

Jixian Zhai

List of Publications by Year in descending order

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77
papers

10,448
citations

50276

46
h-index

71685

76
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91
all docs

91
docs citations

91
times ranked

12126
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome sequencing and analysis of the model grass <i>Brachypodium distachyon</i> . <i>Nature</i> , 2010, 463, 763-768.	27.8	1,685
2	The <i>Medicago</i> genome provides insight into the evolution of rhizobial symbioses. <i>Nature</i> , 2011, 480, 520-524.	27.8	1,166
3	The <i>Amborella</i> Genome and the Evolution of Flowering Plants. <i>Science</i> , 2013, 342, 1241089.	12.6	743
4	MicroRNAs as master regulators of the plant <i>NB-LRR</i> defense gene family via the production of phased, <i>trans</i> -acting siRNAs. <i>Genes and Development</i> , 2011, 25, 2540-2553.	5.9	668
5	Massive Analysis of Rice Small RNAs: Mechanistic Implications of Regulated MicroRNAs and Variants for Differential Target RNA Cleavage. <i>Plant Cell</i> , 2011, 23, 4185-4207.	6.6	341
6	miRNAs trigger widespread epigenetically activated siRNAs from transposons in <i>Arabidopsis</i> . <i>Nature</i> , 2014, 508, 411-415.	27.8	331
7	Spatiotemporally dynamic, cell-type-dependent premeiotic and meiotic phasiRNAs in maize anthers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 3146-3151.	7.1	310
8	Roles of DCL4 and DCL3b in rice phased small RNA biogenesis. <i>Plant Journal</i> , 2012, 69, 462-474.	5.7	289
9	Genome-wide Hi-C Analyses in Wild-Type and Mutants Reveal High-Resolution Chromatin Interactions in <i>Arabidopsis</i> . <i>Molecular Cell</i> , 2014, 55, 694-707.	9.7	283
10	A One Precursor One siRNA Model for Pol IV-Dependent siRNA Biogenesis. <i>Cell</i> , 2015, 163, 445-455.	28.9	260
11	Widespread long-range cis-regulatory elements in the maize genome. <i>Nature Plants</i> , 2019, 5, 1237-1249.	9.3	250
12	The <i>Arabidopsis</i> Nucleotidyl Transferase HESO1 Uridylates Unmethylated Small RNAs to Trigger Their Degradation. <i>Current Biology</i> , 2012, 22, 689-694.	3.9	187
13	Dicer-like 3 produces transposable element-associated 24-nt siRNAs that control agricultural traits in rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 3877-3882.	7.1	181
14	A <i>Phytophthora</i> Effector Suppresses Trans-Kingdom RNAi to Promote Disease Susceptibility. <i>Cell Host and Microbe</i> , 2019, 25, 153-165.e5.	11.0	173
15	An Atlas of Soybean Small RNAs Identifies Phased siRNAs from Hundreds of Coding Genes. <i>Plant Cell</i> , 2014, 26, 4584-4601.	6.6	163
16	SDG714, a Histone H3K9 Methyltransferase, Is Involved in Tos17 DNA Methylation and Transposition in Rice. <i>Plant Cell</i> , 2007, 19, 9-22.	6.6	162
17	CG gene body DNA methylation changes and evolution of duplicated genes in cassava. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13729-13734.	7.1	129
18	Distinct and Cooperative Activities of HESO1 and URT1 Nucleotidyl Transferases in MicroRNA Turnover in <i>Arabidopsis</i> . <i>PLoS Genetics</i> , 2015, 11, e1005119.	3.5	125

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19	Roles of small <sc>RNA</sc>s in soybean defense against <i><sc>P</sc>hytophthora sojae</i> infection. <i>Plant Journal</i> , 2014, 79, 928-940.	5.7	122
20	Short-Read Sequencing Technologies for Transcriptional Analyses. <i>Annual Review of Plant Biology</i> , 2009, 60, 305-333.	18.7	118
21	Plant MicroRNAs Display Differential 3' Truncation and Tailing Modifications That Are ARGONAUTE1 Dependent and Conserved Across Species. <i>Plant Cell</i> , 2013, 25, 2417-2428.	6.6	113
22	Small RNA-Directed Epigenetic Natural Variation in <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2008, 4, e1000056.	3.5	112
23	Plant 22-nt siRNAs mediate translational repression and stress adaptation. <i>Nature</i> , 2020, 581, 89-93.	27.8	112
24	Multiple RNA recognition patterns during microRNA biogenesis in plants. <i>Genome Research</i> , 2013, 23, 1675-1689.	5.5	110
25	RNA-directed DNA methylation involves co-transcriptional small-RNA-guided slicing of polymerase V transcripts in <i>Arabidopsis</i> . <i>Nature Plants</i> , 2018, 4, 181-188.	9.3	106
26	A Comprehensive Online Database for Exploring ~1420,000 Public <i>Arabidopsis</i> RNA-Seq Libraries. <i>Molecular Plant</i> , 2020, 13, 1231-1233.	8.3	103
27	Mutations in the Type II Protein Arginine Methyltransferase AtPRMT5 Result in Pleiotropic Developmental Defects in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2007, 144, 1913-1923.	4.8	99
28	Distinct extremely abundant siRNAs associated with cosuppression in petunia. <i>Rna</i> , 2009, 15, 1965-1970.	3.5	93
29	Rapid construction of parallel analysis of RNA end (PARE) libraries for Illumina sequencing. <i>Methods</i> , 2014, 67, 84-90.	3.8	89
30	Post-transcriptional splicing of nascent RNA contributes to widespread intron retention in plants. <i>Nature Plants</i> , 2020, 6, 780-788.	9.3	87
31	DNA methylome of the 20-gigabase Norway spruce genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E8106-E8113.	7.1	85
32	Biogenesis and function of rice small RNAs from non-coding RNA precursors. <i>Current Opinion in Plant Biology</i> , 2013, 16, 170-179.	7.1	83
33	Identification of micro RNA s and their mRNA targets during soybean nodule development: functional analysis of the role of miR393 in soybean nodulation. <i>New Phytologist</i> , 2015, 207, 748-759.	7.3	82
34	ARGONAUTE10 promotes the degradation of miR165/6 through the SDN1 and SDN2 exonucleases in <i>Arabidopsis</i> . <i>PLoS Biology</i> , 2017, 15, e2001272.	5.6	81
35	The Ca ²⁺ /calmodulin-binding transcription factor TGA3 elevates <sc>LCD</sc> expression and H ₂ S production to bolster Cr ⁶⁺ tolerance in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2017, 91, 1038-1050.	5.7	79
36	Conservation and divergence in eukaryotic DNA methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 9027-9028.	7.1	76

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37	MS23, a master basic helix-loop-helix factor, regulates the specification and development of tapetum in maize. <i>Development (Cambridge)</i> , 2017, 144, 163-172.	2.5	71
38	RNA polymerase V-dependent small RNAs in Arabidopsis originate from small, intergenic loci including most SINE repeats. <i>Epigenetics</i> , 2012, 7, 781-795.	2.7	69
39	Parallel analysis of RNA ends enhances global investigation of microRNAs and target RNAs of <i>Brachypodium distachyon</i> . <i>Genome Biology</i> , 2013, 14, R145.	9.6	67
40	FlsRNA-seq: protoplasting-free full-length single-nucleus RNA profiling in plants. <i>Genome Biology</i> , 2021, 22, 66.	8.8	66
41	sRNAanno—a database repository of uniformly annotated small RNAs in plants. <i>Horticulture Research</i> , 2021, 8, 45.	6.3	63
42	Comprehensive Investigation of MicroRNAs Enhanced by Analysis of Sequence Variants, Expression Patterns, ARGONAUTE Loading, and Target Cleavage. <i>Plant Physiology</i> , 2013, 162, 1225-1245.	4.8	61
43	MTHFD1 controls DNA methylation in Arabidopsis. <i>Nature Communications</i> , 2016, 7, 11640.	12.8	61
44	siRNAs compete with miRNAs for methylation by HEN1 in Arabidopsis. <i>Nucleic Acids Research</i> , 2010, 38, 5844-5850.	14.5	59
45	Mechanism of siRNA production by a plant Dicer-RNA complex in dicing-competent conformation. <i>Science</i> , 2021, 374, 1152-1157.	12.6	58
46	ROR1/RPA2A, a Putative Replication Protein A2, Functions in Epigenetic Gene Silencing and in Regulation of Meristem Development in Arabidopsis. <i>Plant Cell</i> , 2005, 18, 85-103.	6.6	57
47	Plant Public RNA-seq Database: a comprehensive online database for expression analysis of ~45%000 plant public RNA-seq libraries. <i>Plant Biotechnology Journal</i> , 2022, 20, 806-808.	8.3	53
48	Large-scale comparative epigenomics reveals hierarchical regulation of non-CG methylation in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E1069-E1074.	7.1	51
49	Physiological stressors and invasive plant infections alter the small RNA transcriptome of the rice blast fungus, <i>Magnaporthe oryzae</i> . <i>BMC Genomics</i> , 2013, 14, 326.	2.8	49
50	Highly efficient gene silencing using perfect complementary artificial miRNA targeting AP1 or heteromeric artificial miRNA targeting AP1 and CAL genes. <i>Plant Cell Reports</i> , 2009, 28, 469-480.	5.6	43
51	Identification and functional characterization of soybean root hair microRNA expressed in response to <i>Bacteroides japonicum</i> infection. <i>Plant Biotechnology Journal</i> , 2016, 14, 332-341.	8.3	40
52	5'-directed cleavage and nonstoichiometric abundances of 21-nucleotide reproductive phased small interfering RNA in grasses. <i>New Phytologist</i> , 2018, 220, 865-877.	7.3	38
53	Soybean DICER-LIKE2 Regulates Seed Coat Color via Production of Primary 22-Nucleotide Small Interfering RNAs from Long Inverted Repeats. <i>Plant Cell</i> , 2020, 32, 3662-3673.	6.6	35
54	Coordination of MicroRNAs, PhasiRNAs, and NB-CLRR Genes in Response to a Plant Pathogen: Insights from Analyses of a Set of Soybean Rps Gene Near-Linkage Lines. <i>Plant Genome</i> , 2015, 8, eplantgenome2014.09.0044.	2.8	31

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55	MicroRNA482/2118, a miRNA superfamily essential for both disease resistance and plant development. <i>New Phytologist</i> , 2022, 233, 2047-2057.	7.3	29
56	Small RNAs in Plant Immunity and Virulence of Filamentous Pathogens. <i>Annual Review of Phytopathology</i> , 2021, 59, 265-288.	7.8	27
57	FLEP-seq: simultaneous detection of RNA polymerase II position, splicing status, polyadenylation site and poly(A) tail length at genome-wide scale by single-molecule nascent RNA sequencing. <i>Nature Protocols</i> , 2021, 16, 4355-4381.	12.0	24
58	The characterization of Mediator 12 and 13 as conditional positive gene regulators in Arabidopsis. <i>Nature Communications</i> , 2020, 11, 2798.	12.8	22
59	An Online Database for Exploring Over 2,000 Arabidopsis Small RNA Libraries. <i>Plant Physiology</i> , 2020, 182, 685-691.	4.8	19
60	The antagonistic MYB paralogs <i>RH1</i> and <i>RH2</i> govern anthocyanin leaf markings in <i>Medicago truncatula</i> . <i>New Phytologist</i> , 2021, 229, 3330-3344.	7.3	18
61	Substrate deformation regulates DRM2-mediated DNA methylation in plants. <i>Science Advances</i> , 2021, 7, .	10.3	15
62	MicroRNA Processing: Battle of the Bulge. <i>Current Biology</i> , 2010, 20, R68-R70.	3.9	14
63	Multiplex CRISPR-Cas9 editing of DNA methyltransferases in rice uncovers a class of non-CG methylation specific for GC-rich regions. <i>Plant Cell</i> , 2021, 33, 2950-2964.	6.6	13
64	Landscape of transcription termination in Arabidopsis revealed by single-molecule nascent RNA sequencing. <i>Genome Biology</i> , 2021, 22, 322.	8.8	13
65	The Dynamic Kaleidoscope of RNA Biology in Plants. <i>Plant Physiology</i> , 2020, 182, 1-9.	4.8	11
66	Construction of Specific Parallel Amplification of RNA Ends (SPARE) libraries for the systematic identification of plant microRNA processing intermediates. <i>Methods</i> , 2013, 64, 283-291.	3.8	10
67	Characteristics and processing of Pol IV-dependent transcripts in Arabidopsis. <i>Journal of Genetics and Genomics</i> , 2017, 44, 3-6.	3.9	9
68	Deep Sequencing from hen1 Mutants to Identify Small RNA 3' Modifications. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2012, 77, 213-219.	1.1	8
69	The Cornucopia of Small RNAs in Plant Genomes. <i>Rice</i> , 2008, 1, 52-62.	4.0	7
70	Pore-C simultaneously captures genome-wide multi-way chromatin interaction and associated DNA methylation status in Arabidopsis. <i>Plant Biotechnology Journal</i> , 2022, 20, 1009-1011.	8.3	7
71	Solitary fibrous tumor of the abdominal wall re-surfacing as unilateral pleural effusion and mass: A case report and review of the literature. <i>Respiratory Medicine Case Reports</i> , 2018, 23, 4-7.	0.4	4
72	Regulation of DNA Methylation During Plant Endosperm Development. <i>Frontiers in Genetics</i> , 2022, 13, 760690.	2.3	4

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73	Induced Mutation in GmCOP1b Enhances the Performance of Soybean under Dense Planting Conditions. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5394.	4.1	4
74	The chromatin will never forget. <i>Nature Plants</i> , 2020, 6, 1396-1397.	9.3	1
75	A SYBR Gold-based Label-free in vitro Dicing Assay. <i>Bio-protocol</i> , 2022, 12, e4382.	0.4	1
76	Reprint of: Construction of Specific Parallel Amplification of RNA Ends (SPARE) libraries for the systematic identification of plant microRNA processing intermediates. <i>Methods</i> , 2014, 67, 36-44.	3.8	0
77	Safeguard DCL2-Dependent 22-nt siRNA generation by DCL1. <i>Biochemical and Biophysical Research Communications</i> , 2022, 605, 97-103.	2.1	0