Yuhai Cui

List of Publications by Year in descending order

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Ушнат Сш

#	Article	IF	CITATIONS
1	Post-translational modification: a strategicÂresponse to high temperature in plants. ABIOTECH, 2022, 3, 49-64.	3.9	15
2	BLISTER promotes seed maturation and fatty acid biosynthesis by interacting with WRINKLED1 to regulate chromatin dynamics in Arabidopsis. Plant Cell, 2022, 34, 2242-2265.	6.6	11
3	Chromatin-associated SUMOylation controls the transcriptional switch between plant development and heat stress responses. Plant Communications, 2021, 2, 100091.	7.7	14
4	Genomeâ€wide occupancy of <i>Arabidopsis</i> SWI/SNF chromatin remodeler SPLAYED provides insights into its interplay with its close homolog BRAHMA and Polycomb proteins. Plant Journal, 2021, 106, 200-213.	5.7	19
5	CRISPR/Cas9 gene editing in legume crops: Opportunities and challenges. , 2021, 3, e96.		49
6	LEAFY COTYLEDON1 expression in the endosperm enables embryo maturation in Arabidopsis. Nature Communications, 2021, 12, 3963.	12.8	24
7	The Pumilio RNAâ€binding protein APUM24 regulates seed maturation by fineâ€ŧuning the BPMâ€WRI1 module in <i>Arabidopsis</i> . Journal of Integrative Plant Biology, 2021, 63, 1240-1259.	8.5	6
8	Comprehensive Analysis of the SBP Family in Blueberry and Their Regulatory Mechanism Controlling Chlorophyll Accumulation. Frontiers in Plant Science, 2021, 12, 703994.	3.6	6
9	Endosperm–Embryo Communications: Recent Advances and Perspectives. Plants, 2021, 10, 2511.	3.5	7
10	SWI3B and HDA6 interact and are required for transposon silencing in <i>Arabidopsis</i> . Plant Journal, 2020, 102, 809-822.	5.7	30
11	The H3K27me3 Demethylase RELATIVE OF EARLY FLOWERING6 Suppresses Seed Dormancy by Inducing Abscisic Acid Catabolism. Plant Physiology, 2020, 184, 1969-1978.	4.8	33
12	The expression of long non-coding RNAs is associated with H3Ac and H3K4me2 changes regulated by the HDA6-LDL1/2 histone modification complex in Arabidopsis. NAR Genomics and Bioinformatics, 2020, 2, Iqaa066.	3.2	12
13	BRAHMA-interacting proteins BRIP1 and BRIP2 are core subunits of Arabidopsis SWI/SNF complexes. Nature Plants, 2020, 6, 996-1007.	9.3	33
14	Evidence that <i>AGL17</i> is a significant downstream target of CLF in floral transition control. Plant Signaling and Behavior, 2020, 15, 1766851.	2.4	5
15	The complexity of PRC2 catalysts CLF and SWN in plants. Biochemical Society Transactions, 2020, 48, 2779-2789.	3.4	12
16	A SWI/SNF subunit regulates chromosomal dissociation of structural maintenance complex 5 during DNA repair in plant cells. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 15288-15296.	7.1	16
17	Nuclear Prohibitin3 Maintains Genome Integrity and Cell Proliferation in the Root Meristem through Minichromosome Maintenance 2. Plant Physiology, 2019, 179, 1669-1691.	4.8	19
18	RNA polymerase II-independent recruitment of SPT6L at transcription start sites in Arabidopsis. Nucleic Acids Research, 2019, 47, 6714-6725.	14.5	24

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19	Genomeâ€wide occupancy of histone H3K27 methyltransferases <scp>CURLY LEAF</scp> and <scp>SWINGER</scp> in <i>Arabidopsis</i> seedlings. Plant Direct, 2019, 3, e00100.	1.9	70
20	The LDL1/2-HDA6 Histone Modification Complex Interacts With TOC1 and Regulates the Core Circadian Clock Components in Arabidopsis. Frontiers in Plant Science, 2019, 10, 233.	3.6	32
21	Mutagenesis of seed storage protein genes in Soybean using CRISPR/Cas9. BMC Research Notes, 2019, 12, 176.	1.4	61
22	The SWI/SNF subunit SWI3B regulates IAMT1 expression via chromatin remodeling in Arabidopsis leaf development. Plant Science, 2018, 271, 127-132.	3.6	10
23	Verification of <scp>DNA</scp> motifs <i>in Arabidopsis</i> using <scp>CRISPR</scp> /Cas9â€mediated mutagenesis. Plant Biotechnology Journal, 2018, 16, 1446-1451.	8.3	19
24	Genetic mapping and validation of the loci controlling 7S α′ and 11S A-type storage protein subunits in soybean [Glycine max (L.) Merr.]. Theoretical and Applied Genetics, 2018, 131, 659-671.	3.6	17
25	Analysis of a novel mutant allele of GSL8 reveals its key roles in cytokinesis and symplastic trafficking in Arabidopsis. BMC Plant Biology, 2018, 18, 295.	3.6	30
26	The Arabidopsis LDL1/2-HDA6 histone modification complex is functionally associated with CCA1/LHY in regulation of circadian clock genes. Nucleic Acids Research, 2018, 46, 10669-10681.	14.5	52
27	A SUMO Ligase AtMMS21 Regulates the Stability of the Chromatin Remodeler BRAHMA in Root Development. Plant Physiology, 2017, 173, 1574-1582.	4.8	34
28	Conservation and diversification of the miR166 family in soybean and potential roles of newly identified miR166s. BMC Plant Biology, 2017, 17, 32.	3.6	66
29	Cytosolic acetyl-CoA promotes histone acetylation predominantly at H3K27 in Arabidopsis. Nature Plants, 2017, 3, 814-824.	9.3	85
30	Comparative Analysis of Fruit Ripening-Related miRNAs and Their Targets in Blueberry Using Small RNA and Degradome Sequencing. International Journal of Molecular Sciences, 2017, 18, 2767.	4.1	36
31	Comparative proteomics reveals the physiological differences between winter tender shoots and spring tender shoots of a novel tea (Camellia sinensis L.) cultivar evergrowing in winter. BMC Plant Biology, 2017, 17, 206.	3.6	19
32	A DNA element that remembers winter. Nature Genetics, 2016, 48, 1451-1452.	21.4	7
33	Concerted genomic targeting of H3K27 demethylase REF6 and chromatin-remodeling ATPase BRM in Arabidopsis. Nature Genetics, 2016, 48, 687-693.	21.4	193
34	Combinatorial regulation of CLF and SDG8 during Arabidopsis shoot branching. Acta Physiologiae Plantarum, 2016, 38, 1.	2.1	2
35	Regulation of Vegetative Phase Change by SWI2/SNF2 Chromatin Remodeling ATPase BRAHMA. Plant Physiology, 2016, 172, 2416-2428.	4.8	69
36	The Arabidopsis SWI2/SNF2 Chromatin Remodeling ATPase BRAHMA Targets Directly to <i>PINs</i> and Is Required for Root Stem Cell Niche Maintenance. Plant Cell, 2015, 27, 1670-1680.	6.6	88

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37	Arabidopsis BREVIPEDICELLUS Interacts with the SWI2/SNF2 Chromatin Remodeling ATPase BRAHMA to Regulate KNAT2 and KNAT6 Expression in Control of Inflorescence Architecture. PLoS Genetics, 2015, 11, e1005125.	3.5	73
38	The Arabidopsis SWI2/SNF2 Chromatin Remodeler BRAHMA Regulates Polycomb Function during Vegetative Development and Directly Activates the Flowering Repressor Gene SVP. PLoS Genetics, 2015, 11, e1004944.	3.5	111
39	Computational identification of conserved microRNAs and their targets from expression sequence tags of blueberry (<i>Vaccinium corybosum</i>). Plant Signaling and Behavior, 2014, 9, e29462.	2.4	14
40	Genome-wide single nucleotide polymorphism and Insertion-Deletion discovery through next-generation sequencing of reduced representation libraries in common bean. Molecular Breeding, 2014, 33, 769-778.	2.1	29
41	PHYTOCHROME INTERACTING FACTOR3 Associates with the Histone Deacetylase HDA15 in Repression of Chlorophyll Biosynthesis and Photosynthesis in Etiolated <i>Arabidopsis</i> Seedlings Â. Plant Cell, 2013, 25, 1258-1273.	6.6	186
42	Following Vegetative to Embryonic Cellular Changes in Leaves of Arabidopsis Overexpressing <i>LEAFY COTYLEDON2</i> . Plant Physiology, 2013, 162, 1881-1896.	4.8	34
43	Reprogramming cells to study vacuolar development. Frontiers in Plant Science, 2013, 4, 493.	3.6	4
44	HISTONE DEACETYLASE19 Interacts with HSL1 and Participates in the Repression of Seed Maturation Genes in <i>Arabidopsis</i> Seedlings Â. Plant Cell, 2013, 25, 134-148.	6.6	157
45	MicroRNA–Mediated Repression of the Seed Maturation Program during Vegetative Development in Arabidopsis. PLoS Genetics, 2012, 8, e1003091.	3.5	68
46	Histone Deacetylase HDA6 Is Functionally Associated with AS1 in Repression of KNOX Genes in Arabidopsis. PLoS Genetics, 2012, 8, e1003114.	3.5	93
47	HDA6 Directly Interacts with DNA Methyltransferase MET1 and Maintains Transposable Element Silencing in Arabidopsis Â. Plant Physiology, 2012, 158, 119-129.	4.8	141
48	Evidence that the Arabidopsis Ubiquitin C-terminal Hydrolases 1 and 2 associate with the 26S proteasome and the TREX-2 complex. Plant Signaling and Behavior, 2012, 7, 1415-1419.	2.4	7
49	Synergistic repression of the embryonic programme by SET DOMAIN GROUP 8 and EMBRYONIC FLOWER 2 in Arabidopsis seedlings. Journal of Experimental Botany, 2012, 63, 1391-1404.	4.8	71
50	HD2C interacts with HDA6 and is involved in ABA and salt stress response in Arabidopsis. Journal of Experimental Botany, 2012, 63, 3297-3306.	4.8	255
51	Chromatin modifications and remodeling in plant abiotic stress responses. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2012, 1819, 129-136.	1.9	176
52	Transcriptome profiling and methyl homeostasis of an Arabidopsis mutant deficient in S-adenosylhomocysteine hydrolase1 (SAHH1). Plant Molecular Biology, 2012, 79, 315-331.	3.9	25
53	AtRabD2b, a Functional Ortholog of the Yeast Ypt1, Controls Various Growth and Developmental Processes in Arabidopsis. Plant Molecular Biology Reporter, 2012, 30, 275-285.	1.8	5
54	Detection of Protein Interactions in Plant using a Gateway Compatible Bimolecular Fluorescence Complementation (BiFC) System. Journal of Visualized Experiments, 2011, , .	0.3	31

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55	HISTONE DEACETYLASE6 Interacts with FLOWERING LOCUS D and Regulates Flowering in Arabidopsis Â. Plant Physiology, 2011, 156, 173-184.	4.8	199
56	Arabidopsis homolog of the yeast TREX-2 mRNA export complex: components and anchoring nucleoporin. Plant Journal, 2010, 61, 259-270.	5.7	332
57	A mutant deficient in <i>S</i> -adenosylhomocysteine hydrolase in <i>Arabidopsis</i> shows defects in root-hair developmentThis paper is one of a selection of papers published in a Special Issue from the National Research Council of Canada – Plant Biotechnology Institute Botany, 2009, 87, 571-584.	1.0	19
58	The Arabidopsis BRAHMA Chromatin-Remodeling ATPase Is Involved in Repression of Seed Maturation Genes in Leaves Â. Plant Physiology, 2008, 147, 1143-1157.	4.8	97
59	Two naturally occurring deletion mutants of 12S seed storage proteins in Arabidopsis thaliana. Planta, 2005, 222, 512-520.	3.2	12
60	The AtPP gene of the Brassica napus S locus region is specifically expressed in the stigma and encodes a protein similar to a methyltransferase involved in plant defense. Sexual Plant Reproduction, 2001, 13, 309-314.	2.2	3
61	Molecular mechanisms of self-recognition in Brassica self-incompatibility. Trends in Plant Science, 2000, 5, 432-438.	8.8	34
62	Structural and Transcriptional Comparative Analysis of the S Locus Regions in Two Self-Incompatible Brassica napus Lines. Plant Cell, 1999, 11, 2217-2231.	6.6	86
63	Identification and characterization of microRNAs and their targets from expression sequence tags of <i>Ribes nigrum</i> . Canadian Journal of Plant Science, 0, , 1-7.	0.9	14