

Raquel L Chan

List of Publications by Year in descending order

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93
papers

4,415
citations

109137

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118652

62
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all docs

99
docs citations

99
times ranked

4273
citing authors

#	ARTICLE	IF	CITATIONS
1	The Arabidopsis transcription factors AtPHL1 and AtHB23 act together promoting carbohydrate transport from pedicel-silique nodes to seeds. <i>Plant Science</i> , 2022, 315, 111133.	1.7	3
2	Expressing the sunflower transcription factor HaHB11 in maize improves waterlogging and defoliation tolerance. <i>Plant Physiology</i> , 2022, 189, 230-247.	2.3	7
3	The transcription factor AtHB23 modulates starch turnover for root development and plant survival under salinity. <i>Environmental and Experimental Botany</i> , 2022, 201, 104994.	2.0	4
4	The underground life of homeodomain-leucine zipper transcription factors. <i>Journal of Experimental Botany</i> , 2021, 72, 4005-4021.	2.4	21
5	The AtHB1 Transcription Factor Controls the miR164-CUC2 Regulatory Node to Modulate Leaf Development. <i>Plant and Cell Physiology</i> , 2020, 61, 659-670.	1.5	15
6	Key role of the motor protein Kinesin 13B in the activity of homeodomain-leucine zipper I transcription factors. <i>Journal of Experimental Botany</i> , 2020, 71, 6282-6296.	2.4	4
7	Why are second-generation transgenic crops not yet available in the market?. <i>Journal of Experimental Botany</i> , 2020, 71, 6876-6880.	2.4	13
8	An Interdisciplinary Approach to Study the Performance of Second-generation Genetically Modified Crops in Field Trials: A Case Study With Soybean and Wheat Carrying the Sunflower HaHB4 Transcription Factor. <i>Frontiers in Plant Science</i> , 2020, 11, 178.	1.7	26
9	Successful field performance in warm and dry environments of soybean expressing the sunflower transcription factor HB4. <i>Journal of Experimental Botany</i> , 2020, 71, 3142-3156.	2.4	41
10	Lateral root development differs between main and secondary roots and depends on the ecotype. <i>Plant Signaling and Behavior</i> , 2020, 15, 1755504.	1.2	9
11	Maize expressing the sunflower transcription factor HaHB11 has improved productivity in controlled and field conditions. <i>Plant Science</i> , 2019, 287, 110185.	1.7	9
12	AtHB23 participates in the gene regulatory network controlling root branching, and reveals differences between secondary and tertiary roots. <i>Plant Journal</i> , 2019, 100, 1224-1236.	2.8	24
13	Arabidopsis and sunflower plants with increased xylem area show enhanced seed yield. <i>Plant Journal</i> , 2019, 99, 717-732.	2.8	13
14	Field-grown transgenic wheat expressing the sunflower gene <i>HaHB4</i> significantly outyields the wild type. <i>Journal of Experimental Botany</i> , 2019, 70, 1669-1681.	2.4	78
15	<i>Arabidopsis thaliana</i> homeodomain-leucine zipper type I transcription factors contribute to control leaf venation patterning. <i>Plant Signaling and Behavior</i> , 2018, 13, e1448334.	1.2	6
16	The antagonistic basic helix-loop-helix partners BEE and IBH1 contribute to control plant tolerance to abiotic stress. <i>Plant Science</i> , 2018, 271, 143-150.	1.7	17
17	Plant transcription factors from the homeodomain-leucine zipper family I. Role in development and stress responses. <i>IUBMB Life</i> , 2017, 69, 280-289.	1.5	63
18	A uORF Represses the Transcription Factor AtHB1 in Aerial Tissues to Avoid a Deleterious Phenotype. <i>Plant Physiology</i> , 2017, 175, 1238-1253.	2.3	40

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19	A role for LAX2 in regulating xylem development and lateral-vein symmetry in the leaf. <i>Annals of Botany</i> , 2017, 120, 577-590.	1.4	33
20	The sunflower transcription factor HaHB11 confers tolerance to water deficit and salinity to transgenic <i>Arabidopsis</i> and alfalfa plants. <i>Journal of Biotechnology</i> , 2017, 257, 35-46.	1.9	28
21	JUNGBRUNNEN1 Confers Drought Tolerance Downstream of the HD-Zip I Transcription Factor AtHB13. <i>Frontiers in Plant Science</i> , 2017, 8, 2118.	1.7	55
22	A Predictive Coexpression Network Identifies Novel Genes Controlling the Seed-to-Seedling Phase Transition in <i>Arabidopsis thaliana</i> . <i>Plant Physiology</i> , 2016, 170, 2218-2231.	2.3	83
23	A sunflower WRKY transcription factor stimulates the mobilization of seed-stored reserves during germination and post-germination growth. <i>Plant Cell Reports</i> , 2016, 35, 1875-1890.	2.8	27
24	A matter of quantity: Common features in the drought response of transgenic plants overexpressing HD-Zip I transcription factors. <i>Plant Science</i> , 2016, 251, 139-154.	1.7	28
25	The sunflower transcription factor HaHB11 improves yield, biomass and tolerance to flooding in transgenic <i>Arabidopsis</i> plants. <i>Journal of Biotechnology</i> , 2016, 222, 73-83.	1.9	42
26	Homeodomain-“Leucine Zipper Transcription Factors: Structural Features of These Proteins, Unique to Plants. , 2016, , 113-126.		6
27	What Do We Know about Homeodomain-“Leucine Zipper I Transcription Factors? Functional and Biotechnological Considerations. , 2016, , 343-356.		3
28	<i>Arabidopsis thaliana</i> HomeoBox 1 (At<sc>HB</sc>1), a Homeodomain-“Leucine Zipper I (<sc>HD</sc>-“Zip I) transcription factor, is regulated by PHYTOCHROME-INTERACTING FACTOR 1 to promote hypocotyl elongation. <i>New Phytologist</i> , 2015, 207, 669-682.	3.5	69
29	Functional characterization of the homeodomain leucine zipper I transcription factor AtHB13 reveals a crucial role in <i>Arabidopsis</i> development. <i>Journal of Experimental Botany</i> , 2015, 66, 5929-5943.	2.4	48
30	The rice transcription factor OsWRKY47 is a positive regulator of the response to water deficit stress. <i>Plant Molecular Biology</i> , 2015, 88, 401-413.	2.0	92
31	The sunflower transcription factor HaWRKY76 confers drought and flood tolerance to <i>Arabidopsis thaliana</i> plants without yield penalty. <i>Plant Cell Reports</i> , 2015, 34, 2065-2080.	2.8	60
32	Plant science with relevance to biotechnology. <i>Journal of Biotechnology</i> , 2014, 174, iv.	1.9	1
33	Plant homeodomain-leucine zipper I transcription factors exhibit different functional AHA motifs that selectively interact with TBP or/and TFIIB. <i>Plant Cell Reports</i> , 2014, 33, 955-967.	2.8	42
34	<i>Arabidopsis</i> AtHB7 and AtHB12 evolved divergently to fine tune processes associated with growth and responses to water stress. <i>BMC Plant Biology</i> , 2014, 14, 150.	1.6	120
35	Two Direct Targets of Cytokinin Signaling Regulate Symbiotic Nodulation in <i>Medicago truncatula</i> . <i>Plant Cell</i> , 2012, 24, 3838-3852.	3.1	136
36	Role of recently evolved miRNA regulation of sunflower <i>HaWRKY6</i> in response to temperature damage. <i>New Phytologist</i> , 2012, 195, 766-773.	3.5	118

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37	RNAi-mediated silencing of the HD-Zip gene HD20 in <i>Nicotiana attenuata</i> affects benzyl acetone emission from corollas via ABA levels and the expression of metabolic genes. <i>BMC Plant Biology</i> , 2012, 12, 60.	1.6	16
38	The homologous HD-Zip I transcription factors HaHB1 and AtHB13 confer cold tolerance via the induction of pathogenesis-related and glucanase proteins. <i>Plant Journal</i> , 2012, 69, 141-153.	2.8	80
39	The homologous homeodomain-leucine zipper transcription factors HaHB1 and AtHB13 confer tolerance to drought and salinity stresses via the induction of proteins that stabilize membranes. <i>Plant Biotechnology Journal</i> , 2012, 10, 815-825.	4.1	75
40	Uncharacterized conserved motifs outside the HD-Zip domain in HD-Zip subfamily I transcription factors; a potential source of functional diversity. <i>BMC Plant Biology</i> , 2011, 11, 42.	1.6	70
41	HAHB10, a sunflower HD-Zip II transcription factor, participates in the induction of flowering and in the control of phytohormone-mediated responses to biotic stress. <i>Journal of Experimental Botany</i> , 2011, 62, 1061-1076.	2.4	68
42	<i>Nicotiana attenuata</i> NaHD20 plays a role in leaf ABA accumulation during water stress, benzylacetone emission from flowers, and the timing of bolting and flower transitions. <i>Journal of Experimental Botany</i> , 2011, 62, 155-166.	2.4	40
43	The LOB-like transcription factor MtLBD1 controls <i>Medicago truncatula</i> root architecture under salt stress. <i>Plant Signaling and Behavior</i> , 2010, 5, 1666-1668.	1.2	39
44	Transcriptional Control of a Plant Stem Cell Niche. <i>Developmental Cell</i> , 2010, 18, 841-853.	3.1	221
45	Expression analyses indicate the involvement of sunflower WRKY transcription factors in stress responses, and phylogenetic reconstructions reveal the existence of a novel clade in the Asteraceae. <i>Plant Science</i> , 2010, 178, 398-410.	1.7	32
46	Environmental Regulation of Lateral Root Emergence in <i>Medicago truncatula</i> Requires the HD-Zip I Transcription Factor HB1. <i>Plant Cell</i> , 2010, 22, 2171-2183.	3.1	156
47	Transient transformation of sunflower leaf discs via an <i>Agrobacterium</i> -mediated method: applications for gene expression and silencing studies. <i>Nature Protocols</i> , 2009, 4, 1699-1707.	5.5	54
48	Two ABREs, two redundant root-specific and one W-box cis-acting elements are functional in the sunflower HAHB4 promoter. <i>Plant Physiology and Biochemistry</i> , 2008, 46, 860-867.	2.8	21
49	HAHB4, a sunflower HD-Zip protein, integrates signals from the jasmonic acid and ethylene pathways during wounding and biotic stress responses. <i>Plant Journal</i> , 2008, 56, 376-388.	2.8	85
50	The sunflower HD-Zip transcription factor HAHB4 is up-regulated in darkness, reducing the transcription of photosynthesis-related genes. <i>Journal of Experimental Botany</i> , 2008, 59, 3143-3155.	2.4	36
51	Patents on Plant Transcription Factors. <i>Recent Patents on Biotechnology</i> , 2008, 2, 209-217.	0.4	17
52	The true story of the HD-Zip family. <i>Trends in Plant Science</i> , 2007, 12, 419-426.	4.3	508
53	The intron of the <i>Arabidopsis thaliana</i> COX5c gene is able to improve the drought tolerance conferred by the sunflower Hahb-4 transcription factor. <i>Planta</i> , 2007, 226, 1143-1154.	1.6	25
54	Cross-talk between ethylene and drought signalling pathways is mediated by the sunflower Hahb-4 transcription factor. <i>Plant Journal</i> , 2006, 48, 125-137.	2.8	169

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55	Hahb-4, a sunflower homeobox-leucine zipper gene, is a developmental regulator and confers drought tolerance to <i>Arabidopsis thaliana</i> plants. <i>Transgenic Research</i> , 2005, 14, 429-440.	1.3	134
56	The leader intron of <i>Arabidopsis thaliana</i> genes encoding cytochrome c oxidase subunit 5c promotes high-level expression by increasing transcript abundance and translation efficiency. <i>Journal of Experimental Botany</i> , 2005, 56, 2563-2571.	2.4	51
57	Hahb-10, a Sunflower Homeobox-Leucine Zipper Gene, is Regulated by Light Quality and Quantity, and Promotes Early Flowering when Expressed in <i>Arabidopsis</i> . <i>Plant and Cell Physiology</i> , 2005, 46, 1954-1963.	1.5	46
58	The promoter of the sunflower HD-Zip protein gene Hahb4 directs tissue-specific expression and is inducible by water stress, high salt concentrations and ABA. <i>Plant Science</i> , 2005, 169, 447-456.	1.7	36
59	Site-directed mutagenesis and footprinting analysis of the interaction of the sunflower KNOX protein HAKN1 with DNA. <i>FEBS Journal</i> , 2005, 272, 190-202.	2.2	7
60	The promoter of the <i>Arabidopsis</i> nuclear gene COX5b-1, encoding subunit 5b of the mitochondrial cytochrome c oxidase, directs tissue-specific expression by a combination of positive and negative regulatory elements. <i>Journal of Experimental Botany</i> , 2004, 55, 1997-2004.	2.4	33
61	Site-directed mutagenesis and footprinting analysis of the interaction of the sunflower KNOX protein HAKN1 with DNA. <i>FEBS Journal</i> , 2004, 272, 190-202.	2.2	15
62	Homeodomain-leucine Zipper Proteins Interact with a Plant Homologue of the Transcriptional Co-activator Multiprotein Bridging Factor 1. <i>BMB Reports</i> , 2004, 37, 320-334.	1.1	6
63	Nuclear and mitochondrial genes encoding cytochrome c oxidase subunits respond differently to the same metabolic factors. <i>Plant Physiology and Biochemistry</i> , 2003, 41, 689-693.	2.8	24
64	Knotted1-like genes are strongly expressed in differentiated cell types in sunflower. <i>Journal of Experimental Botany</i> , 2003, 54, 681-690.	2.4	13
65	Identification of three MADS-box genes expressed in sunflower capitulum. <i>Journal of Experimental Botany</i> , 2003, 54, 1637-1639.	2.4	16
66	Redox Regulation of Plant Homeodomain Transcription Factors. <i>Journal of Biological Chemistry</i> , 2002, 277, 34800-34807.	1.6	86
67	Genes encoding cytochrome c oxidase subunit 5c from sunflower (<i>Helianthus annuus</i> L.) are regulated by nitrate and oxygen availability. <i>Plant Science</i> , 2002, 163, 897-905.	1.7	10
68	Hahb-4, a homeobox-leucine zipper gene potentially involved in abscisic acid-dependent responses to water stress in sunflower*. <i>Plant, Cell and Environment</i> , 2002, 25, 633-640.	2.8	84
69	Metabolic regulation of genes encoding cytochrome c and cytochrome c oxidase subunit Vb in <i>Arabidopsis</i> . <i>Plant, Cell and Environment</i> , 2002, 25, 1605-1615.	2.8	37
70	Positively charged residues at the N-terminal arm of the homeodomain are required for efficient DNA binding by homeodomain-leucine zipper proteins ¹¹ Edited by M. Yaniv. <i>Journal of Molecular Biology</i> , 2001, 308, 39-47.	2.0	37
71	Combinatorial interactions of two amino acids with a single base pair define target site specificity in plant dimeric homeodomain proteins. <i>Nucleic Acids Research</i> , 2001, 29, 4866-4872.	6.5	36
72	Cell-Type-Specific Expression of Plant Cytochrome c mRNA in Developing Flowers and Roots. <i>Plant Physiology</i> , 2001, 125, 1603-1610.	2.3	23

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73	The Cytochrome c Gene from the Green Alga <i>Chlamydomonas reinhardtii</i> . Structure and Expression in Wild-Type Cells and in Obligate Photoautotrophic (dk) Mutants. <i>Plant and Cell Physiology</i> , 2000, 41, 1149-1156.	1.5	7
74	A monomer-dimer equilibrium modulates the interaction of the sunflower homeodomain leucine-zipper protein Hahb-4 with DNA. <i>Biochemical Journal</i> , 1999, 341, 81-87.	1.7	68
75	A monomer-dimer equilibrium modulates the interaction of the sunflower homeodomain leucine-zipper protein Hahb-4 with DNA. <i>Biochemical Journal</i> , 1999, 341, 81.	1.7	51
76	Homeoboxes in plant development. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1998, 1442, 1-19.	2.4	192
77	Expression of Sunflower Homeodomain Containing Proteins in <i>Escherichia coli</i> : Purification and Functional Studies. <i>Protein Expression and Purification</i> , 1998, 13, 97-103.	0.6	22
78	Isolation and expression pattern of hahr1, a homeobox-containing cDNA from <i>Helianthus annuus</i> . <i>Gene</i> , 1997, 196, 61-68.	1.0	16
79	Expression of sunflower cytochrome c mRNA is tissue-specific and controlled by nitrate and light. <i>Physiologia Plantarum</i> , 1997, 99, 342-347.	2.6	11
80	Interaction between proteins containing homeodomains associated to leucine zippers from sunflower. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1997, 1351, 137-149.	2.4	29
81	A novel type of dimerization motif, related to leucine zippers, is present in plant homeodomain proteins. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1997, 1352, 203-212.	2.4	9
82	Expression of sunflower cytochrome c mRNA is tissue-specific and controlled by nitrate and light. <i>Physiologia Plantarum</i> , 1997, 99, 342-347.	2.6	2
83	A cDNA Encoding an HD-Zip Protein from Sunflower. <i>Plant Physiology</i> , 1994, 106, 1687-1688.	2.3	23
84	Screening cDNA libraries by PCR using 5' sequencing primers and degenerate oligonucleotides. <i>Trends in Genetics</i> , 1993, 9, 231-232.	2.9	16
85	In <i>Euglena</i> , spliced-leader RNA (SL-RNA) and 5S rRNA genes are tandemly repeated. <i>Nucleic Acids Research</i> , 1992, 20, 1711-1715.	6.5	36
86	The <i>Euglena gracilis</i> rbcS gene contains introns with unusual borders. <i>FEBS Letters</i> , 1992, 304, 252-255.	1.3	13
87	Post-transcriptional regulation by light of the biosynthesis of <i>Euglena</i> ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit. <i>Plant Molecular Biology</i> , 1991, 17, 73-82.	2.0	35
88	Biosynthesis and Distribution of the Ferredoxin-NADP Oxidoreductase Binding Protein. , 1990, , 1831-1834.		0
89	Immunological studies of the binding protein for chloroplast ferredoxin-NADP+ reductase. <i>Archives of Biochemistry and Biophysics</i> , 1987, 253, 56-61.	1.4	17
90	Trimeric structure and other properties of the chloroplast reductase binding protein. <i>FEBS Letters</i> , 1985, 190, 165-168.	1.3	23

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91	Isolation and sequencing of an active-site peptide from spinach ferredoxin-NADP+ oxidoreductase after affinity labeling with periodate-oxidized NADP+. Archives of Biochemistry and Biophysics, 1985, 240, 172-177.	1.4	34
92	A fast and sensitive micromethod for the manual sequencing of peptides using O-phthalaldehyde as derivatizing reagent. Journal of Proteomics, 1984, 10, 49-54.	2.4	5
93	Affinity labeling of spinach ferredoxin-NADP+ oxidoreductase with periodate-oxidized NADP+. Archives of Biochemistry and Biophysics, 1984, 229, 340-347.	1.4	11