

Xiaofeng Cao

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89
papers

6,940
citations

39
h-index

83
g-index

97
ext. papers

8,769
ext. citations

13.3
avg, IF

5.97
L-index

#	Paper	IF	Citations
89	Requirement of CHROMOMETHYLASE3 for maintenance of CpXpG methylation. <i>Science</i> , 2001 , 292, 2077-80	33.9	678
88	Role of the arabidopsis DRM methyltransferases in de novo DNA methylation and gene silencing. <i>Current Biology</i> , 2002 , 12, 1138-44	6.3	597
87	Locus-specific control of asymmetric and CpNpG methylation by the DRM and CMT3 methyltransferase genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99 Suppl 4, 16491-8	11.5	454
86	Role of the DRM and CMT3 methyltransferases in RNA-directed DNA methylation. <i>Current Biology</i> , 2003 , 13, 2212-7	6.3	411
85	Histone methylation in higher plants. <i>Annual Review of Plant Biology</i> , 2010 , 61, 395-420	30.7	387
84	MicroRNAs inhibit the translation of target mRNAs on the endoplasmic reticulum in Arabidopsis. <i>Cell</i> , 2013 , 153, 562-74	56.2	353
83	Arabidopsis REF6 is a histone H3 lysine 27 demethylase. <i>Nature Genetics</i> , 2011 , 43, 715-9	36.3	259
82	MicroRNAs and Their Regulatory Roles in Plant-Environment Interactions. <i>Annual Review of Plant Biology</i> , 2019 , 70, 489-525	30.7	234
81	Roles of DCL4 and DCL3b in rice phased small RNA biogenesis. <i>Plant Journal</i> , 2012 , 69, 462-74	6.9	224
80	Epigenetic reprogramming that prevents transgenerational inheritance of the vernalized state. <i>Nature</i> , 2014 , 515, 587-90	50.4	171
79	Arginine methylation mediated by the Arabidopsis homolog of PRMT5 is essential for proper pre-mRNA splicing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 19114-9	11.5	135
78	ROS accumulation and antiviral defence control by microRNA528 in rice. <i>Nature Plants</i> , 2017 , 3, 16203	11.5	134
77	Comparative analysis of JmjC domain-containing proteins reveals the potential histone demethylases in Arabidopsis and rice. <i>Journal of Integrative Plant Biology</i> , 2008 , 50, 886-96	8.3	134
76	Degradome sequencing reveals endogenous small RNA targets in rice (<i>Oryza sativa</i> L. ssp. indica). <i>Frontiers in Biology</i> , 2010 , 5, 67-90		132
75	RNase Z(S1) processes UBL40 mRNAs and controls thermosensitive genic male sterility in rice. <i>Nature Communications</i> , 2014 , 5, 4884	17.4	127
74	Concerted genomic targeting of H3K27 demethylase REF6 and chromatin-remodeling ATPase BRM in Arabidopsis. <i>Nature Genetics</i> , 2016 , 48, 687-93	36.3	122
73	Mutation of a major CG methylase in rice causes genome-wide hypomethylation, dysregulated genome expression, and seedling lethality. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 10642-7	11.5	119

72	JMJ14 is an H3K4 demethylase regulating flowering time in Arabidopsis. <i>Cell Research</i> , 2010 , 20, 387-90	24.7	117
71	<i>Oryza sativa</i> dicer-like4 reveals a key role for small interfering RNA silencing in plant development. <i>Plant Cell</i> , 2007 , 19, 2705-18	11.6	115
70	NOT2 proteins promote polymerase II-dependent transcription and interact with multiple MicroRNA biogenesis factors in Arabidopsis. <i>Plant Cell</i> , 2013 , 25, 715-27	11.6	113
69	REF6 recognizes a specific DNA sequence to demethylate H3K27me3 and regulate organ boundary formation in Arabidopsis. <i>Nature Genetics</i> , 2016 , 48, 694-9	36.3	96
68	ABI4 mediates antagonistic effects of abscisic acid and gibberellins at transcript and protein levels. <i>Plant Journal</i> , 2016 , 85, 348-61	6.9	90
67	Integrated analysis of phenome, genome, and transcriptome of hybrid rice uncovered multiple heterosis-related loci for yield increase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E6026-E6035	11.5	79
66	Control of transposon activity by a histone H3K4 demethylase in rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 1953-8	11.5	78
65	An H3K27me3 demethylase-HSFA2 regulatory loop orchestrates transgenerational thermomemory in Arabidopsis. <i>Cell Research</i> , 2019 , 29, 379-390	24.7	76
64	Mutations in the Type II protein arginine methyltransferase AtPRMT5 result in pleiotropic developmental defects in Arabidopsis. <i>Plant Physiology</i> , 2007 , 144, 1913-23	6.6	75
63	Rice RNA-dependent RNA polymerase 6 acts in small RNA biogenesis and spikelet development. <i>Plant Journal</i> , 2012 , 71, 378-89	6.9	70
62	Involvement of the Histone Acetyltransferase ATHAC1 in the Regulation of Flowering Time via Repression of FLOWERING LOCUS C in Arabidopsis. <i>Plant Physiology</i> , 2007 , 143, 1660-1668	6.6	67
61	Epigenetic Mutation of RAV6 Affects Leaf Angle and Seed Size in Rice. <i>Plant Physiology</i> , 2015 , 169, 2118-28	6.5	65
60	Integrative genome-wide analysis reveals HLP1, a novel RNA-binding protein, regulates plant flowering by targeting alternative polyadenylation. <i>Cell Research</i> , 2015 , 25, 864-76	24.7	61
59	WRKY71 accelerates flowering via the direct activation of FLOWERING LOCUS T and LEAFY in Arabidopsis thaliana. <i>Plant Journal</i> , 2016 , 85, 96-106	6.9	60
58	Nitric Oxide Regulates Protein Methylation during Stress Responses in Plants. <i>Molecular Cell</i> , 2017 , 67, 702-710.e4	17.6	57
57	ARGONAUTE10 promotes the degradation of miR165/6 through the SDN1 and SDN2 exonucleases in Arabidopsis. <i>PLoS Biology</i> , 2017 , 15, e2001272	9.7	56
56	Arabidopsis protein arginine methyltransferase 3 is required for ribosome biogenesis by affecting precursor ribosomal RNA processing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 16190-5	11.5	48
55	The Histone H3K4 Demethylase JMJ16 Represses Leaf Senescence in Arabidopsis. <i>Plant Cell</i> , 2019 , 31, 430-443	11.6	47

54	Transposon-mediated epigenetic regulation contributes to phenotypic diversity and environmental adaptation in rice. <i>Current Opinion in Plant Biology</i> , 2017 , 36, 111-118	9.9	45
53	The Arabidopsis H3K27me3 demethylase JUMONJI 13 is a temperature and photoperiod dependent flowering repressor. <i>Nature Communications</i> , 2019 , 10, 1303	17.4	45
52	Epigenetic regulation and functional exaptation of transposable elements in higher plants. <i>Current Opinion in Plant Biology</i> , 2014 , 21, 83-88	9.9	44
51	RNA Binding Proteins RZ-1B and RZ-1C Play Critical Roles in Regulating Pre-mRNA Splicing and Gene Expression during Development in Arabidopsis. <i>Plant Cell</i> , 2016 , 28, 55-73	11.6	40
50	Transcriptional Regulation of miR528 by OsSPL9 Orchestrates Antiviral Response in Rice. <i>Molecular Plant</i> , 2019 , 12, 1114-1122	14.4	39
49	The effect of transposable elements on phenotypic variation: insights from plants to humans. <i>Science China Life Sciences</i> , 2016 , 59, 24-37	8.5	36
48	C-terminal domains of a histone demethylase interact with a pair of transcription factors and mediate specific chromatin association. <i>Cell Discovery</i> , 2015 , 1,	22.3	33
47	Roles of pre-mRNA splicing and polyadenylation in plant development. <i>Current Opinion in Plant Biology</i> , 2017 , 35, 45-53	9.9	33
46	Plant PRMTs broaden the scope of arginine methylation. <i>Journal of Genetics and Genomics</i> , 2012 , 39, 195-208	4	32
45	Epigenetic regulation and epigenomic landscape in rice. <i>National Science Review</i> , 2016 , 3, 309-327	10.8	31
44	Fine-Tuning of MiR528 Accumulation Modulates Flowering Time in Rice. <i>Molecular Plant</i> , 2019 , 12, 1103-1113	14.4	30
43	Post-transcriptional splicing of nascent RNA contributes to widespread intron retention in plants. <i>Nature Plants</i> , 2020 , 6, 780-788	11.5	30
42	Rice InVivo RNA Structurome Reveals RNA Secondary Structure Conservation and Divergence in Plants. <i>Molecular Plant</i> , 2018 , 11, 607-622	14.4	29
41	The ATPase hCINAP regulates 18S rRNA processing and is essential for embryogenesis and tumour growth. <i>Nature Communications</i> , 2016 , 7, 12310	17.4	28
40	Recruitment of the NineTeen Complex to the activated spliceosome requires AtPRMT5. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 5447-52	11.5	27
39	Structure of the Arabidopsis JM14-H3K4me3 Complex Provides Insight into the Substrate Specificity of KDM5 Subfamily Histone Demethylases. <i>Plant Cell</i> , 2018 , 30, 167-177	11.6	26
38	DNA methylation repels targeting of Arabidopsis REF6. <i>Nature Communications</i> , 2019 , 10, 2063	17.4	25
37	RNA G-quadruplex structures exist and function in vivo in plants. <i>Genome Biology</i> , 2020 , 21, 226	18.3	23

36	Retrospective and perspective of plant epigenetics in China. <i>Journal of Genetics and Genomics</i> , 2018 , 45, 621-638	4	22
35	The seekers: how epigenetic modifying enzymes find their hidden genomic targets in Arabidopsis. <i>Current Opinion in Plant Biology</i> , 2018 , 45, 75-81	9.9	21
34	COR27 and COR28 encode nighttime repressors integrating Arabidopsis circadian clock and cold response. <i>Journal of Integrative Plant Biology</i> , 2017 , 59, 78-85	8.3	20
33	TarHunter, a tool for predicting conserved microRNA targets and target mimics in plants. <i>Bioinformatics</i> , 2018 , 34, 1574-1576	7.2	19
32	Impact of poly(A)-tail G-content on Arabidopsis PAB binding and their role in enhancing translational efficiency. <i>Genome Biology</i> , 2019 , 20, 189	18.3	18
31	Whole genome sequencing of cotton--a new chapter in cotton genomics. <i>Science China Life Sciences</i> , 2015 , 58, 515-6	8.5	18
30	FIERY1 promotes microRNA accumulation by suppressing rRNA-derived small interfering RNAs in Arabidopsis. <i>Nature Communications</i> , 2019 , 10, 4424	17.4	17
29	Ribosomal RNA Biogenesis and Its Response to Chilling Stress in. <i>Plant Physiology</i> , 2018 , 177, 381-397	6.6	17
28	CPSF30-L-mediated recognition of mRNA mA modification controls alternative polyadenylation of nitrate signaling-related gene transcripts in Arabidopsis. <i>Molecular Plant</i> , 2021 , 14, 688-699	14.4	16
27	An epiallele of rice AK1 affects photosynthetic capacity. <i>Journal of Integrative Plant Biology</i> , 2017 , 59, 158-163	8.3	15
26	Drosophila Homolog of FMRP Maintains Genome Integrity by Interacting with Piwi. <i>Journal of Genetics and Genomics</i> , 2016 , 43, 11-24	4	13
25	Trip to ER: MicroRNA-mediated translational repression in plants. <i>RNA Biology</i> , 2013 , 10, 1586-92	4.8	13
24	Developmental Cytoplasmic-to-Nuclear Translocation of RNA-Binding Protein HuR Is Required for Adult Neurogenesis. <i>Cell Reports</i> , 2019 , 29, 3101-3117.e7	10.6	12
23	Histone methylation in epigenetic regulation and temperature responses. <i>Current Opinion in Plant Biology</i> , 2021 , 61, 102001	9.9	9
22	Modulation of Auxin Signaling and Development by Polyadenylation Machinery. <i>Plant Physiology</i> , 2019 , 179, 686-699	6.6	9
21	Context and Complexity: Analyzing Methylation in Trinucleotide Sequences. <i>Trends in Plant Science</i> , 2017 , 22, 351-353	13.1	8
20	Extensive profiling of the expressions of tRNAs and tRNA-derived fragments (tRFs) reveals the complexities of tRNA and tRF populations in plants. <i>Science China Life Sciences</i> , 2021 , 64, 495-511	8.5	8
19	DEAD-BOX RNA HELICASE 27 regulates microRNA biogenesis, zygote division, and stem cell homeostasis. <i>Plant Cell</i> , 2021 , 33, 66-84	11.6	7

18	The histone H3K27 demethylase REF6/JMJ12 promotes thermomorphogenesis in .. <i>National Science Review</i> , 2022 , 9, nwab213	10.8	4
17	An engineered prime editor with enhanced editing efficiency in plants.. <i>Nature Biotechnology</i> , 2022 ,	44.5	4
16	New players in ABA signaling: identification of PUB12/13 involved in degradation of ABA co-receptor ABI1. <i>Science China Life Sciences</i> , 2015 , 58, 1173-4	8.5	3
15	Cell-type-dependent histone demethylase specificity promotes meiotic chromosome condensation in Arabidopsis. <i>Nature Plants</i> , 2020 , 6, 823-837	11.5	3
14	Processing of coding and non-coding RNAs in plant development and environmental responses. <i>Essays in Biochemistry</i> , 2020 , 64, 931-945	7.6	3
13	Plant transfer RNA-derived fragments: Biogenesis and functions. <i>Journal of Integrative Plant Biology</i> , 2021 , 63, 1399-1409	8.3	2
12	Cotton variant genomes-a breakthrough in population genetics analysis. <i>Science China Life Sciences</i> , 2018 , 61, 869-870	8.5	2
11	Reproductive tissue-specific translome of a rice thermo-sensitive genic male sterile line.. <i>Journal of Genetics and Genomics</i> , 2022 ,	4	1
10	Landscape of transcription termination in Arabidopsis revealed by single-molecule nascent RNA sequencing. <i>Genome Biology</i> , 2021 , 22, 322	18.3	1
9	Protein arginine methyltransferase 3 fine-tunes the assembly/disassembly of pre-ribosomes to repress nucleolar stress by interacting with RPS2B in arabidopsis. <i>Molecular Plant</i> , 2021 , 14, 223-236	14.4	1
8	The rice histone methylation regulates hub species of the root microbiota. <i>Journal of Genetics and Genomics</i> , 2021 , 48, 836-843	4	1
7	Targeted DNA demethylation produces heritable epialleles in rice. <i>Science China Life Sciences</i> , 2021 , 1	8.5	1
6	Small RNA flow from tapetum cells to germ cells in plants. <i>Science China Life Sciences</i> , 2021 , 64, 1977-1979	8.5	0
5	Precise editing of methylated cytosine in Arabidopsis thaliana using a human APOBEC3Bctd-Cas9 fusion. <i>Science China Life Sciences</i> , 2021 , 1	8.5	0
4	Epigenetic regulation of thermomorphogenesis in Arabidopsis thaliana. <i>ABIOTECH</i> , 2022 , 3, 12-24	3.9	0
3	Small RNA Extraction and Detection in Rice (<i>Oryza sativa</i>). <i>Current Protocols in Plant Biology</i> , 2016 , 1, 79-87	2.8	
2	Biogenesis, action and biological functions of an Arabidopsis 5Utrf, 5Utr-Ala.. <i>Science China Life Sciences</i> , 2022 , 1	8.5	
1	Thermotolerance in rice.. <i>Science China Life Sciences</i> , 2022 , 1	8.5	

