Xin-Jian He

List of Publications by Year
in descending order

54 papers	4,778 citations	168829 31 h-index	182931 54 g-index
54 all docs	54 docs citations	54 times ranked	6659 citing authors

#	Article	IF	Citations
1	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.	3.5	5
2	The <i>Arabidopsis</i> NuA4 histone acetyltransferase complex is required for chlorophyll biosynthesis and photosynthesis. Journal of Integrative Plant Biology, 2022, 64, 901-914.	4.1	17
3	Characterization of an autonomous pathway complex that promotes flowering in <i>Arabidopsis</i>. Nucleic Acids Research, 2022, 50, 7380-7395.	6.5	9
4	The CBP/p300 histone acetyltransferases function as plantâ€specific MEDIATOR subunits in <i>Arabidopsis</i>. Journal of Integrative Plant Biology, 2021, 63, 755-771.	4.1	29
5	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.	4.1	19
6	FVE promotes RNAâ€directed DNA methylation by facilitating the association of RNA polymerase V with chromatin. Plant Journal, 2021, 107, 467-479.	2.8	5
7	Arabidopsis RPD3-like histone deacetylases form multiple complexes involved in stress response. Journal of Genetics and Genomics, 2021, 48, 369-383.	1.7	18
8	Three functionally redundant plant-specific paralogs are core subunits of the SAGA histone acetyltransferase complex in Arabidopsis. Molecular Plant, 2021, 14, 1071-1087.	3.9	20
9	COMPASS functions as a module of the INO80 chromatin remodeling complex to mediate histone H3K4 methylation in Arabidopsis. Plant Cell, 2021, 33, 3250-3271.	3.1	17
10	DREAM complex suppresses DNA methylation maintenance genes and precludes DNA hypermethylation. Nature Plants, 2020, 6, 942-956.	4.7	52
11	Dual Recognition of H3K4me3 and DNA by the ISWI Component ARID5 Regulates the Floral Transition in Arabidopsis. Plant Cell, 2020, 32, 2178-2195.	3.1	34
12	FHA2 is a plantâ€specific ISWI subunit responsible for stamen development and plant fertility. Journal of Integrative Plant Biology, 2020, 62, 1703-1716.	4.1	9
13	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.	2.8	10
14	A plantâ€specific SWR1 chromatinâ€remodeling complex couples histone H2A.Z deposition with nucleosome sliding. EMBO Journal, 2020, 39, e102008.	3.5	57
15	Exogenously overexpressed intronic long noncoding RNAs activate host gene expression by affecting histone modification in Arabidopsis. Scientific Reports, 2020, 10, 3094.	1.6	20
16	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.	2.8	51
17	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.	4.1	45
18	<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.	4.1	27

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19	Sumoylation of SUVR2 contributes to its role in transcriptional gene silencing. Science China Life Sciences, 2018, 61, 235-243.	2.3	3
20	Arabidopsis AGDP1 links H3K9me2 to DNA methylation in heterochromatin. Nature Communications, 2018, 9, 4547.	5.8	66
21	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.	1.1	5
22	The <scp>PEAT</scp> protein complexes are required for histone deacetylation and heterochromatin silencing. EMBO Journal, 2018, 37, .	3.5	42
23	Tetrahydrofolate Modulates Floral Transition through Epigenetic Silencing. Plant Physiology, 2017, 174, 1274-1284.	2.3	9
24	<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.	3.5	54
25	The Arabidopsis acetylated histone-binding protein BRAT1 forms a complex with BRP1 and prevents transcriptional silencing. Nature Communications, 2016, 7, 11715.	5.8	16
26	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.	3.1	31
27	A Dicer-Independent Route for Biogenesis of siRNAs that Direct DNA Methylation in Arabidopsis. Molecular Cell, 2016, 61, 222-235.	4.5	134
28	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.	1.5	43
29	The Cytosolic Iron-Sulfur Cluster Assembly Protein MMS19 Regulates Transcriptional Gene Silencing, DNA Repair, and Flowering Time in Arabidopsis. PLoS ONE, 2015, 10, e0129137.	1.1	17
30	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.	6.5	94
31	The Splicing Factor PRP31 Is Involved in Transcriptional Gene Silencing and Stress Response in Arabidopsis. Molecular Plant, 2015, 8, 1053-1068.	3.9	36
32	SUVR2 is involved in transcriptional gene silencing by associating with SNF2-related chromatin-remodeling proteins in Arabidopsis. Cell Research, 2014, 24, 1445-1465.	5.7	38
33	The SET Domain Proteins SUVH2 and SUVH9 Are Required for Pol V Occupancy at RNA-Directed DNA Methylation Loci. PLoS Genetics, 2014, 10, e1003948.	1.5	152
34	Non-Coding RNA Transcription and RNA-Directed DNA Methylation in Arabidopsis. Molecular Plant, 2014, 7, 1406-1414.	3.9	28
35	The splicing machinery promotes RNA-directed DNA methylation and transcriptional silencing in Arabidopsis. EMBO Journal, 2013, 32, 1128-1140.	3.5	52
36	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.	3.3	158

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37	A Pre-mRNA-Splicing Factor Is Required for RNA-Directed DNA Methylation in Arabidopsis. PLoS Genetics, 2013, 9, e1003779.	1.5	58
38	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.	6.5	40
39	Folate Polyglutamylation Is Involved in Chromatin Silencing by Maintaining Global DNA Methylation and Histone H3K9 Dimethylation in Arabidopsis. Plant Cell, 2013, 25, 2545-2559.	3.1	54
40	IDN2 and Its Paralogs Form a Complex Required for RNAâ€“Directed DNA Methylation. PLoS Genetics, 2012, 8, e1002693.	1.5	52
41	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.	5.7	33
42	Regulation and function of DNA methylation in plants and animals. Cell Research, 2011, 21, 442-465.	5.7	421
43	An SGS3-like protein functions in RNA-directed DNA methylation and transcriptional gene silencing in Arabidopsis. Plant Journal, 2010, 62, 92-99.	2.8	55
44	A conserved transcriptional regulator is required for RNA-directed DNA methylation and plant development. Genes and Development, 2009, 23, 2717-2722.	2.7	92
45	Oxidative Stress Function of the <i>Saccharomyces cerevisiae</i> Skn7 Receiver Domain. Eukaryotic Cell, 2009, 8, 768-778.	3.4	53
46	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.	2.7	126
47	An Effector of RNA-Directed DNA Methylation in Arabidopsis Is an ARGONAUTE 4- and RNA-Binding Protein. Cell, 2009, 137, 498-508.	13.5	220
48	The <i>Arabidopsis</i> NFYA5 Transcription Factor Is Regulated Transcriptionally and Posttranscriptionally to Promote Drought Resistance. Plant Cell, 2008, 20, 2238-2251.	3.1	812
49	Modulation of Ethylene Responses Affects Plant Salt-Stress Responses. Plant Physiology, 2007, 143, 707-719.	2.3	474
50	Identification of novel Yap1p and Skn7p binding sites involved in the oxidative stress response of Saccharomyces cerevisiae. Molecular Microbiology, 2005, 58, 1454-1467.	1.2	80
51	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.	2.8	634
52	Characterization of a novel cell cycle-related gene from Arabidopsis. Journal of Experimental Botany, 2005, 56, 807-816.	2.4	16
53	A rice transcription factor OsbHLH1 is involved in cold stress response. Theoretical and Applied Genetics, 2003, 107, 1402-1409.	1.8	106
54	Spatial Expression and Characterization of a Putative Ethylene Receptor Protein NTHK1 in Tobacco. Plant and Cell Physiology, 2002, 43, 810-815.	1.5	30