA Metabolism and Mouse Fertility. Molecular Cell, 2013, 49, 18-29.	4.5	2,549
2	Nuclear m 6 A Reader YTHDC1 Regulates mRNA Splicing. Molecular Cell, 2016, 61, 507-519.	4.5	1,432
3	FTO-dependent demethylation of N6-methyladenosine regulates mRNA splicing and is required for adipogenesis. Cell Research, 2014, 24, 1403-1419.	5.7	869
4	GOEAST: a web-based software toolkit for Gene Ontology enrichment analysis. Nucleic Acids Research, 2008, 36, W358-W363.	6.5	569
5	ETCM: an encyclopaedia of traditional Chinese medicine. Nucleic Acids Research, 2019, 47, D976-D982.	6.5	507
6	m6A RNA Methylation Is Regulated by MicroRNAs and Promotes Reprogramming to Pluripotency. Cell Stem Cell, 2015, 16, 289-301.	5.2	483
7	PsRobot: a web-based plant small RNA meta-analysis toolbox. Nucleic Acids Research, 2012, 40, W22-W28.	6.5	448
8	Distinct catalytic and non-catalytic roles of ARGONAUTE4 in RNA-directed DNA methylation. Nature, 2006, 443, 1008-1012.	13.7	416
9	Widespread Long Noncoding RNAs as Endogenous Target Mimics for MicroRNAs in Plants Â. Plant Physiology, 2013, 161, 1875-1884.	2.3	400
10	N6-Methyl-Adenosine (m6A) in RNA: An Old Modification with A Novel Epigenetic Function. Genomics, Proteomics and Bioinformatics, 2013 , 11 , 8 - 17 .	3.0	368
11	A complex system of small RNAs in the unicellular green alga Chlamydomonas reinhardtii. Genes and Development, 2007, 21, 1190-1203.	2.7	367
12	Comprehensive comparison of Pacific Biosciences and Oxford Nanopore Technologies and their applications to transcriptome analysis. F1000Research, 2017, 6, 100.	0.8	366
13	Potential inhibitors against 2019-nCoV coronavirus M protease from clinically approved medicines. Journal of Genetics and Genomics, 2020, 47, 119-121.	1.7	331
14	Mettl3-mediated m6A regulates spermatogonial differentiation and meiosis initiation. Cell Research, 2017, 27, 1100-1114.	5.7	306
15	Roles of DCL4 and DCL3b in rice phased small RNA biogenesis. Plant Journal, 2012, 69, 462-474.	2.8	289
16	Activation of the Imprinted Dlk1-Dio3 Region Correlates with Pluripotency Levels of Mouse Stem Cells. Journal of Biological Chemistry, 2010, 285, 19483-19490.	1.6	253
17	Genome-wide prediction and identification of cis-natural antisense transcripts in Arabidopsis thaliana. Genome Biology, 2005, 6, R30.	13.9	240
18	METTL3-mediated m6A modification is required for cerebellar development. PLoS Biology, 2018, 16, e2004880.	2.6	216

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19	Combining metabolomics and transcriptomics to characterize tanshinone biosynthesis in Salvia miltiorrhiza. BMC Genomics, 2014, 15, 73.	1.2	165
20	METTL3-mediated N6-methyladenosine mRNA modification enhances long-term memory consolidation. Cell Research, 2018, 28, 1050-1061.	5.7	146
21	Direct reprogramming of Sertoli cells into multipotent neural stem cells by defined factors. Cell Research, 2012, 22, 208-218.	5.7	135
22	Deep sequencing of small RNAs specifically associated with Arabidopsis AGO1 and AGO4 uncovers new AGO functions. Plant Journal, 2011, 67, 292-304.	2.8	114
23	Small RNA Profiling in Two <i>Brassica napus</i> Cultivars Identifies MicroRNAs with Oil Productionand Development-Correlated Expression and New Small RNA Classes Â. Plant Physiology, 2012, 158, 813-823.	2.3	111
24	Geminivirus-encoded TrAP suppressor inhibits the histone methyltransferase SUVH4/KYP to counter host defense. ELife, 2015, 4, e06671.	2.8	92
25	Mir-24 Regulates Junctophilin-2 Expression in Cardiomyocytes. Circulation Research, 2012, 111, 837-841.	2.0	87
26	Genetic Modification and Screening in Rat Using Haploid Embryonic Stem Cells. Cell Stem Cell, 2014, 14, 404-414.	5.2	85
27	In Vivo Suppression of MicroRNA-24 Prevents the Transition Toward Decompensated Hypertrophy in Aortic-Constricted Mice. Circulation Research, 2013, 112, 601-605.	2.0	84
28	MED25 connects enhancer–promoter looping and MYC2-dependent activation of jasmonate signalling. Nature Plants, 2019, 5, 616-625.	4.7	82
29	Conserved miRNA analysis in Gossypium hirsutum through small RNA sequencing. Genomics, 2009, 94, 263-268.	1.3	79
30	Prediction of trans-antisense transcripts in Arabidopsis thaliana. Genome Biology, 2006, 7, R92.	13.9	72
31	Arabidopsis AGO3 predominantly recruits 24-nt small RNAs to regulate epigenetic silencing. Nature Plants, 2016, 2, 16049.	4.7	64
32	Differentiated regulation of immune-response related genes between LUAD and LUSC subtypes of lung cancers. Oncotarget, 2017, 8, 133-144.	0.8	54
33	Sequential de novo centromere formation and inactivation on a chromosomal fragment in maize. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E1263-E1271.	3.3	46
34	Generation and Application of Mouse-Rat Allodiploid Embryonic Stem Cells. Cell, 2016, 164, 279-292.	13.5	46
35	IDP-ASE: haplotyping and quantifying allele-specific expression at the gene and gene isoform level by hybrid sequencing. Nucleic Acids Research, 2017, 45, e32-e32.	6.5	42
36	Birth of fertile bimaternal offspring following intracytoplasmic injection of parthenogenetic haploid embryonic stem cells. Cell Research, 2016, 26, 135-138.	5.7	40

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37	Perivascular adipose tissueâ€derived stromal cells contribute to vascular remodeling during aging. Aging Cell, 2019, 18, e12969.	3.0	40
38	Mice generated from tetraploid complementation competent iPS cells show similar developmental features as those from ES cells but are prone to tumorigenesis. Cell Research, 2011, 21, 1634-1637.	5.7	39
39	Genome-wide annotation and analysis of zebra finch microRNA repertoire reveal sex-biased expression. BMC Genomics, 2012, 13, 727.	1.2	39
40	Accurate and fast cell marker gene identification with COSG. Briefings in Bioinformatics, 2022, 23, .	3.2	39
41	Ubiquitously expressed genes participate in cellâ€specific functions via alternative promoter usage. EMBO Reports, 2016, 17, 1304-1313.	2.0	26
42	Endogenous Small RNA Clusters in Plants. Genomics, Proteomics and Bioinformatics, 2014, 12, 64-71.	3.0	24
43	Dynamic chromatin changes associated with <i>de novo</i> centromere formation in maize euchromatin. Plant Journal, 2016, 88, 854-866.	2.8	23
44	Inhibition of endoplasmic reticulum stress by intermedin1-53 attenuates angiotensin Il–induced abdominal aortic aneurysm in ApoE KO Mice. Endocrine, 2018, 62, 90-106.	1.1	22
45	A multi-axis robot-based bioprinting system supporting natural cell function preservation and cardiac tissue fabrication. Bioactive Materials, 2022, 18, 138-150.	8.6	21
46	Durable pluripotency and haploidy in epiblast stem cells derived from haploid embryonic stem cellsin vitro. Journal of Molecular Cell Biology, 2015, 7, 326-337.	1.5	19
47	Bioinformatic analysis of microRNA biogenesis and function related proteins in eleven animal genomes. Journal of Genetics and Genomics, 2009, 36, 591-601.	1.7	16
48	Dynamic and Coordinated Expression Changes of Rice Small RNAs in Response to Xanthomonas oryzae pv. oryzae. Journal of Genetics and Genomics, 2015, 42, 625-637.	1.7	16
49	An Integrative Analysis of the Effects of Auxin on Jasmonic Acid Biosynthesis in Arabidopsis thaliana. Journal of Integrative Plant Biology, 2006, 48, 99-103.	4.1	14
50	Identification and Characterization of Small RNAs in the Hyperthermophilic Archaeon Sulfolobus solfataricus. PLoS ONE, 2012, 7, e35306.	1.1	14
51	A non-invasive method to determine the pluripotent status of stem cells by culture medium microRNA expression detection. Scientific Reports, 2016, 6, 22380.	1.6	14
52	Novel roles of an intragenic G-quadruplex in controlling microRNA expression and cardiac function. Nucleic Acids Research, 2021, 49, 2522-2536.	6.5	14
53	ISRNA: an integrative online toolkit for short reads from high-throughput sequencing data. Bioinformatics, 2014, 30, 434-436.	1.8	9
54	Evolutionary and Functional Analysis of the Key Pluripotency Factor Oct4 and Its Family Proteins. Journal of Genetics and Genomics, 2013, 40, 399-412.	1.7	7

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55	Long noncoding RNA <i>lnc-NAP</i> sponges mmu-miR-139-5p to modulate <i>Nanog</i> functions in mouse ESCs and embryos. RNA Biology, 2021, 18, 875-887.	1.5	6
56	Influence of feeder cells on transcriptomic analysis of pluripotent stem cells. Cell Proliferation, 2022, 55, e13189.	2.4	6
57	Rising from Ashes: Non-Coding RNAs Come of Age. Journal of Genetics and Genomics, 2013, 40, 141-142.	1.7	3
58	Dynamic transcriptome landscape in the song nucleus HVC between juvenile and adult zebra finches. Genetics & Genomics Next, 2021, 2, e10035.	0.8	3
59	Intermedin1–53 Inhibits NLRP3 Inflammasome Activation by Targeting IRE1α in Cardiac Fibrosis. Inflammation, 2022, 45, 1568-1584.	1.7	3
60	Bioinformaticians wrestling with the big biomedical data. Journal of Genetics and Genomics, 2017, 44, 223-225.	1.7	2
61	Early transcriptomic profiling variation caused by cluster allergen immunotherapy. Chinese Medical Journal, 2020, 133, 1366-1368.	0.9	1
62	Stinging Insect Allergens. Current Protein and Peptide Science, 2020, 21, 142-152.	0.7	1
63	Regulation beyond genome sequences: DNA and histone methylation in embryonic stem cells. Frontiers in Biology, 2010, 5, 41-47.	0.7	0
64	Bayesian networks: a powerful tool for systems biology study. Frontiers in Biology, 2010, 5, 95-96.	0.7	0
65	Omics tools for the needle out of haystack?. Journal of Genetics and Genomics, 2018, 45, 343-344.	1.7	0
66	Identification of dysregulated microRNAs involved in arachidonic acid metabolism regulation in dilated cardiomyopathy-mediated heart failure patients. Acta Physiologica Sinica, 2021, 73, 584-596.	0.5	0