

Blocking histone deacetylation in Arabidopsis induces p regulation and development

Proceedings of the National Academy of Sciences of the United States of America
98, 200-5

DOI: [10.1073/pnas.011347998](https://doi.org/10.1073/pnas.011347998)

Citation Report

#	ARTICLE	IF	CITATIONS
1	Epigenetic developmental mechanisms in plants: molecules and targets of plant epigenetic regulation. <i>Current Opinion in Genetics and Development</i> , 2001, 11, 215-220.	1.5	67
2	Gene silencing and DNA methylation processes. <i>Current Opinion in Plant Biology</i> , 2001, 4, 123-129.	3.5	141
3	Chromatin remodelling. <i>Current Opinion in Plant Biology</i> , 2001, 4, 457-462.	3.5	30
4	Chromatin remodeling in plants. <i>Current Opinion in Plant Biology</i> , 2001, 4, 494-500.	3.5	99
5	Identification of Arabidopsis Histone Deacetylase HDA6 Mutants That Affect Transgene Expression. <i>Plant Cell</i> , 2001, 13, 1047-1061.	3.1	204
6	Transcriptional Regulation: a Genomic Overview. <i>The Arabidopsis Book</i> , 2002, 1, e0085.	0.5	55
7	Suppressors of transcriptional transgenic silencing in <i>Chlamydomonas</i> are sensitive to DNA-damaging agents and reactivate transposable elements. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 1076-1081.	3.3	96
8	Tissue-specific silencing of a transgene in rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 10881-10886.	3.3	29
9	Disruption of a DNA Topoisomerase I Gene Affects Morphogenesis in Arabidopsis. <i>Plant Cell</i> , 2002, 14, 2085-2093.	3.1	51
10	Remembrance of Things Past: Chromatin Remodeling in Plant Development. <i>Annual Review of Cell and Developmental Biology</i> , 2002, 18, 707-746.	4.0	87
11	GENEEXPRESSION INNEMATODEFEEDINGSITES. <i>Annual Review of Phytopathology</i> , 2002, 40, 191-219.	3.5	282
12	Genetic and epigenetic processes in seed development. <i>Current Opinion in Plant Biology</i> , 2002, 5, 19-25.	3.5	25
13	Chromatin dynamics in plants. <i>Current Opinion in Plant Biology</i> , 2002, 5, 560-567.	3.5	59
14	Chromatin as a eukaryotic template of genetic information. <i>Current Opinion in Cell Biology</i> , 2002, 14, 269-278.	2.6	25
15	Epigenetic inheritance of expression states in plant development: the role of Polycomb group proteins. <i>Current Opinion in Cell Biology</i> , 2002, 14, 773-779.	2.6	61
16	DNA methylation controls histone H3 lysine 9 methylation and heterochromatin assembly in Arabidopsis. <i>EMBO Journal</i> , 2002, 21, 6549-6559.	3.5	439
17	HDA6, a putative histone deacetylase needed to enhance DNA methylation induced by double-stranded RNA. <i>EMBO Journal</i> , 2002, 21, 6832-6841.	3.5	286
18	Genomic Imprinting and Endosperm Development in Flowering Plants. <i>Molecular Biotechnology</i> , 2003, 25, 149-184.	1.3	80

#	ARTICLE	IF	CITATIONS
19	CHB2, a member of theSWI3gene family, is a global regulator inArabidopsis. Plant Molecular Biology, 2003, 52, 1125-1134.	2.0	32
20	Arabidopsis MBD proteins show different binding specificities and nuclear localization. Plant Molecular Biology, 2003, 53, 755-771.	2.0	51
21	Changes in gene expression in response to altered SHL transcript levels. Plant Molecular Biology, 2003, 53, 805-820.	2.0	10
22	Fertilization induces strong accumulation of a histone deacetylase (HD2) and of other chromatin-remodeling proteins in restricted areas of the ovules. Plant Molecular Biology, 2003, 53, 759-769.	2.0	22
23	Ageing in Plants: Conserved Strategies and Novel Pathways. Plant Biology, 2003, 5, 455-464.	1.8	51
24	A maize histone deacetylase and retinoblastoma-related protein physically interact and cooperate in repressing gene transcription. Plant Molecular Biology, 2003, 51, 401-413.	2.0	61
25	Chromatin dynamics and Arabidopsis development. Chromosome Research, 2003, 11, 277-304.	1.0	30
26	Chromatin regulation of plant development. Current Opinion in Plant Biology, 2003, 6, 20-28.	3.5	111
27	Repression of gene expression by Arabidopsis HD2 histone deacetylases. Plant Journal, 2003, 34, 241-247.	2.8	70
28	Ten members of the Arabidopsis gene family encoding methyl-CpG-binding domain proteins are transcriptionally active and at least one, AtMBD11, is crucial for normal development. Nucleic Acids Research, 2003, 31, 5291-5304.	6.5	56
29	Regulation and Processing of Maize Histone Deacetylase Hda1 by Limited Proteolysis. Plant Cell, 2003, 15, 1904-1917.	3.1	19
30	The Transcriptional Enhancer of the Pea Plastocyanin Gene Associates with the Nuclear Matrix and Regulates Gene Expression through Histone Acetylation. Plant Cell, 2003, 15, 1468-1479.	3.1	98
31	Expression Profile and Cellular Localization of Maize Rpd3-Type Histone Deacetylases during Plant Development. Plant Physiology, 2003, 133, 606-617.	2.3	58
32	Arabidopsis Histone Acetyltransferase AtGCN5 Regulates the Floral Meristem Activity through the WUSCHEL/AGAMOUS Pathway. Journal of Biological Chemistry, 2003, 278, 28246-28251.	1.6	141
33	Arabidopsis Histone Deacetylase HDA6 Is Required for Maintenance of Transcriptional Gene Silencing and Determines Nuclear Organization of rDNA Repeats. Plant Cell, 2004, 16, 1021-1034.	3.1	264
34	Stochastic and Epigenetic Changes of Gene Expression in Arabidopsis Polyploids. Genetics, 2004, 167, 1961-1973.	1.2	323
35	An auxin-responsive SCARECROW-like transcriptional activator interacts with histone deacetylase. Plant Molecular Biology, 2004, 55, 417-431.	2.0	78
36	A plant dialect of the histone language. Trends in Plant Science, 2004, 9, 84-90.	4.3	146

#	ARTICLE	IF	CITATIONS
37	Dynamic Histone Acetylation of Late Embryonic Genes during Seed Germination. <i>Plant Molecular Biology</i> , 2005, 59, 909-925.	2.0	73
38	Reversible Histone Acetylation and Deacetylation Mediate Genome-Wide, Promoter-Dependent and Locus-Specific Changes in Gene Expression During Plant Development. <i>Genetics</i> , 2005, 169, 337-345.	1.2	157
39	Role of an Arabidopsis AP2/EREBP-Type Transcriptional Repressor in Abscisic Acid and Drought Stress Responses. <i>Plant Cell</i> , 2005, 17, 2384-2396.	3.1	479
40	HISTONE DEACETYLASE19 Is Involved in Jasmonic Acid and Ethylene Signaling of Pathogen Response in Arabidopsis. <i>Plant Cell</i> , 2005, 17, 1196-1204.	3.1	407
41	Suppression of Histone H1 Genes in Arabidopsis Results in Heritable Developmental Defects and Stochastic Changes in DNA Methylation. <i>Genetics</i> , 2005, 169, 997-1008.	1.2	91
42	The bromodomain protein GTE6 controls leaf development in Arabidopsis by histone acetylation at ASYMMETRIC LEAVES1. <i>Genes and Development</i> , 2005, 19, 2245-2254.	2.7	56
43	The elongata mutants identify a functional Elongator complex in plants with a role in cell proliferation during organ growth. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 7754-7759.	3.3	154
44	Regulation of meristem activity by chromatin remodelling. <i>Trends in Plant Science</i> , 2005, 10, 332-338.	4.3	38
45	Analysis of the Transcription Factor WUSCHEL and Its Functional Homologue in Antirrhinum Reveals a Potential Mechanism for Their Roles in Meristem Maintenance. <i>Plant Cell</i> , 2006, 18, 560-573.	3.1	203
46	DNA Methylation in Plants. , 2006, 301, 67-122.		70
47	Arabidopsis thaliana histone deacetylase 1 (AtHD1) is localized in euchromatic regions and demonstrates histone deacetylase activity in vitro. <i>Cell Research</i> , 2006, 16, 479-488.	5.7	37
48	Molecular cell biology: Epigenetic gene silencing in plants. , 2006, , 101-133.		10
49	AtSAP18, An Orthologue of Human SAP18, is Involved in the Regulation of Salt Stress and Mediates Transcriptional Repression in Arabidopsis. <i>Plant Molecular Biology</i> , 2006, 60, 241-257.	2.0	122
50	Large-Scale Analysis of mRNA Translation States during Sucrose Starvation in Arabidopsis Cells Identifies Cell Proliferation and Chromatin Structure as Targets of Translational Control. <i>Plant Physiology</i> , 2006, 141, 663-673.	2.3	99
51	The Balance between the MIR164A and CUC2 Genes Controls Leaf Margin Serration in Arabidopsis. <i>Plant Cell</i> , 2006, 18, 2929-2945.	3.1	513
52	Arabidopsis GCN5, HD1, and TAF1/HAF2 Interact to Regulate Histone Acetylation Required for Light-Responsive Gene Expression. <i>Plant Cell</i> , 2006, 18, 2893-2903.	3.1	302
53	The Transcription Corepressor LEUNIG Interacts with the Histone Deacetylase HDA19 and Mediator Components MED14 (SWP) and CDK8 (HEN3) To Repress Transcription. <i>Molecular and Cellular Biology</i> , 2007, 27, 5306-5315.	1.1	123
54	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.	2.3	80

#	ARTICLE	IF	CITATIONS
55	Impact of Core Histone Modifications on Transcriptional Regulation and Plant Growth. <i>Critical Reviews in Plant Sciences</i> , 2007, 26, 243-263.	2.7	32
56	Maize Histone Deacetylase hda101 Is Involved in Plant Development, Gene Transcription, and Sequence-Specific Modulation of Histone Modification of Genes and Repeats. <i>Plant Cell</i> , 2007, 19, 1145-1162.	3.1	68
57	Conserved functions of retinoblastoma proteins: From purple retina to green plant cells. <i>Plant Science</i> , 2007, 172, 671-683.	1.7	14
58	Roles of dynamic and reversible histone acetylation in plant development and polyploidy. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2007, 1769, 295-307.	2.4	195
59	Groucho/Tup1 family co-repressors in plant development. <i>Trends in Plant Science</i> , 2008, 13, 137-144.	4.3	122
60	Variation of metabolic profiles in developing maize kernels up- and down-regulated for the hda101 gene. <i>Journal of Experimental Botany</i> , 2008, 59, 3913-3924.	2.4	14
61	The Arabidopsis Histone Deacetylases HDA6 and HDA19 Contribute to the Repression of Embryonic Properties after Germination. <i>Plant Physiology</i> , 2008, 146, 149-161.	2.3	269
62	<i>Arabidopsis</i> WRKY38 and WRKY62 Transcription Factors Interact with Histone Deacetylase 19 in Basal Defense. <i>Plant Cell</i> , 2008, 20, 2357-2371.	3.1	481
63	The <i>Arabidopsis</i> onset of leaf death5 Mutation of Quinolinate Synthase Affects Nicotinamide Adenine Dinucleotide Biosynthesis and Causes Early Ageing. <i>Plant Cell</i> , 2008, 20, 2909-2925.	3.1	106
64	Histone Modifications and Expression of Light-Regulated Genes in Arabidopsis Are Cooperatively Influenced by Changing Light Conditions. <i>Plant Physiology</i> , 2008, 147, 2070-2083.	2.3	80
65	Epigenetic regulation of stress responses in plants. <i>Current Opinion in Plant Biology</i> , 2009, 12, 133-139.	3.5	984
66	Why so repressed? Turning off transcription during plant growth and development. <i>Current Opinion in Plant Biology</i> , 2009, 12, 628-636.	3.5	54
67	Phylogenetic analysis, subcellular localization, and expression patterns of RPD3/HDA1 family histone deacetylases in plants. <i>BMC Plant Biology</i> , 2009, 9, 37.	1.6	117
68	Generation of Arabidopsis Mutants by Heterologous Expression of a Full-Length cDNA Library from Tomato Fruits. <i>Plant Molecular Biology Reporter</i> , 2009, 27, 454-461.	1.0	5
69	Biosynthesis and Role in Virulence of the Histone Deacetylase Inhibitor Depudecin from <i>Alternaria brassicicola</i> . <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 1258-1267.	1.4	79
70	Genome-wide profiling of histone H3 lysine 9 acetylation and dimethylation in Arabidopsis reveals correlation between multiple histone marks and gene expression. <i>Plant Molecular Biology</i> , 2010, 72, 585-595.	2.0	167
71	Epigenetic Chromatin Modifiers in Barley: II. Characterization and Expression Analysis of the HDA1 Family of Barley Histone Deacetylases During Development and in Response to Jasmonic Acid. <i>Plant Molecular Biology Reporter</i> , 2010, 28, 9-21.	1.0	28
72	Epigenetic control of plant immunity. <i>Molecular Plant Pathology</i> , 2010, 11, 563-576.	2.0	167

#	ARTICLE	IF	CITATIONS
73	Senescence and death of plant organs: Nutrient recycling and developmental regulation. <i>Comptes Rendus - Biologies</i> , 2010, 333, 382-391.	0.1	171
74	Histone modifications in transcriptional activation during plant development. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2011, 1809, 567-576.	0.9	195
75	Chromatin remodelling in plant light signalling. <i>Physiologia Plantarum</i> , 2011, 142, 305-313.	2.6	43
76	A potato skin SSH library yields new candidate genes for suberin biosynthesis and periderm formation. <i>Planta</i> , 2011, 233, 933-945.	1.6	39
77	Role of HD2 genes in seed germination and early seedling growth in Arabidopsis. <i>Plant Cell Reports</i> , 2011, 30, 1969-1979.	2.8	56
78	Proteins of Diverse Function and Subcellular Location Are Lysine Acetylated in Arabidopsis. <i>Plant Physiology</i> , 2011, 155, 1779-1790.	2.3	233
79	Coordinated histone modifications are associated with gene expression variation within and between species. <i>Genome Research</i> , 2011, 21, 590-598.	2.4	140
80	Decomposition Rates and Residue-Colonizing Microbial Communities of <i>Bacillus thuringiensis</i> Insecticidal Protein Cry3Bb-Expressing (Bt) and Non-Bt Corn Hybrids in the Field. <i>Applied and Environmental Microbiology</i> , 2011, 77, 839-846.	1.4	30
81	Lysine Acetylation Is a Widespread Protein Modification for Diverse Proteins in Arabidopsis. <i>Plant Physiology</i> , 2011, 155, 1769-1778.	2.3	198
82	HD2 proteins interact with RPD3-type histone deacetylases. <i>Plant Signaling and Behavior</i> , 2012, 7, 608-610.	1.2	29
83	Diverse roles of Groucho/Tup1 co-repressors in plant growth and development. <i>Plant Signaling and Behavior</i> , 2012, 7, 86-92.	1.2	33
84	Histone deacetylase HD2 interacts with ERF1 and is involved in longan fruit senescence. <i>Journal of Experimental Botany</i> , 2012, 63, 441-454.	2.4	83
85	Chromatin modifications and remodeling in plant abiotic stress responses. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2012, 1819, 129-136.	0.9	176
86	A new RNASeq-based reference transcriptome for sugar beet and its application in transcriptome-scale analysis of vernalization and gibberellin responses. <i>BMC Genomics</i> , 2012, 13, 99.	1.2	54
87	The Complex Regulation of Senescence. <i>Critical Reviews in Plant Sciences</i> , 2012, 31, 124-147.	2.7	80
88	Aberrant promoter methylation occurred from multicopy transgene and SU(VAR)3-9 homolog 9 (SUVH9) gene in transgenic <i>Nicotiana benthamiana</i> . <i>Functional Plant Biology</i> , 2012, 39, 764.	1.1	7
89	Subcellular Localization of Class II HDAs in Arabidopsis thaliana: Nucleocytoplasmic Shuttling of HDA15 Is Driven by Light. <i>PLoS ONE</i> , 2012, 7, e30846.	1.1	55
90	Characterization and differential expression analysis of complete coding sequences of <i>Vitis vinifera</i> L. sirtuin genes. <i>Plant Physiology and Biochemistry</i> , 2012, 54, 123-132.	2.8	15

#	ARTICLE	IF	CITATIONS
91	Chromatin modification and remodelling: a regulatory landscape for the control of Arabidopsis defence responses upon pathogen attack. Cellular Microbiology, 2012, 14, 829-839.	1.1	65
92	Inhibition of histone deacetylation alters Arabidopsis root growth in response to auxin via PIN1 degradation. Plant Cell Reports, 2013, 32, 1625-1636.	2.8	39
93	Determinate primary root growth as an adaptation to aridity in Cactaceae: towards an understanding of the evolution and genetic control of the trait. Annals of Botany, 2013, 112, 239-252.	1.4	19
94	Epigenetic and small RNA regulation of senescence. Plant Molecular Biology, 2013, 82, 529-537.	2.0	31
95	Histone deacetylases and their functions in plants. Plant Cell Reports, 2013, 32, 465-478.	2.8	120
96	Histone Deacetylase Complex1 Expression Level Titrates Plant Growth and Abscisic Acid Sensitivity in Arabidopsis. Plant Cell, 2013, 25, 3491-3505.	3.1	92
97	Transcriptome Comparative Profiling of Barley eibi1 Mutant Reveals Pleiotropic Effects of HvABCG31 Gene on Cuticle Biogenesis and Stress Responsive Pathways. International Journal of Molecular Sciences, 2013, 14, 20478-20491.	1.8	9
98	Arabidopsis Paired Amphipathic Helix Proteins SNL1 and SNL2 Redundantly Regulate Primary Seed Dormancy via Abscisic Acid-Ethylene Antagonism Mediated by Histone Deacetylation. Plant Cell, 2013, 25, 149-166.	3.1	140
99	Profiling of Differentially Expressed Genes in Roots of Robinia pseudoacacia during Nodule Development Using Suppressive Subtractive Hybridization. PLoS ONE, 2013, 8, e63930.	1.1	13
100	Protein Profiling and Histone Deacetylation Activities in Somaclonal Variants of Oil Palm (Elaeis Tj ETQq1 1 0.784314 rgBT /Overl	0.8	16
101	QTL meta-analysis in Arabidopsis reveals an interaction between leaf senescence and resource allocation to seeds. Journal of Experimental Botany, 2014, 65, 3949-3962.	2.4	42
102	Genetic and epigenetic changes in a genomic region containing MIR172 in Arabidopsis allopolyploids and their progenitors. Heredity, 2014, 112, 207-214.	1.2	9
103	Plants Release Precursors of Histone Deacetylase Inhibitors to Suppress Growth of Competitors. Plant Cell, 2015, 27, 3175-3189.	3.1	86
104	DNA Damage Repair in the Context of Plant Chromatin. Plant Physiology, 2015, 168, 1206-1218.	2.3	55
105	SCARECROW-LIKE15 interacts with HISTONE DEACETYLASE19 and is essential for repressing the seed maturation programme. Nature Communications, 2015, 6, 7243.	5.8	58
106	Histone H2B Monoubiquitination Mediated by HISTONE MONOUBIQUITINATION1 and HISTONE MONOUBIQUITINATION2 Is Involved in Anther Development by Regulating Tapetum Degradation-Related Genes in Rice. Plant Physiology, 2015, 168, 1389-1405.	2.3	78
107	Identification and characterization of histone deacetylases in tomato (Solanum lycopersicum). Frontiers in Plant Science, 2014, 5, 760.	1.7	58
108	Overexpression of a truncated CTF7 construct leads to pleiotropic defects in reproduction and vegetative growth in Arabidopsis. BMC Plant Biology, 2015, 15, 74.	1.6	3

#	ARTICLE	IF	CITATIONS
109	POWERDRESS interacts with HISTONE DEACETYLASE 9 to promote aging in Arabidopsis. <i>ELife</i> , 2016, 5, .	2.8	143
110	AtHD2D Gene Plays a Role in Plant Growth, Development, and Response to Abiotic Stresses in <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 310.	1.7	90
111	Long-Term Boron-Excess-Induced Alterations of Gene Profiles in Roots of Two Citrus Species Differing in Boron-Tolerance Revealed by cDNA-AFLP. <i>Frontiers in Plant Science</i> , 2016, 7, 898.	1.7	9
112	<i>Arabidopsis</i> DNA polymerase β recruits components of Polycomb repressor complex to mediate epigenetic gene silencing. <i>Nucleic Acids Research</i> , 2016, 44, 5597-5614.	6.5	34
113	The WD40 Domain Protein MSI1 Functions in a Histone Deacetylase Complex to Fine-Tune Abscisic Acid Signaling. <i>Plant Cell</i> , 2016, 28, 42-54.	3.1	116
114	Epigenetic Modifications and Plant Hormone Action. <i>Molecular Plant</i> , 2016, 9, 57-70.	3.9	146
115	Fine mapping identifies CsGCN5 encoding a histone acetyltransferase as putative candidate gene for tendril-less1 mutation (td-1) in cucumber. <i>Theoretical and Applied Genetics</i> , 2017, 130, 1549-1558.	1.8	39
116	Heterologous protein-DNA interactions lead to biased allelic expression of circadian clock genes in interspecific hybrids. <i>Scientific Reports</i> , 2017, 7, 45087.	1.6	10
117	Identification and expression analysis of genes involved in histone acetylation in <i>Hevea brasiliensis</i> . <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	7
118	Characterization and Expression Analysis of Common Bean <i>Histone Deacetylase 6</i> during Development and Cold Stress Response. <i>International Journal of Genomics</i> , 2017, 2017, 1-12.	0.8	10
119	Control of Maize Vegetative and Reproductive Development, Fertility, and rRNAs Silencing by <i>HISTONE DEACETYLASE 108</i> . <i>Genetics</i> , 2018, 208, 1443-1466.	1.2	30
120	Characterization and subcellular localization of histone deacetylases and their roles in response to abiotic stresses in soybean. <i>BMC Plant Biology</i> , 2018, 18, 226.	1.6	38
121	Histone acetyltransferase GCN5-mediated regulation of long non-coding RNA At4 contributes to phosphate starvation response in <i>Arabidopsis</i> . <i>Journal of Experimental Botany</i> , 2019, 70, 6337-6348.	2.4	30
122	Diurnal regulation of SDG2 and JMJ14 by circadian clock oscillators orchestrates histone modification rhythms in <i>Arabidopsis</i> . <i>Genome Biology</i> , 2019, 20, 170.	3.8	22
123	Histone Deacetylase HDT1 is Involved in Stem Vascular Development in <i>Arabidopsis</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 3452.	1.8	6
124	Different Modes of Action of Genetic and Chemical Downregulation of Histone Deacetylases with Respect to Plant Development and Histone Modifications. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5093.	1.8	14
125	The <i>HAC1</i> histone acetyltransferase promotes leaf senescence and regulates the expression of <i>ERF022</i> . <i>Plant Direct</i> , 2019, 3, e00159.	0.8	27
126	Dissecting the pathways coordinating patterning and growth by plant boundary domains. <i>PLoS Genetics</i> , 2019, 15, e1007913.	1.5	36

#	ARTICLE	IF	CITATIONS
127	Interactive roles of chromatin regulation and circadian clock function in plants. <i>Genome Biology</i> , 2019, 20, 62.	3.8	26
128	Molecular cloning and subcellular localization of six HDACs and their roles in response to salt and drought stress in kenaf (<i>Hibiscus cannabinus</i> L.). <i>Biological Research</i> , 2019, 52, 20.	1.5	24
129	HOS15 Interacts with the Histone Deacetylase HDA9 and the Evening Complex to Epigenetically Regulate the Floral Activator <i>GIGANTEA</i> . <i>Plant Cell</i> , 2019, 31, 37-51.	3.1	65
130	Genome-wide Target Mapping Shows Histone Deacetylase Complex1 Regulates Cell Proliferation in Cucumber Fruit. <i>Plant Physiology</i> , 2020, 182, 167-184.	2.3	47
131	The Interplay between Toxic and Essential Metals for Their Uptake and Translocation Is Likely Governed by DNA Methylation and Histone Deacetylation in Maize. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6959.	1.8	17
132	Epigenetic Landmarks of Leaf Senescence and Crop Improvement. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5125.	1.8	18
133	Genome-wide identification and expression patterns analysis of the RPD3/HDA1 gene family in cotton. <i>BMC Genomics</i> , 2020, 21, 643.	1.2	11
134	Integrative transcriptomics reveals genotypic impact on sugar beet storability. <i>Plant Molecular Biology</i> , 2020, 104, 359-378.	2.0	9
135	Histone Deacetylase HDA9 With ABI4 Contributes to Abscisic Acid Homeostasis in Drought Stress Response. <i>Frontiers in Plant Science</i> , 2020, 11, 143.	1.7	59
136	Cell identity specification in plants: lessons from flower development. <i>Journal of Experimental Botany</i> , 2021, 72, 4202-4217.	2.4	16
138	Insights Into the Molecular Evolution of AT-Hook Motif Nuclear Localization Genes in <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 714305.	1.7	5
139	Genetic Mechanisms Enhancing Plant Biodiversity. <i>Sustainable Agriculture Reviews</i> , 2011, , 51-86.	0.6	1
141	Chromatin, Aging, and Cellular Senescence. , 2003, , .		0
142	Gene Silencing and its Applications in Plants. , 2011, , 241-251.		0
143	Epigenetic Mechanisms of Senescence in Plants. <i>Cells</i> , 2022, 11, 251.	1.8	9
144	Local Rather than Global H3K27me3 Dynamics Are Associated with Differential Gene Expression in <i>Verticillium dahliae</i> . <i>MBio</i> , 2022, 13, e0356621.	1.8	14
145	An Efficient and Universal Protoplast Isolation Protocol Suitable for Transient Gene Expression Analysis and Single-Cell RNA Sequencing. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3419.	1.8	19
146	Profiling of H3K4me3 and H3K27me3 and Their Roles in Gene Subfunctionalization in Allotetraploid Cotton. <i>Frontiers in Plant Science</i> , 2021, 12, 761059.	1.7	8

#	ARTICLE	IF	CITATIONS
147	Genome-wide identification and expression analysis of the HD2 protein family and its response to drought and salt stress in <i>Gossypium</i> species. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	1