

Raquel L Chan

List of Publications by Year in descending order

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93
papers

4,415
citations

109321

35
h-index

118850

62
g-index

99
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. | 3.6 | 3 |
| 2 | Expressing the sunflower transcription factor HaHB11 in maize improves waterlogging and defoliation tolerance. <i>Plant Physiology</i> , 2022, 189, 230-247. | 4.8 | 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. | 4.2 | 4 |
| 4 | The underground life of homeodomain-leucine zipper transcription factors. <i>Journal of Experimental Botany</i> , 2021, 72, 4005-4021. | 4.8 | 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. | 3.1 | 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. | 4.8 | 4 |
| 7 | Why are second-generation transgenic crops not yet available in the market?. <i>Journal of Experimental Botany</i> , 2020, 71, 6876-6880. | 4.8 | 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. | 3.6 | 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. | 4.8 | 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. | 2.4 | 9 |
| 11 | Maize expressing the sunflower transcription factor HaHB11 has improved productivity in controlled and field conditions. <i>Plant Science</i> , 2019, 287, 110185. | 3.6 | 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. | 5.7 | 24 |
| 13 | Arabidopsis and sunflower plants with increased xylem area show enhanced seed yield. <i>Plant Journal</i> , 2019, 99, 717-732. | 5.7 | 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. | 4.8 | 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. | 2.4 | 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. | 3.6 | 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. | 3.4 | 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. | 4.8 | 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. | 2.9 | 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. | 3.8 | 28 |
| 21 | JUNGBRUNNEN1 Confers Drought Tolerance Downstream of the HD-Zip I Transcription Factor AtHB13. <i>Frontiers in Plant Science</i> , 2017, 8, 2118. | 3.6 | 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. | 4.8 | 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. | 5.6 | 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. | 3.6 | 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. | 3.8 | 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. | 7.3 | 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. | 4.8 | 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. | 3.9 | 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. | 5.6 | 60 |
| 32 | Plant science with relevance to biotechnology. <i>Journal of Biotechnology</i> , 2014, 174, iv. | 3.8 | 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. | 5.6 | 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. | 3.6 | 120 |
| 35 | Two Direct Targets of Cytokinin Signaling Regulate Symbiotic Nodulation in <i>Medicago truncatula</i> . <i>Plant Cell</i> , 2012, 24, 3838-3852. | 6.6 | 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. | 7.3 | 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. | 3.6 | 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. | 5.7 | 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. | 8.3 | 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. | 3.6 | 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. | 4.8 | 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. | 4.8 | 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. | 2.4 | 39 |
| 44 | Transcriptional Control of a Plant Stem Cell Niche. <i>Developmental Cell</i> , 2010, 18, 841-853. | 7.0 | 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. | 3.6 | 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. | 6.6 | 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. | 12.0 | 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. | 5.8 | 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. | 5.7 | 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. | 4.8 | 36 |
| 51 | Patents on Plant Transcription Factors. <i>Recent Patents on Biotechnology</i> , 2008, 2, 209-217. | 0.8 | 17 |
| 52 | The true story of the HD-Zip family. <i>Trends in Plant Science</i> , 2007, 12, 419-426. | 8.8 | 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. | 3.2 | 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. | 5.7 | 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. | 2.4 | 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. | 4.8 | 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. | 3.1 | 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. | 3.6 | 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. | 4.7 | 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. | 4.8 | 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. | 4.7 | 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. | 2.4 | 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. | 5.8 | 24 |
| 64 | Knotted1-like genes are strongly expressed in differentiated cell types in sunflower. <i>Journal of Experimental Botany</i> , 2003, 54, 681-690. | 4.8 | 13 |
| 65 | Identification of three MADS-box genes expressed in sunflower capitulum. <i>Journal of Experimental Botany</i> , 2003, 54, 1637-1639. | 4.8 | 16 |
| 66 | Redox Regulation of Plant Homeodomain Transcription Factors. <i>Journal of Biological Chemistry</i> , 2002, 277, 34800-34807. | 3.4 | 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. | 3.6 | 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. | 5.7 | 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. | 5.7 | 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. | 4.2 | 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. | 14.5 | 36 |
| 72 | Cell-Type-Specific Expression of Plant Cytochrome c mRNA in Developing Flowers and Roots. <i>Plant Physiology</i> , 2001, 125, 1603-1610. | 4.8 | 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. | 3.1 | 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. | 3.7 | 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. | 3.7 | 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. | 1.3 | 22 |
| 78 | Isolation and expression pattern of hahr1, a homeobox-containing cDNA from <i>Helianthus annuus</i> . <i>Gene</i> , 1997, 196, 61-68. | 2.2 | 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. | 5.2 | 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. | 5.2 | 2 |
| 83 | A cDNA Encoding an HD-Zip Protein from Sunflower. <i>Plant Physiology</i> , 1994, 106, 1687-1688. | 4.8 | 23 |
| 84 | Screening cDNA libraries by PCR using 5' sequencing primers and degenerate oligonucleotides. <i>Trends in Genetics</i> , 1993, 9, 231-232. | 6.7 | 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. | 14.5 | 36 |
| 86 | The <i>Euglena gracilis</i> rbcS gene contains introns with unusual borders. <i>FEBS Letters</i> , 1992, 304, 252-255. | 2.8 | 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. | 3.9 | 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. | 3.0 | 17 |
| 90 | Trimeric structure and other properties of the chloroplast reductase binding protein. <i>FEBS Letters</i> , 1985, 190, 165-168. | 2.8 | 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. | 3.0 | 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. | 3.0 | 11 |