

# Wen-Hui Shen

## List of Publications by Year in descending order

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110  
papers

6,530  
citations

50276

46  
h-index

71685

76  
g-index

112  
all docs

112  
docs citations

112  
times ranked

5379  
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.  | 6.6  | 13        |
| 2  | H3K36 methyltransferase SDG708 enhances drought tolerance by promoting abscisic acid biosynthesis in rice. <i>New Phytologist</i> , 2021, 230, 1967-1984.   | 7.3  | 18        |
| 3  | OsChz1 acts as a histone chaperone in modulating chromatin organization and genome function in rice. <i>Nature Communications</i> , 2020, 11, 5717.   | 12.8 | 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.                         | 7.1  | 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.  | 5.7  | 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.  | 7.3  | 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.                                  | 3.6  | 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.  | 7.1  | 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.  | 2.8  | 27        |
| 10 | H3K4me2 functions as a repressive epigenetic mark in plants. <i>Epigenetics and Chromatin</i> , 2019, 12, 40.   | 3.9  | 51        |
| 11 | The transcription factor OsSUF4 interacts with SDG725 in promoting H3K36me3 establishment. <i>Nature Communications</i> , 2019, 10, 2999.   | 12.8 | 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.   | 7.3  | 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.                             | 3.6  | 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.  | 3.6  | 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. | 7.3  | 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.   | 5.7  | 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.                        | 8.5  | 30        |
| 18 | Linking PHYTOCHROME-INTERACTING FACTOR to Histone Modification in Plant Shade Avoidance. <i>Plant Physiology</i> , 2018, 176, 1341-1351.  | 4.8  | 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.   | 4.8 | 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.                                      | 4.2 | 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.  | 5.7 | 26        |
| 22 | Chromatin modulation and gene regulation in plants: insight about PRC1 function. <i>Biochemical Society Transactions</i> , 2018, 46, 957-966.   | 3.4 | 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.  | 2.7 | 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.  | 6.6 | 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.  | 4.8 | 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.  | 7.3 | 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.      | 3.5 | 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.  | 8.5 | 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.   | 3.8 | 30        |
| 30 | The evolutionary landscape of PRC1 core components in green lineage. <i>Planta</i> , 2016, 243, 825-846.  | 3.2 | 20        |
| 31 | ZRF1 Chromatin Regulators Have Polycomb Silencing and Independent Roles in Development. <i>Plant Physiology</i> , 2016, 172, 1746-1759.   | 4.8 | 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. | 5.7 | 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.  | 7.3 | 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.                     | 1.9 | 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.  | 5.7 | 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.                                    | 5.7 | 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. | 7.1 | 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.  | 5.7 | 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.                | 3.5 | 176       |
| 41 | Dynamic regulation and function of histone monoubiquitination in plants. <i>Frontiers in Plant Science</i> , 2014, 5, 83.  | 3.6 | 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.  | 7.3 | 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.                                   | 3.1 | 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.  | 5.7 | 72        |
| 45 | Functional conservation and divergence of J-domain-containing ZUO1/ZRF orthologs throughout evolution. <i>Planta</i> , 2014, 239, 1159-1173.   | 3.2 | 27        |
| 46 | Epigenetic regulation of rice flowering and reproduction. <i>Frontiers in Plant Science</i> , 2014, 5, 803.  | 3.6 | 61        |
| 47 | H3K36 Methylation Is Involved in Promoting Rice Flowering. <i>Molecular Plant</i> , 2013, 6, 975-977.  | 8.3 | 42        |
| 48 | The Polycomb Complex PRC1: Composition and Function in Plants. <i>Journal of Genetics and Genomics</i> , 2013, 40, 231-238.  | 3.9 | 59        |
| 49 | A LIM Domain Protein from Tobacco Involved in Actin-Bundling and Histone Gene Transcription. <i>Molecular Plant</i> , 2013, 6, 483-502.  | 8.3 | 33        |
| 50 | SDG2-Mediated H3K4 Methylation Is Required for Proper Arabidopsis Root Growth and Development. <i>PLoS ONE</i> , 2013, 8, e56537.  | 2.5 | 69        |
| 51 | NAP1 Family Histone Chaperones Are Required for Somatic Homologous Recombination in Arabidopsis. <i>Plant Cell</i> , 2012, 24, 1437-1447.  | 6.6 | 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.  | 1.9 | 83        |
| 53 | H3K36 methylation is critical for brassinosteroidâ€regulated plant growth and development in rice. <i>Plant Journal</i> , 2012, 70, 340-347.   | 5.7 | 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.  | 5.7 | 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.  | 2.1  | 65        |
| 56 | Histone modifications in transcriptional activation during plant development. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2011, 1809, 567-576.   | 1.9  | 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.   | 5.7  | 79        |
| 58 | Phylogenetic analysis and classification of the Brassica rapa SET-domain protein family. <i>BMC Plant Biology</i> , 2011, 11, 175.   | 3.6  | 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. | 7.1  | 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.   | 8.5  | 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.  | 4.8  | 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.  | 6.6  | 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.  | 12.0 | 143       |
| 64 | Chromatin Remodeling in Stem Cell Maintenance in Arabidopsis thaliana. <i>Molecular Plant</i> , 2009, 2, 600-609.  | 8.3  | 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.   | 8.3  | 45        |
| 66 | An update on histone lysine methylation in plants. <i>Progress in Natural Science: Materials International</i> , 2009, 19, 407-413.  | 4.4  | 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.                       | 5.7  | 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.       | 5.7  | 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.   | 8.5  | 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.  | 4.8  | 102       |
| 71 | Polycomb Silencing of KNOX Genes Confines Shoot Stem Cell Niches in Arabidopsis. <i>Current Biology</i> , 2008, 18, 1966-1971.   | 3.9  | 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.           | 2.3  | 283       |

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|----|--|------|-----------|
| 73 | Chromatin Remodeling in Arabidopsis Root Growth. <i>Plant Signaling and Behavior</i> , 2007, 2, 160-162.   | 2.4  | 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.   | 3.6  | 16        |
| 76 | Plant SET- and RING-associated domain proteins in heterochromatinization. <i>Plant Journal</i> , 2007, 52, 914-926.  | 5.7  | 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.   | 6.6  | 125       |
| 78 | Molecular and functional characterization of Arabidopsis Cullin 3A. <i>Plant Journal</i> , 2005, 41, 386-399.  | 5.7  | 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.  | 10.3 | 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.  | 4.8  | 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.             | 3.1  | 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.                              | 5.7  | 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.                 | 3.8  | 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.   | 3.2  | 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.  | 6.6  | 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.                              | 3.4  | 59        |
| 87 | Null Mutation of AtCUL1 Causes Arrest in Early Embryogenesis in Arabidopsis. <i>Molecular Biology of the Cell</i> , 2002, 13, 1916-1928.   | 2.1  | 153       |
| 88 | The plant E2F-Rb pathway and epigenetic control. <i>Trends in Plant Science</i> , 2002, 7, 505-511.  | 8.8  | 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.                 | 2.2  | 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. | 5.7  | 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.  | 3.9 | 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.   | 5.7 | 52        |
| 93  | The plant cell cycle: G1/S regulation. <i>Euphytica</i> , 2001, 118, 223-236.  | 1.2 | 14        |
| 94  | Cell cycle-dependent proteolysis and ectopic overexpression of cyclin B1 in tobacco BY2 cells. <i>Plant Journal</i> , 2000, 24, 763-773.   | 5.7 | 93        |
| 95  | Regulation of biosynthesis and cellular localization of Sp32 annexins in tobacco BY2 cells. <i>Plant Molecular Biology</i> , 1999, 39, 361-372.  | 3.9 | 44        |
| 96  | T-DNA Transfer to Maize Plants. <i>Molecular Biotechnology</i> , 1999, 13, 165-170.  | 2.4 | 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.   | 3.9 | 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.  | 7.1 | 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.  | 2.9 | 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.   | 5.7 | 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. | 7.1 | 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.  | 5.7 | 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.   | 5.7 | 0         |
| 108 | Mutational analysis of the small intergenic region of maize streak virus. <i>Virology</i> , 1991, 183, 721-730.  | 2.4 | 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.  | 4.8 | 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. | 7.1 | 216       |