## Xin-Jian He

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3773893/publications.pdf Version: 2024-02-01



XIN-IIAN HE

#	Article	IF	CITATIONS
1	The <i>Arabidopsis</i> NFYA5 Transcription Factor Is Regulated Transcriptionally and Posttranscriptionally to Promote Drought Resistance. Plant Cell, 2008, 20, 2238-2251.	6.6	812
2	AtNAC2, a transcription factor downstream of ethylene and auxin signaling pathways, is involved in salt stress response and lateral root development. Plant Journal, 2005, 44, 903-916.	5.7	634
3	Modulation of Ethylene Responses Affects Plant Salt-Stress Responses. Plant Physiology, 2007, 143, 707-719.	4.8	474
4	Regulation and function of DNA methylation in plants and animals. Cell Research, 2011, 21, 442-465.	12.0	421
5	An Effector of RNA-Directed DNA Methylation in Arabidopsis Is an ARGONAUTE 4- and RNA-Binding Protein. Cell, 2009, 137, 498-508.	28.9	220
6	DTF1 is a core component of RNA-directed DNA methylation and may assist in the recruitment of Pol IV. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 8290-8295.	7.1	158
7	The SET Domain Proteins SUVH2 and SUVH9 Are Required for Pol V Occupancy at RNA-Directed DNA Methylation Loci. PLoS Genetics, 2014, 10, e1003948.	3.5	152
8	A Dicer-Independent Route for Biogenesis of siRNAs that Direct DNA Methylation in Arabidopsis. Molecular Cell, 2016, 61, 222-235.	9.7	134
9	NRPD4, a protein related to the RPB4 subunit of RNA polymerase II, is a component of RNA polymerases IV and V and is required for RNA-directed DNA methylation. Genes and Development, 2009, 23, 318-330.	5.9	126
10	A rice transcription factor OsbHLH1 is involved in cold stress response. Theoretical and Applied Genetics, 2003, 107, 1402-1409.	3.6	106
11	Two novel NAC transcription factors regulate gene expression and flowering time by associating with the histone demethylase JMJ14. Nucleic Acids Research, 2015, 43, 1469-1484.	14.5	94
12	A conserved transcriptional regulator is required for RNA-directed DNA methylation and plant development. Genes and Development, 2009, 23, 2717-2722.	5.9	92
13	Identification of novel Yap1p and Skn7p binding sites involved in the oxidative stress response of Saccharomyces cerevisiae. Molecular Microbiology, 2005, 58, 1454-1467.	2.5	80
14	Arabidopsis AGDP1 links H3K9me2 to DNA methylation in heterochromatin. Nature Communications, 2018, 9, 4547.	12.8	66
15	A Pre-mRNA-Splicing Factor Is Required for RNA-Directed DNA Methylation in Arabidopsis. PLoS Genetics, 2013, 9, e1003779.	3.5	58
16	A plantâ€specific SWR1 chromatinâ€remodeling complex couples histone H2A.Z deposition with nucleosome sliding. EMBO Journal, 2020, 39, e102008.	7.8	57
17	An SGS3-like protein functions in RNA-directed DNA methylation and transcriptional gene silencing in Arabidopsis. Plant Journal, 2010, 62, 92-99.	5.7	55
18	Folate Polyglutamylation Is Involved in Chromatin Silencing by Maintaining Global DNA Methylation and Histone H3K9 Dimethylation in Arabidopsis. Plant Cell, 2013, 25, 2545-2559.	6.6	54

Xin-Jian He

#	Article	IF	CITATIONS
19	<i><scp>RDM</scp>4</i> modulates cold stress resistance in <i>Arabidopsis</i> partially through the <i><scp>CBF</scp></i> â€mediated pathway. New Phytologist, 2016, 209, 1527-1539.	7.3	54
20	Oxidative Stress Function of the <i>Saccharomyces cerevisiae</i> Skn7 Receiver Domain. Eukaryotic Cell, 2009, 8, 768-778.	3.4	53
21	IDN2 and Its Paralogs Form a Complex Required for RNA–Directed DNA Methylation. PLoS Genetics, 2012, 8, e1002693.	3.5	52
22	The splicing machinery promotes RNA-directed DNA methylation and transcriptional silencing in Arabidopsis. EMBO Journal, 2013, 32, 1128-1140.	7.8	52
23	DREAM complex suppresses DNA methylation maintenance genes and precludes DNA hypermethylation. Nature Plants, 2020, 6, 942-956.	9.3	52
24	The <scp>HDA</scp> 19 histone deacetylase complex is involved in the regulation of flowering time in a photoperiodâ€dependent manner. Plant Journal, 2019, 98, 448-464.	5.7	51
25	A methylatedâ€DNAâ€binding complex required for plant development mediates transcriptional activation of promoter methylated genes. Journal of Integrative Plant Biology, 2019, 61, 120-139.	8.5	45
26	Two Components of the RNA-Directed DNA Methylation Pathway Associate with MORC6 and Silence Loci Targeted by MORC6 in Arabidopsis. PLoS Genetics, 2016, 12, e1006026.	3.5	43
27	The <scp>PEAT</scp> protein complexes are required for histone deacetylation and heterochromatin silencing. EMBO Journal, 2018, 37, .	7.8	42
28	The PRP6-like splicing factor STA1 is involved in RNA-directed DNA methylation by facilitating the production of Pol V-dependent scaffold RNAs. Nucleic Acids Research, 2013, 41, 8489-8502.	14.5	40
29	SUVR2 is involved in transcriptional gene silencing by associating with SNF2-related chromatin-remodeling proteins in Arabidopsis. Cell Research, 2014, 24, 1445-1465.	12.0	38
30	The Splicing Factor PRP31 Is Involved in Transcriptional Gene Silencing and Stress Response in Arabidopsis. Molecular Plant, 2015, 8, 1053-1068.	8.3	36
31	Dual Recognition of H3K4me3 and DNA by the ISWI Component ARID5 Regulates the Floral Transition in Arabidopsis. Plant Cell, 2020, 32, 2178-2195.	6.6	34
32	An atypical component of RNA-directed DNA methylation machinery has both DNA methylation-dependent and -independent roles in locus-specific transcriptional gene silencing. Cell Research, 2011, 21, 1691-1700.	12.0	33
33	The SUMO E3 Ligase-Like Proteins PIAL1 and PIAL2 Interact with MOM1 and Form a Novel Complex Required for Transcriptional Silencing. Plant Cell, 2016, 28, 1215-1229.	6.6	31
34	Spatial Expression and Characterization of a Putative Ethylene Receptor Protein NTHK1 in Tobacco. Plant and Cell Physiology, 2002, 43, 810-815.	3.1	30
35	The CBP/p300 histone acetyltransferases function as plantâ€specific MEDIATOR subunits in <i>Arabidopsis</i> . Journal of Integrative Plant Biology, 2021, 63, 755-771.	8.5	29
36	Non-Coding RNA Transcription and RNA-Directed DNA Methylation in Arabidopsis. Molecular Plant, 2014, 7, 1406-1414.	8.3	28

Xin-Jian He

#	Article	IF	CITATIONS
37	<i>Arabidopsis</i> PWWP domain proteins mediate H3K27 trimethylation on <i>FLC</i> and regulate flowering time. Journal of Integrative Plant Biology, 2018, 60, 362-368.	8.5	27
38	Exogenously overexpressed intronic long noncoding RNAs activate host gene expression by affecting histone modification in Arabidopsis. Scientific Reports, 2020, 10, 3094.	3.3	20
39	Three functionally redundant plant-specific paralogs are core subunits of the SAGA histone acetyltransferase complex in Arabidopsis. Molecular Plant, 2021, 14, 1071-1087.	8.3	20
40	A histone H3K27me3 reader cooperates with a family of PHD fingerâ€containing proteins to regulate flowering time in <i>Arabidopsis</i> . Journal of Integrative Plant Biology, 2021, 63, 787-802.	8.5	19
41	Arabidopsis RPD3-like histone deacetylases form multiple complexes involved in stress response. Journal of Genetics and Genomics, 2021, 48, 369-383.	3.9	18
42	The Cytosolic Iron-Sulfur Cluster Assembly Protein MMS19 Regulates Transcriptional Gene Silencing, DNA Repair, and Flowering Time in Arabidopsis. PLoS ONE, 2015, 10, e0129137.	2.5	17
43	COMPASS functions as a module of the INO80 chromatin remodeling complex to mediate histone H3K4 methylation in Arabidopsis. Plant Cell, 2021, 33, 3250-3271.	6.6	17
44	The <i>Arabidopsis</i> NuA4 histone acetyltransferase complex is required for chlorophyll biosynthesis and photosynthesis. Journal of Integrative Plant Biology, 2022, 64, 901-914.	8.5	17
45	Characterization of a novel cell cycle-related gene from Arabidopsis. Journal of Experimental Botany, 2005, 56, 807-816.	4.8	16
46	The Arabidopsis acetylated histone-binding protein BRAT1 forms a complex with BRP1 and prevents transcriptional silencing. Nature Communications, 2016, 7, 11715.	12.8	16
47	The CCR4â€NOT complex component NOT1 regulates RNAâ€directed DNA methylation and transcriptional silencing by facilitating Pol IVâ€dependent siRNA production. Plant Journal, 2020, 103, 1503-1515.	5.7	10
48	Tetrahydrofolate Modulates Floral Transition through Epigenetic Silencing. Plant Physiology, 2017, 174, 1274-1284.	4.8	9
49	FHA2 is a plantâ€specific ISWI subunit responsible for stamen development and plant fertility. Journal of Integrative Plant Biology, 2020, 62, 1703-1716.	8.5	9
50	Characterization of an autonomous pathway complex that promotes flowering in <i>Arabidopsis</i> . Nucleic Acids Research, 2022, 50, 7380-7395.	14.5	9
51	Exploring potential roles for the interaction of MOM1 with SUMO and the SUMO E3 ligase-like protein PIAL2 in transcriptional silencing. PLoS ONE, 2018, 13, e0202137.	2.5	5
52	FVE promotes RNAâ€directed DNA methylation by facilitating the association of RNA polymerase V with chromatin. Plant Journal, 2021, 107, 467-479.	5.7	5
53	The RNA recognition motifâ€containing protein UBA2c prevents early flowering by promoting transcription of the flowering repressor <i>FLM</i> in Arabidopsis. New Phytologist, 2022, 233, 751-765. 	7.3	5
54	Sumoylation of SUVR2 contributes to its role in transcriptional gene silencing. Science China Life Sciences, 2018, 61, 235-243.	4.9	3