

# Songling Bai

## List of Publications by Year in descending order

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54  
papers

2,929  
citations

147801

31  
h-index

175258

52  
g-index

55  
all docs

55  
docs citations

55  
times ranked

2103  
citing authors

#	ARTICLE	IF	CITATIONS
1	BBX16, a B-box protein, positively regulates light-induced anthocyanin accumulation by activating MYB10 in red pear. <i>Plant Biotechnology Journal</i> , 2019, 17, 1985-1997.	8.3	184
2	Dormancy-associated MADS-box genes and microRNAs jointly control dormancy transition in pear ( <i>Pyrus pyrifolia</i> white pear group) flower bud. <i>Journal of Experimental Botany</i> , 2016, 67, 239-257.	4.8	170
3	Transcriptome Analysis of Japanese Pear ( <i>Pyrus pyrifolia</i> Nakai) Flower Buds Transitioning Through Endodormancy. <i>Plant and Cell Physiology</i> , 2013, 54, 1132-1151.	3.1	147
4	An apple B-box protein, MdCOL11, is involved in UV-B- and temperature-induced anthocyanin biosynthesis. <i>Planta</i> , 2014, 240, 1051-1062.	3.2	123
5	Ethylene response factors Pp4ERF24 and Pp12ERF96 regulate blue light-induced anthocyanin biosynthesis in "Red Zaosu" pear fruits by interacting with MYB114. <i>Plant Molecular Biology</i> , 2019, 99, 67-78.	3.9	123
6	Two B-box proteins, PpBBX18 and PpBBX21, antagonistically regulate anthocyanin biosynthesis via competitive association with <i>Pyrus pyrifolia</i> ELONGATED HYPOCOTYL 5 in the peel of pear fruit. <i>Plant Journal</i> , 2019, 100, 1208-1223.	5.7	115
7	Histone modification and signalling cascade of the dormancy-associated MADS-box gene, PpMADS13, in Japanese pear ( <i>Pyrus</i> ) Tj ETQq1 10.784314 rBT/Overload	5.7	106
8	Ethylene mediates the branching of the jasmonate-induced flavonoid biosynthesis pathway by suppressing anthocyanin biosynthesis in red Chinese pear fruits. <i>Plant Biotechnology Journal</i> , 2020, 18, 1223-1240.	8.3	101
9	The crucial role of PpMYB10.1 in anthocyanin accumulation in peach and relationships between its allelic type and skin color phenotype. <i>BMC Plant Biology</i> , 2015, 15, 280.	3.6	100
10	Dormancy-Associated MADS-Box (DAM) and the Abscisic Acid Pathway Regulate Pear Endodormancy Through a Feedback Mechanism. <i>Plant and Cell Physiology</i> , 2017, 58, 1378-1390.	3.1	99
11	The blue light signal transduction pathway is involved in anthocyanin accumulation in "Red Zaosu" pear. <i>Planta</i> , 2018, 248, 37-48.	3.2	97
12	Expression and genomic structure of the dormancy-associated MADS box genes MADS13 in Japanese pears ( <i>Pyrus pyrifolia</i> Nakai) that differ in their chilling requirement for endodormancy release. <i>Tree Physiology</i> , 2013, 33, 654-667.	3.1	91
13	Cloning and Characterization of miRNAs and Their Targets, Including a Novel miRNA-Targeted NBS-LRR Protein Class Gene in Apple (Golden Delicious). <i>Molecular Plant</i> , 2014, 7, 218-230.	8.3	83
14	A mobile signal transported over a long distance induces systemic transcriptional gene silencing in a grafted partner. <i>Journal of Experimental Botany</i> , 2011, 62, 4561-4570.	4.8	77
15	Ethylene-activated PpERF105 induces the expression of the repressor-type R2R3-MYB gene PpMYB140 to inhibit anthocyanin biosynthesis in red pear fruit. <i>Plant Journal</i> , 2021, 105, 167-181.	5.7	76
16	ABA-responsive ABRE-BINDING FACTOR3 activates DAM3 expression to promote bud dormancy in Asian pear. <i>Plant, Cell and Environment</i> , 2020, 43, 1360-1375.	5.7	75
17	Abscisic Acid (ABA) Promotes the Induction and Maintenance of Pear ( <i>Pyrus pyrifolia</i> White Pear) Tj ETQq1 10.784314 rBT/Overload	4.1	74
18	Response of miR156-SPL Module during the Red Peel Coloration of Bagging-Treated Chinese Sand Pear ( <i>Pyrus pyrifolia</i> Nakai). <i>Frontiers in Physiology</i> , 2017, 8, 550.	2.8	71

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19	Transcriptome analysis of bagging-treated red Chinese sand pear peels reveals light-responsive pathway functions in anthocyanin accumulation. <i>Scientific Reports</i> , 2017, 7, 63.	3.3	67
20	Bud endodormancy in deciduous fruit trees: advances and prospects. <i>Horticulture Research</i> , 2021, 8, 139.	6.3	60
21	Involvement of <i>EARLY BUD-BREAK</i> , an AP2/ERF Transcription Factor Gene, in Bud Break in Japanese Pear ( <i>Pyrus pyrifolia</i> Nakai) Lateral Flower Buds: Expression, Histone Modifications and Possible Target Genes. <i>Plant and Cell Physiology</i> , 2016, 57, 1038-1047.	3.1	49
22	Epigenetic regulation of MdMYB1 is associated with paper bagging-induced red pigmentation of apples. <i>Planta</i> , 2016, 244, 573-586.	3.2	47
23	Light-Induced Basic/Helix-Loop-Helix64 Enhances Anthocyanin Biosynthesis and Undergoes CONSTITUTIVELY PHOTOMORPHOGENIC1-Mediated Degradation in Pear. <i>Plant Physiology</i> , 2020, 184, 1684-1701.	4.8	46
24	R2R3-MYB transcription factor PpMYB17 positively regulates flavonoid biosynthesis in pear fruit. <i>Planta</i> , 2020, 252, 59.	3.2	46
25	High-quality genome assembly of 'Cuiguan' pear ( <i>Pyrus pyrifolia</i> ) as a reference genome for identifying regulatory genes and epigenetic modifications responsible for bud dormancy. <i>Horticulture Research</i> , 2021, 8, 197.	6.3	44
26	Graft-Transmitted siRNA Signal from the Root Induces Visual Manifestation of Endogenous Post-Transcriptional Gene Silencing in the Scion. <i>PLoS ONE</i> , 2011, 6, e16895.	2.5	43
27	PpyGAST1 is potentially involved in bud dormancy release by integrating the GA biosynthesis and ABA signaling in 'Suli' pear ( <i>Pyrus pyrifolia</i> White Pear Group). <i>Environmental and Experimental Botany</i> , 2019, 162, 302-312.	4.2	42
28	Insertion of a transposon-like sequence in the 5' flanking region of the <i>YUCCA</i> gene causes the stony hard phenotype. <i>Plant Journal</i> , 2018, 96, 815-827.	5.7	41
29	Transcriptome analysis provides new insights into the transcriptional regulation of methyl jasmonate-induced flavonoid biosynthesis in pear calli. <i>BMC Plant Biology</i> , 2020, 20, 388.	3.6	40
30	Knockdown of Carotenoid Cleavage Dioxygenase 4 (CCD4) via Virus-Induced Gene Silencing Confers Yellow Coloration in Peach Fruit: Evaluation of Gene Function Related to Fruit Traits. <i>Plant Molecular Biology Reporter</i> , 2016, 34, 257-264.	1.8	38
31	Development of flower buds in the Japanese pear ( <i>Pyrus pyrifolia</i> ) from late autumn to early spring. <i>Tree Physiology</i> , 2015, 35, 653-662.	3.1	36
32	Robustness improvement of NIR-based determination of soluble solids in apple fruit by local calibration. <i>Postharvest Biology and Technology</i> , 2018, 139, 82-90.	6.0	36
33	Genome wide identification and predicted functional analyses of NAC transcription factors in Asian pears. <i>BMC Plant Biology</i> , 2018, 18, 214.	3.6	36
34	Epigenome Editing of Potato by Grafting Using Transgenic Tobacco as siRNA Donor. <i>PLoS ONE</i> , 2016, 11, e0161729.	2.5	34
35	Repression of TERMINAL FLOWER1 primarily mediates floral induction in pear ( <i>Pyrus pyrifolia</i> Nakai) concomitant with change in gene expression of plant hormone-related genes and transcription factors. <i>Journal of Experimental Botany</i> , 2017, 68, 4899-4914.	4.8	31
36	Physiological differences between bud breaking and flowering after dormancy completion revealed by <i>DAM</i> and <i>FT/TFL1</i> expression in Japanese pear ( <i>Pyrus pyrifolia</i> ). <i>Tree Physiology</i> , 2016, 36, 109-120.	3.1	30

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37	PpHB22, a member of HD-Zip proteins, activates PpDAM1 to regulate bud dormancy transition in ‘Suli’™ pear ( <i>Pyrus pyrifolia</i> White Pear Group). <i>Plant Physiology and Biochemistry</i> , 2018, 127, 355-365.	5.8	30
38	Identification, classification, and transcription profiles of the B-type response regulator family in pear. <i>PLoS ONE</i> , 2017, 12, e0171523.	2.5	28
39	PpCBFs selectively regulate PpDAMs and contribute to the pear bud endodormancy process. <i>Plant Molecular Biology</i> , 2019, 99, 575-586.	3.9	26
40	Small RNA and PARE sequencing in flower bud reveal the involvement of sRNAs in endodormancy release of Japanese pear ( <i>Pyrus pyrifolia</i> 'Kosui'). <i>BMC Genomics</i> , 2016, 17, 230.	2.8	25
41	Phylogenetic, Molecular, and Functional Characterization of PpyCBF Proteins in Asian Pears ( <i>Pyrus</i> ) Tj ETQq1 1 0.784314 rgBT /Overl	4.1	19
42	Changes in phytohormone content and associated gene expression throughout the stages of pear ( <i>Pyrus pyrifolia</i> Nakai) dormancy. <i>Tree Physiology</i> , 2021, 41, 529-543.	3.1	19
43	Genome-wide identification, characterization, and expression analysis of the dehydrin gene family in Asian pear ( <i>Pyrus pyrifolia</i> ). <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	1.6	17
44	Genome-wide survey and analysis of the TIFY gene family and its potential role in anthocyanin synthesis in Chinese sand pear ( <i>Pyrus pyrifolia</i> ). <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	1.6	16
45	Characterization of 10 MADS-box genes from <i>Pyrus pyrifolia</i> and their differential expression during fruit development and ripening. <i>Gene</i> , 2013, 528, 183-194.	2.2	14
46	Distribution of <i>MdACS3</i> null alleles in apple ( <i>Malus domestica</i> Borkh.) and its relevance to the fruit ripening characters. <i>Breeding Science</i> , 2012, 62, 46-52.	1.9	13
47	Determination S-Genotypes and Identification of Five Novel S-RNase Alleles in Wild <i>Malus</i> Species. <i>Plant Molecular Biology Reporter</i> , 2012, 30, 453-461.	1.8	13
48	Retrotransposon-based sequence-specific amplification polymorphism markers reveal that cultivated <i>Pyrus ussuriensis</i> originated from an interspecific hybridization. <i>European Journal of Horticultural Science</i> , 2016, 81, 264-272.	0.7	11
49	Alternative splicing of the dormancy-associated MADS-box transcription factor gene PpDAM1 is associated with flower bud dormancy in ‘Dangshansu’™ pear ( <i>Pyrus pyrifolia</i> white pear group). <i>Plant Physiology and Biochemistry</i> , 2021, 166, 1096-1108.	5.8	7
50	Efficient Breeding and Cultivation of Type 2 Red-fleshed Apple Cultivars Using a Search System for Suitable Apple Cultivar Combination. <i>Horticultural Plant Journal</i> , 2018, 4, 219-225.	5.0	6
51	Isolation and S-genotyping application of S-allelic polymorphic <i>MdSLFBs</i> in apple ( <i>Malus domestica</i> ) Tj ETQq1 1 0.784314 rgBT /Overl	2.1	5
52	Studies on pear parthenocarpy induced by exogenous plant growth regulators. <i>Acta Horticulturae</i> , 2018, , 21-26.	0.2	2
53	Application of Systemic Transcriptional Gene Silencing for Plant Breeding. , 2018, , 247-263.		0
54	Functional Genomics. <i>Compendium of Plant Genomes</i> , 2019, , 265-277.	0.5	0