

# Wen-Hui Shen

## List of Publications by Year in descending order

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110  
papers

6,530  
citations

57681

46  
h-index

81351

76  
g-index

112  
all docs

112  
docs citations

112  
times ranked

5978  
citing authors

#	ARTICLE	IF	CITATIONS
1	Arabidopsis CHROMATIN REMODELING 19 acts as a transcriptional repressor and contributes to plant pathogen resistance. <i>Plant Cell</i> , 2022, 34, 1100-1116.	3.1	13
2	H3K36 methyltransferase SDG708 enhances drought tolerance by promoting abscisic acid biosynthesis in rice. <i>New Phytologist</i> , 2021, 230, 1967-1984.	3.5	18
3	OsChz1 acts as a histone chaperone in modulating chromatin organization and genome function in rice. <i>Nature Communications</i> , 2020, 11, 5717.	5.8	9
4	NAP1-Related Protein 1 (NRP1) has multiple interaction modes for chaperoning histones H2A-H2B. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 30391-30399.	3.3	13
5	The histone methylation readers MRC1/MRC2 and the histone chaperones NRP1/NRP2 associate in fine-tuning Arabidopsis flowering time. <i>Plant Journal</i> , 2020, 103, 1010-1024.	2.8	13
6	MRC1/2 histone methylation readers and HD2C histone deacetylase associate in repression of the florigen gene <i>FT</i> to set a proper flowering time in response to daylength changes. <i>New Phytologist</i> , 2020, 227, 1453-1466.	3.5	22
7	Arabidopsis SDG8 Potentiates the Sustainable Transcriptional Induction of the Pathogenesis-Related Genes PR1 and PR2 During Plant Defense Response. <i>Frontiers in Plant Science</i> , 2020, 11, 277.	1.7	36
8	AtINO80 represses photomorphogenesis by modulating nucleosome density and H2A.Z incorporation in light-related genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 33679-33688.	3.3	22
9	Evolution and conservation of polycomb repressive complex 1 core components and putative associated factors in the green lineage. <i>BMC Genomics</i> , 2019, 20, 533.	1.2	27
10	H3K4me2 functions as a repressive epigenetic mark in plants. <i>Epigenetics and Chromatin</i> , 2019, 12, 40.	1.8	51
11	The transcription factor OsSUF4 interacts with SDG725 in promoting H3K36me3 establishment. <i>Nature Communications</i> , 2019, 10, 2999.	5.8	29
12	AtINO80 and AtARP5 physically interact and play common as well as distinct roles in regulating plant growth and development. <i>New Phytologist</i> , 2019, 223, 336-353.	3.5	21
13	Functional Coordination of the Chromatin-Remodeling Factor AtINO80 and the Histone Chaperones NRP1/2 in Inflorescence Meristem and Root Apical Meristem. <i>Frontiers in Plant Science</i> , 2019, 10, 115.	1.7	12
14	Arabidopsis ZUOTIN RELATED FACTOR1 Proteins Are Required for Proper Embryonic and Post-Embryonic Root Development. <i>Frontiers in Plant Science</i> , 2019, 10, 1498.	1.7	3
15	Interactive and noninteractive roles of histone H2B monoubiquitination and H3K36 methylation in the regulation of active gene transcription and control of plant growth and development. <i>New Phytologist</i> , 2019, 221, 1101-1116.	3.5	53
16	Histone chaperones play crucial roles in maintenance of stem cell niche during plant root development. <i>Plant Journal</i> , 2018, 95, 86-100.	2.8	20
17	Chromatin remodeling factor OsINO80 is involved in regulation of gibberellin biosynthesis and is crucial for rice plant growth and development. <i>Journal of Integrative Plant Biology</i> , 2018, 60, 144-159.	4.1	30
18	Linking PHYTOCHROME-INTERACTING FACTOR to Histone Modification in Plant Shade Avoidance. <i>Plant Physiology</i> , 2018, 176, 1341-1351.	2.3	55

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19	jaw-1D: a gain-of-function mutation responsive to paramutation-like induction of epigenetic silencing. <i>Journal of Experimental Botany</i> , 2018, 70, 459-468.	2.4	4
20	Structural Analysis of the Arabidopsis AL2-PAL and PRC1 Complex Provides Mechanistic Insight into Active-to-Repressive Chromatin State Switch. <i>Journal of Molecular Biology</i> , 2018, 430, 4245-4259.	2.0	11
21	Histone lysine methyltransferases Bna<scp>SDG</scp>8.A and Bna<scp>SDG</scp>8.C are involved in the floral transition in <i>Brassica napus</i> . <i>Plant Journal</i> , 2018, 95, 672-685.	2.8	26
22	Chromatin modulation and gene regulation in plants: insight about PRC1 function. <i>Biochemical Society Transactions</i> , 2018, 46, 957-966.	1.6	31
23	Conservation and diversification of polycomb repressive complex 2 (PRC2) proteins in the green lineage. <i>Briefings in Functional Genomics</i> , 2017, 16, 106-119.	1.3	24
24	The Histone Chaperone NRP1 Interacts with WEREWOLF to Activate <i>GLABRA2</i> in Arabidopsis Root Hair Development. <i>Plant Cell</i> , 2017, 29, 260-276.	3.1	35
25	SDG2-Mediated H3K4me3 Is Crucial for Chromatin Condensation and Mitotic Division during Male Gametogenesis in Arabidopsis. <i>Plant Physiology</i> , 2017, 174, 1205-1215.	2.3	32
26	SET DOMAIN GROUP701 encodes a H3K4-specific methyltransferase and regulates multiple key processes of rice plant development. <i>New Phytologist</i> , 2017, 215, 609-623.	3.5	44
27	Arabidopsis Flower and Embryo Developmental Genes are Repressed in Seedlings by Different Combinations of Polycomb Group Proteins in Association with Distinct Sets of Cis-regulatory Elements. <i>PLoS Genetics</i> , 2016, 12, e1005771.	1.5	125
28	Transcription factors AS1 and AS2 interact with LHP1 to repress <i>KNOX</i> genes in <i>Arabidopsis</i> . <i>Journal of Integrative Plant Biology</i> , 2016, 58, 959-970.	4.1	45
29	Arabidopsis PRC1 core component AtRING1 regulates stem cell-determining carpel development mainly through repression of class I KNOX genes. <i>BMC Biology</i> , 2016, 14, 112.	1.7	30
30	The evolutionary landscape of PRC1 core components in green lineage. <i>Planta</i> , 2016, 243, 825-846.	1.6	20
31	ZRF1 Chromatin Regulators Have Polycomb Silencing and Independent Roles in Development. <i>Plant Physiology</i> , 2016, 172, 1746-1759.	2.3	23
32	Distinct roles of the histone chaperones <scp>NAP</scp>1 and <scp>NRP</scp> and the chromatin remodeling factor <scp>INO</scp>80 in somatic homologous recombination in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2016, 88, 397-410.	2.8	44
33	SET DOMAIN GROUP 708, a histone H3 lysine 36-specific methyltransferase, controls flowering time in rice ( <i>Oryza sativa</i> ). <i>New Phytologist</i> , 2016, 210, 577-588.	3.5	49
34	Interplay of the histone methyltransferases SDG8 and SDG26 in the regulation of transcription and plant flowering and development. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2016, 1859, 581-590.	0.9	27
35	Genome-wide gene expression profiling to investigate molecular phenotypes of Arabidopsis mutants deprived in distinct histone methyltransferases and demethylases. <i>Genomics Data</i> , 2015, 4, 143-145.	1.3	18
36	The chromatin remodeling factor At<scp>INO</scp>80 plays crucial roles in genome stability maintenance and in plant development. <i>Plant Journal</i> , 2015, 82, 655-668.	2.8	57

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37	The trx<sc>G</sc> family histone methyltransferase <sc>SET DOMAIN GROUP</sc>Â26 promotes flowering via a distinctive genetic pathway. <i>Plant Journal</i> , 2015, 81, 316-328.	2.8	61
38	A methyltransferase required for proper timing of the vernalization response in <i>Arabidopsis</i>. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 2269-2274.	3.3	43
39	Histone H2A/H2B chaperones: from molecules to chromatinâ€based functions in plant growth and development. <i>Plant Journal</i> , 2015, 83, 78-95.	2.8	83
40	Arabidopsis AL PHD-PRC1 Complexes Promote Seed Germination through H3K4me3-to-H3K27me3 Chromatin State Switch in Repression of Seed Developmental Genes. <i>PLoS Genetics</i> , 2014, 10, e1004091.	1.5	176
41	Dynamic regulation and function of histone monoubiquitination in plants. <i>Frontiers in Plant Science</i> , 2014, 5, 83.	1.7	64
42	Combinatorial functions of diverse histone methylations in <i><sc>A</sc>rabidopsis thaliana</i> flowering time regulation. <i>New Phytologist</i> , 2014, 201, 312-322.	3.5	66
43	Histone H2B Monoubiquitination is Involved in the Regulation of Cutin and Wax Composition in <i>Arabidopsis thaliana</i> . <i>Plant and Cell Physiology</i> , 2014, 55, 455-466.	1.5	86
44	Histone chaperone <sc>ASF1</sc> is involved in gene transcription activation in response to heat stress in <sc><i>A</i></sc><i>rabidopsis thaliana</i>. <i>Plant, Cell and Environment</i> , 2014, 37, 2128-2138.	2.8	72
45	Functional conservation and divergence of J-domain-containing ZUO1/ZRF orthologs throughout evolution. <i>Planta</i> , 2014, 239, 1159-1173.	1.6	27
46	Epigenetic regulation of rice flowering and reproduction. <i>Frontiers in Plant Science</i> , 2014, 5, 803.	1.7	61
47	H3K36 Methylation Is Involved in Promoting Rice Flowering. <i>Molecular Plant</i> , 2013, 6, 975-977.	3.9	42
48	The Polycomb Complex PRC1: Composition and Function in Plants. <i>Journal of Genetics and Genomics</i> , 2013, 40, 231-238.	1.7	59
49	A LIM Domain Protein from Tobacco Involved in Actin-Bundling and Histone Gene Transcription. <i>Molecular Plant</i> , 2013, 6, 483-502.	3.9	33
50	SDG2-Mediated H3K4 Methylation Is Required for Proper Arabidopsis Root Growth and Development. <i>PLoS ONE</i> , 2013, 8, e56537.	1.1	69
51	NAP1 Family Histone Chaperones Are Required for Somatic Homologous Recombination in Arabidopsis. <i>Plant Cell</i> , 2012, 24, 1437-1447.	3.1	77
52	Histone variants and chromatin assembly in plant abiotic stress responses. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2012, 1819, 343-348.	0.9	83
53	H3K36 methylation is critical for brassinosteroidâ€regulated plant growth and development in rice. <i>Plant Journal</i> , 2012, 70, 340-347.	2.8	93
54	TCP transcription factors interact with AS2 in the repression of classâ€ <i>KNOX</i> genes in <i>Arabidopsis thaliana</i>. <i>Plant Journal</i> , 2012, 71, 99-107.	2.8	94

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55	Chromatin modification and remodelling: a regulatory landscape for the control of Arabidopsis defence responses upon pathogen attack. <i>Cellular Microbiology</i> , 2012, 14, 829-839.	1.1	65
56	Histone modifications in transcriptional activation during plant development. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2011, 1809, 567-576.	0.9	195
57	<i>Arabidopsis</i> homologues of the histone chaperone ASF1 are crucial for chromatin replication and cell proliferation in plant development. <i>Plant Journal</i> , 2011, 66, 443-455.	2.8	79
58	Phylogenetic analysis and classification of the Brassica rapa SET-domain protein family. <i>BMC Plant Biology</i> , 2011, 11, 175.	1.6	42
59	HIGH NITROGEN INSENSITIVE 9 (HNI9)-mediated systemic repression of root NO <sub>3</sub> uptake is associated with changes in histone methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 13329-13334.	3.3	108
60	SDG714 Regulates Specific Gene Expression and Consequently Affects Plant Growth via H3K9 Dimethylation. <i>Journal of Integrative Plant Biology</i> , 2010, 52, 420-430.	4.1	12
61	Arabidopsis Histone Methyltransferase SET DOMAIN GROUP8 Mediates Induction of the Jasmonate/Ethylene Pathway Genes in Plant Defense Response to Necrotrophic Fungi. <i>Plant Physiology</i> , 2010, 154, 1403-1414.	2.3	181
62	<i>Arabidopsis</i> SET DOMAIN GROUP2 Is Required for H3K4 Trimethylation and Is Crucial for Both Sporophyte and Gametophyte Development. <i>Plant Cell</i> , 2010, 22, 3232-3248.	3.1	156
63	The Arabidopsis PRC1-like ring-finger proteins are necessary for repression of embryonic traits during vegetative growth. <i>Cell Research</i> , 2010, 20, 1332-1344.	5.7	143
64	Chromatin Remodeling in Stem Cell Maintenance in Arabidopsis thaliana. <i>Molecular Plant</i> , 2009, 2, 600-609.	3.9	68
65	A Truncated Arabidopsis NUCLEOSOME ASSEMBLY PROTEIN 1, AtNAP1;3T, Alters Plant Growth Responses to Abscisic Acid and Salt in the Atnap1;3-2 Mutant. <i>Molecular Plant</i> , 2009, 2, 688-699.	3.9	45
66	An update on histone lysine methylation in plants. <i>Progress in Natural Science: Materials International</i> , 2009, 19, 407-413.	1.8	29
67	The E2 ubiquitin-conjugating enzymes, AtUBC1 and AtUBC2, play redundant roles and are involved in activation of <i>FLC</i> expression and repression of flowering in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2009, 57, 279-288.	2.8	162
68	Molecular and reverse genetic characterization of <i>NUCLEOSOME ASSEMBLY PROTEIN1</i> ( <i>NAP1</i> ) genes unravels their function in transcription and nucleotide excision repair in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2009, 59, 27-38.	2.8	71
69	A Non-canonical Transferred DNA Insertion at the <i>BRI1</i> Locus in <i>Arabidopsis thaliana</i> . <i>Journal of Integrative Plant Biology</i> , 2009, 51, 367-373.	4.1	8
70	<i>SET DOMAIN GROUP25</i> Encodes a Histone Methyltransferase and Is Involved in <i>FLOWERING LOCUS C</i> Activation and Repression of Flowering. <i>Plant Physiology</i> , 2009, 151, 1476-1485.	2.3	102
71	Polycomb Silencing of KNOX Genes Confines Shoot Stem Cell Niches in Arabidopsis. <i>Current Biology</i> , 2008, 18, 1966-1971.	1.8	246
72	Di- and Tri- but Not Monomethylation on Histone H3 Lysine 36 Marks Active Transcription of Genes Involved in Flowering Time Regulation and Other Processes in <i>Arabidopsis thaliana</i> . <i>Molecular and Cellular Biology</i> , 2008, 28, 1348-1360.	1.1	283

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73	Chromatin Remodeling in Arabidopsis Root Growth. <i>Plant Signaling and Behavior</i> , 2007, 2, 160-162.	1.2	3
74	G1/S Transition and the Rb-E2F Pathway. <i>Plant Cell Monographs</i> , 2007, , 59-73.	0.4	2
75	Molecular characterization of three rice SET-domain proteins. <i>Plant Science</i> , 2007, 172, 1072-1078.	1.7	16
76	Plant SET- and RING-associated domain proteins in heterochromatinization. <i>Plant Journal</i> , 2007, 52, 914-926.	2.8	48
77	Arabidopsis NRP1 and NRP2 Encode Histone Chaperones and Are Required for Maintaining Postembryonic Root Growth. <i>Plant Cell</i> , 2006, 18, 2879-2892.	3.1	125
78	Molecular and functional characterization of Arabidopsis Cullin 3A. <i>Plant Journal</i> , 2005, 41, 386-399.	2.8	91
79	Prevention of early flowering by expression of FLOWERING LOCUS C requires methylation of histone H3 K36. <i>Nature Cell Biology</i> , 2005, 7, 1256-1260.	4.6	277
80	Interacting Proteins and Differences in Nuclear Transport Reveal Specific Functions for the NAP1 Family Proteins in Plants. <i>Plant Physiology</i> , 2005, 138, 1446-1456.	2.3	61
81	Ectopic Expression of the NtSET1 Histone Methyltransferase Inhibits Cell Expansion, and Affects Cell Division and Differentiation in Tobacco Plants. <i>Plant and Cell Physiology</i> , 2004, 45, 1715-1719.	1.5	18
82	Molecular characterization of the tobacco SET domain protein NtSET1 unravels its role in histone methylation, chromatin binding, and segregation. <i>Plant Journal</i> , 2004, 40, 699-711.	2.8	52
83	Plants Contain a High Number of Proteins Showing Sequence Similarity to the Animal SUV39H Family of Histone Methyltransferases. <i>Annals of the New York Academy of Sciences</i> , 2004, 1030, 661-669.	1.8	21
84	Regulation of biosynthesis and intracellular localization of rice and tobacco homologues of nucleosome assembly protein 1. <i>Planta</i> , 2003, 216, 561-570.	1.6	47
85	The Tobacco A-Type Cyclin, Nicta;CYCA3;2, at the Nexus of Cell Division and Differentiation. <i>Plant Cell</i> , 2003, 15, 2763-2777.	3.1	117
86	The AtRbx1 Protein Is Part of Plant SCF Complexes, and Its Down-regulation Causes Severe Growth and Developmental Defects. <i>Journal of Biological Chemistry</i> , 2002, 277, 50069-50080.	1.6	59
87	Null Mutation of AtCUL1 Causes Arrest in Early Embryogenesis in Arabidopsis. <i>Molecular Biology of the Cell</i> , 2002, 13, 1916-1928.	0.9	153
88	The plant E2F-Rb pathway and epigenetic control. <i>Trends in Plant Science</i> , 2002, 7, 505-511.	4.3	102
89	A gene trap Dissociation insertion line, associated with a RING-H2 finger gene, shows tissue specific and developmental regulated expression of the gene in Arabidopsis. <i>Gene</i> , 2002, 290, 63-71.	1.0	14
90	NtSET1, a member of a newly identified subgroup of plant SET-domain-containing proteins, is chromatin-associated and its ectopic overexpression inhibits tobacco plant growth. <i>Plant Journal</i> , 2002, 28, 371-383.	2.8	35

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91	The subcellular localization of an unusual rice calmodulin isoform, OsCaM61, depends on its prenylation status. <i>Plant Molecular Biology</i> , 2002, 48, 203-210.	2.0	33
92	Sub-cellular localisation of GFP-tagged tobacco mitotic cyclins during the cell cycle and after spindle checkpoint activation. <i>Plant Journal</i> , 2001, 28, 569-581.	2.8	52
93	The plant cell cycle: G1/S regulation. <i>Euphytica</i> , 2001, 118, 223-236.	0.6	14
94	Cell cycle-dependent proteolysis and ectopic overexpression of cyclin B1 in tobacco BY2 cells. <i>Plant Journal</i> , 2000, 24, 763-773.	2.8	93
95	Regulation of biosynthesis and cellular localization of Sp32 annexins in tobacco BY2 cells. <i>Plant Molecular Biology</i> , 1999, 39, 361-372.	2.0	44
96	T-DNA Transfer to Maize Plants. <i>Molecular Biotechnology</i> , 1999, 13, 165-170.	1.3	3
97	Excision of Ds1 from the genome of maize streak virus in response to different transposase-encoding genes. <i>Plant Molecular Biology</i> , 1998, 36, 387-392.	2.0	9
98	Protein complexes binding to cis elements of the plant histone gene promoters: multiplicity, phosphorylation and cell cycle alteration. , 1997, 33, 367-379.		35
99	Multiple A-type cyclins express sequentially during the cell cycle in <i>Nicotiana tabacum</i> BY2 cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 13819-13824.	3.3	108
100	The binding motifs for Ac transposase are absolutely required for excision of Ds1 in maize. <i>Molecular Genetics and Genomics</i> , 1995, 248, 527-534.	2.4	15
101	Vectors based on maize streak virus can replicate to high copy numbers in maize plants. <i>Journal of General Virology</i> , 1995, 76, 965-969.	1.3	35
102	T-DNA Transfer to Maize Plants. , 1995, 44, 343-350.		0
103	Amplification and expression of the beta-glucuronidase gene in maize plants by vectors based on maize streak virus. <i>Plant Journal</i> , 1994, 5, 227-236.	2.8	40
104	T-DNA transfer to maize cells: histochemical investigation of beta-glucuronidase activity in maize tissues.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1993, 90, 1488-1492.	3.3	59
105	Mechanism of Ds1 excision from the genome of maize streak virus. <i>Molecular Genetics and Genomics</i> , 1992, 233, 388-394.	2.4	14
106	Excision of a transposable element from a viral vector introduced into maize plants by agroinfection.. <i>Plant Journal</i> , 1992, 2, 35-42.	2.8	26
107	Excision of a transposable element from a viral vector introduced into maize plants by agroinfection. <i>Plant Journal</i> , 1992, 2, 35-42.	2.8	0
108	Mutational analysis of the small intergenic region of maize streak virus. <i>Virology</i> , 1991, 183, 721-730.	1.1	27

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109	High Sensitivity to Auxin is a Common Feature of Hairy Root. <i>Plant Physiology</i> , 1990, 94, 554-560.	2.3	73
110	Hairy roots are more sensitive to auxin than normal roots. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1988, 85, 3417-3421.	3.3	216