Xiaofeng Cao

List of Publications by Year
in descending order

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95	9,951	46984 47	38368 95
papers	citations	h-index	g-index

97	97	97	9116
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Requirement of CHROMOMETHYLASE3 for Maintenance of CpXpG Methylation. Science, 2001, 292, 2077-2080.	6.0	820
2	Role of the Arabidopsis DRM Methyltransferases in De Novo DNA Methylation and Gene Silencing. Current Biology, 2002, 12, 1138-1144.	1.8	679
3	Histone Methylation in Higher Plants. Annual Review of Plant Biology, 2010, 61, 395-420.	8.6	526
4	Locus-specific control of asymmetric and CpNpG methylation by the DRM and CMT3 methyltransferase genes. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 16491-16498.	3.3	511
5	Role of the DRM and CMT3 Methyltransferases in RNA-Directed DNA Methylation. Current Biology, 2003, 13, 2212-2217.	1.8	462
6	MicroRNAs and Their Regulatory Roles in Plantâ€“Environment Interactions. Annual Review of Plant Biology, 2019, 70, 489-525.	8.6	454
7	MicroRNAs Inhibit the Translation of Target mRNAs on the Endoplasmic Reticulum in Arabidopsis. Cell, 2013, 153, 562-574.	13.5	451
8	Arabidopsis REF6 is a histone H3 lysine 27 demethylase. Nature Genetics, 2011, 43, 715-719.	9.4	351
9	Roles of DCL4 and DCL3b in rice phased small RNA biogenesis. Plant Journal, 2012, 69, 462-474.	2.8	289
10	Epigenetic reprogramming that prevents transgenerational inheritance of the vernalized state. Nature, 2014, 515, 587-590.	13.7	227
11	Concerted genomic targeting of H3K27 demethylase REF6 and chromatin-remodeling ATPase BRM in Arabidopsis. Nature Genetics, 2016, 48, 687-693.	9.4	193
12	ROS accumulation and antiviral defence control by microRNA528 in rice. Nature Plants, 2017, 3, 16203.	4.7	189
13	Comparative Analysis of JmjC Domainâ€containing Proteins Reveals the Potential Histone Demethylases in Arabidopsis and Rice. Journal of Integrative Plant Biology, 2008, 50, 886-896.	4.1	178
14	RNase ZS1 processes UbL40 mRNAs and controls thermosensitive genic male sterility in rice. Nature Communications, 2014, 5, 4884.	5.8	177
15	Arginine methylation mediated by the Arabidopsis homolog of PRMT5 is essential for proper pre-mRNA splicing. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 19114-19119.	3.3	174
16	<scp>ABI</scp>4 mediates antagonistic effects of abscisic acid and gibberellins at transcript and protein levels. Plant Journal, 2016, 85, 348-361.	2.8	164
17	JMJ14 is an H3K4 demethylase regulating flowering time in Arabidopsis. Cell Research, 2010, 20, 387-390.	5.7	154
18	Degradome sequencing reveals endogenous small RNA targets in rice (Oryza sativa L. ssp. indica). Frontiers in Biology, 2010, 5, 67-90.	0.7	152

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19	Mutation of a major CG methylase in rice causes genome-wide hypomethylation, dysregulated genome expression, and seedling lethality. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 10642-10647.	3.3	149
20	An H3K27me3 demethylase-HSFA2 regulatory loop orchestrates transgenerational thermomemory in Arabidopsis. Cell Research, 2019, 29, 379-390.	5.7	149
21	REF6 recognizes a specific DNA sequence to demethylate H3K27me3 and regulate organ boundary formation in Arabidopsis. Nature Genetics, 2016, 48, 694-699.	9.4	148
22	NOT2 Proteins Promote Polymerase IIâ€“Dependent Transcription and Interact with Multiple MicroRNA Biogenesis Factors in Arabidopsis Â Â. Plant Cell, 2013, 25, 715-727.	3.1	147
23	Oryza sativa Dicer-like4Reveals a Key Role for Small Interfering RNA Silencing in Plant Development. Plant Cell, 2007, 19, 2705-2718.	3.1	136
24	Integrated analysis of phenome, genome, and transcriptome of hybrid rice uncovered multiple heterosis-related loci for yield increase. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E6026-E6035.	3.3	126
25	<scp>WRKY</scp>71 accelerates flowering via the direct activation of <scp>FLOWERING LOCUS</scp> T and <scp>LEAFY</scp> in Arabidopsis thaliana. Plant Journal, 2016, 85, 96-106.	2.8	113
26	Nitric Oxide Regulates Protein Methylation during Stress Responses in Plants. Molecular Cell, 2017, 67, 702-710.e4.	4.5	104
27	Control of transposon activity by a histone H3K4 demethylase in rice. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 1953-1958.	3.3	100
28	Mutations in the Type II Protein Arginine Methyltransferase AtPRMT5 Result in Pleiotropic Developmental Defects in Arabidopsis. Plant Physiology, 2007, 144, 1913-1923.	2.3	99
29	Rice RNAâ€dependent RNA polymerase 6 acts in small RNA biogenesis and spikelet development. Plant Journal, 2012, 71, 378-389.	2.8	98
30	The Arabidopsis H3K27me3 demethylase JUMONJI 13 is a temperature and photoperiod dependent flowering repressor. Nature Communications, 2019, 10, 1303.	5.8	98
31	Involvement of the Histone Acetyltransferase AtHAC1 in the Regulation of Flowering Time via Repression of FLOWERING LOCUS C in Arabidopsis. Plant Physiology, 2007, 143, 1660-1668.	2.3	97
32	Integrative genome-wide analysis reveals HLP1, a novel RNA-binding protein, regulates plant flowering by targeting alternative polyadenylation. Cell Research, 2015, 25, 864-876.	5.7	94
33	Epigenetic Mutation of RAV6 Affects Leaf Angle and Seed Size in Rice Â. Plant Physiology, 2015, 169, 2118-2128.	2.3	94
34	The Histone H3K4 Demethylase JMJ16 Represses Leaf Senescence in Arabidopsis. Plant Cell, 2019, 31, 430-443.	3.1	89
35	An engineered prime editor with enhanced editing efficiency in plants. Nature Biotechnology, 2022, 40, 1394-1402.	9.4	89
36	Post-transcriptional splicing of nascent RNA contributes to widespread intron retention in plants. Nature Plants, 2020, 6, 780-788.	4.7	87

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37	ARGONAUTE10 promotes the degradation of miR165/6 through the SDN1 and SDN2 exonucleases in Arabidopsis. PLoS Biology, 2017, 15, e2001272.	2.6	81
38	RNA Binding Proteins RZ-1B and RZ-1C Play Critical Roles in Regulating Pre-mRNA Splicing and Gene Expression during Development in Arabidopsis. Plant Cell, 2016, 28, 55-73.	3.1	79
39	RNA G-quadruplex structures exist and function in vivo in plants. Genome Biology, 2020, 21, 226.	3.8	75
40	CPSF30-L-mediated recognition of mRNA m6A modification controls alternative polyadenylation of nitrate signaling-related gene transcripts in Arabidopsis. Molecular Plant, 2021, 14, 688-699.	3.9	75
41	Roles of pre-mRNA splicing and polyadenylation in plant development. Current Opinion in Plant Biology, 2017, 35, 45-53.	3.5	74
42	Transcriptional Regulation of miR528 by OsSPL9 Orchestrates Antiviral Response in Rice. Molecular Plant, 2019, 12, 1114-1122.	3.9	73
43	Arabidopsis protein arginine methyltransferase 3 is required for ribosome biogenesis by affecting precursor ribosomal RNA processing. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 16190-16195.	3.3	68
44	Fine-Tuning of MiR528 Accumulation Modulates Flowering Time in Rice. Molecular Plant, 2019, 12, 1103-1113.	3.9	67
45	Transposon-mediated epigenetic regulation contributes to phenotypic diversity and environmental adaptation in rice. Current Opinion in Plant Biology, 2017, 36, 111-118.	3.5	61
46	Epigenetic regulation and functional exaptation of transposable elements in higher plants. Current Opinion in Plant Biology, 2014, 21, 83-88.	3.5	59
47	The effect of transposable elements on phenotypic variation: insights from plants to humans. Science China Life Sciences, 2016, 59, 24-37.	2.3	58
48	DNA methylation repels targeting of Arabidopsis REF6. Nature Communications, 2019, 10, 2063.	5.8	53
49	Impact of poly(A)-tail G-content on Arabidopsis PAB binding and their role in enhancing translational efficiency. Genome Biology, 2019, 20, 189.	3.8	49
50	C-terminal domains of histone demethylase JMJ14 interact with a pair of NAC transcription factors to mediate specific chromatin association. Cell Discovery, 2015, 1, .	3.1	47
51	Rice InÂVivo RNA Structurome Reveals RNA Secondary Structure Conservation and Divergence in Plants. Molecular Plant, 2018, 11, 607-622.	3.9	46
52	Ribosomal RNA Biogenesis and Its Response to Chilling Stress in Oryza sativa. Plant Physiology, 2018, 177, 381-397.	2.3	46
53	Recruitment of the NineTeen Complex to the activated spliceosome requires AtPRMT5. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 5447-5452.	3.3	45
54	Retrospective and perspective of plant epigenetics in China. Journal of Genetics and Genomics, 2018, 45, 621-638.	1.7	45

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55	Histone methylation in epigenetic regulation and temperature responses. Current Opinion in Plant Biology, 2021, 61, 102001.	3.5	44
56	Plant PRMTs Broaden the Scope of Arginine Methylation. Journal of Genetics and Genomics, 2012, 39, 195-208.	1.7	43
57	Epigenetic regulation and epigenomic landscape in rice. National Science Review, 2016, 3, 309-327.	4.6	41
58	Structure of the Arabidopsis JMJ14-H3K4me3 Complex Provides Insight into the Substrate Specificity of KDM5 Subfamily Histone Demethylases. Plant Cell, 2018, 30, 167-177.	3.1	40
59	COR27 and COR28 encode nighttime repressors integrating Arabidopsis circadian clock and cold response. Journal of Integrative Plant Biology, 2017, 59, 78-85.	4.1	39
60	The ATPase hCINAP regulates 18S rRNA processing and is essential for embryogenesis and tumour growth. Nature Communications, 2016, 7, 12310.	5.8	36
61	An epiallele of rice AK1 affects photosynthetic capacity. Journal of Integrative Plant Biology, 2017, 59, 158-163.	4.1	32
62	The seekers: how epigenetic modifying enzymes find their hidden genomic targets in Arabidopsis. Current Opinion in Plant Biology, 2018, 45, 75-81.	3.5	32
63	Noncoding RNA: from dark matter to bright star. Science China Life Sciences, 2020, 63, 463-468.	2.3	32
64	TarHunter, a tool for predicting conserved microRNA targets and target mimics in plants. Bioinformatics, 2018, 34, 1574-1576.	1.8	29
65	FIERY1 promotes microRNA accumulation by suppressing rRNA-derived small interfering RNAs in Arabidopsis. Nature Communications, 2019, 10, 4424.	5.8	28
66	Developmental Cytoplasmic-to-Nuclear Translocation of RNA-Binding Protein HuR Is Required for Adult Neurogenesis. Cell Reports, 2019, 29, 3101-3117.e7.	2.9	26
67	Extensive profiling of the expressions of tRNAs and tRNA-derived fragments (tRFs) reveals the complexities of tRNA and tRF populations in plants. Science China Life Sciences, 2021, 64, 495-511.	2.3	23
68	DEAD-BOX RNA HELICASE 27 regulates microRNA biogenesis, zygote division, and stem cell homeostasis. Plant Cell, 2021, 33, 66-84.	3.1	23
69	Whole genome sequencing of cottonâ€”a new chapter in cotton genomics. Science China Life Sciences, 2015, 58, 515-516.	2.3	20
70	The histone H3K27 demethylase REF6/JMJ12 promotes thermomorphogenesis in Arabidopsis. National Science Review, 2022, 9, nwab213.	4.6	20
71	Trip to ER. RNA Biology, 2013, 10, 1586-1592.	1.5	16
72	Plant transfer RNAâ€derived fragments: Biogenesis and functions. Journal of Integrative Plant Biology, 2021, 63, 1399-1409.	4.1	16

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73	Drosophila Homolog of FMRP Maintains Genome Integrity by Interacting with Piwi. Journal of Genetics and Genomics, 2016, 43, 11-24.	1.7	15
74	Modulation of Auxin Signaling and Development by Polyadenylation Machinery. Plant Physiology, 2019, 179, 686-699.	2.3	15
75	Cell-type-dependent histone demethylase specificity promotes meiotic chromosome condensation in Arabidopsis. Nature Plants, 2020, 6, 823-837.	4.7	13
76	Landscape of transcription termination in Arabidopsis revealed by single-molecule nascent RNA sequencing. Genome Biology, 2021, 22, 322.	3.8	13
77	Protein arginine methyltransferase 3 fine-tunes the assembly/disassembly of pre-ribosomes to repress nucleolar stress by interacting with RPS2B in arabidopsis. Molecular Plant, 2021, 14, 223-236.	3.9	11
78	Context and Complexity: Analyzing Methylation in Trinucleotide Sequences. Trends in Plant Science, 2017, 22, 351-353.	4.3	9
79	The rice histone methylation regulates hub species of the root microbiota. Journal of Genetics and Genomics, 2021, 48, 836-843.	1.7	9
80	Targeted DNA demethylation produces heritable epialleles in rice. Science China Life Sciences, 2022, 65, 753-756.	2.3	9
81	Precise editing of methylated cytosine in Arabidopsis thaliana using a human APOBEC3Bctd-Cas9 fusion. Science China Life Sciences, 2022, 65, 219-222.	2.3	8
82	Processing of coding and non-coding RNAs in plant development and environmental responses. Essays in Biochemistry, 2020, 64, 931-945.	2.1	7
83	Epigenetic regulation of thermomorphogenesis in Arabidopsis thaliana. ABIOTECH, 2022, 3, 12-24.	1.8	5
84	Control of <scp>OsARF3a</scp> by <scp>OsKANADI1</scp> contributes to lemma development in rice. Plant Journal, 2022, 110, 1717-1730.	2.8	5
85	New players in ABA signaling: identification of PUB12/13 involved in degradation of ABA co-receptor ABI1. Science China Life Sciences, 2015, 58, 1173-1174.	2.3	4
86	Reproductive tissue-specific translatome of a rice thermo-sensitive genic male sterile line. Journal of Genetics and Genomics, 2022, 49, 624-635.	1.7	4
87	Cotton variant genomesâ€"a breakthrough in population genetics analysis. Science China Life Sciences, 2018, 61, 869-870.	2.3	2
88	Biogenesis, action and biological functions of an Arabidopsis 5â€² tRF, 5â€² tsR-Ala. Science China Life Sciences, 2022, , 1.	2.3	2
89	Reconciliation between high yield and disease resistance. Nature Reviews Genetics, 2022, , .	7.7	2
90	Special issue on epigenetic inheritance by histone modifications, histone variants and non-coding RNAs. Frontiers in Biology, 2011, 6, 87-87.	0.7	1

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91	Small RNA Extraction and Detection in Rice (Oryza sativa). Current Protocols in Plant Biology, 2016, 1, 79-87.	2.8	1
92	Small RNA flow from tapetum cells to germ cells in plants. Science China Life Sciences, 2021, 64, 1977-1979.	2.3	1
93	A new thermosensor from rice. Molecular Plant, 2022, , .	3.9	1
94	Editorial overview: Cell signalling and gene regulation â€" communication and control as the twin pillars of systems biology. Current Opinion in Plant Biology, 2015, 27, v-viii.	3.5	0
95	Thermotolerance in rice. Science China Life Sciences, 2022, , 1.	2.3	0