

# Shaomin Bian

## List of Publications by Year in descending order

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Version: 2024-02-01

20  
papers

529  
citations

759233

12  
h-index

794594

19  
g-index

20  
all docs

20  
docs citations

20  
times ranked

687  
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of ARF family in blueberry and its potential involvement of fruit development and pH stress response. <i>BMC Genomics</i> , 2022, 23, 329.	2.8	9
2	Genome-wide occupancy of <i>Arabidopsis</i> SWI/SNF chromatin remodeler SPLAYED provides insights into its interplay with its close homolog BRAHMA and Polycomb proteins. <i>Plant Journal</i> , 2021, 106, 200-213.	5.7	19
3	LEAFY COTYLEDON1 expression in the endosperm enables embryo maturation in <i>Arabidopsis</i> . <i>Nature Communications</i> , 2021, 12, 3963.	12.8	24
4	Comprehensive Analysis of the SBP Family in Blueberry and Their Regulatory Mechanism Controlling Chlorophyll Accumulation. <i>Frontiers in Plant Science</i> , 2021, 12, 703994.	3.6	6
5	Soybean GmMYB133 Inhibits Hypocotyl Elongation and Confers Salt Tolerance in <i>Arabidopsis</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 764074.	3.6	5
6	Identification and functional characterization of the Aux/IAA gene VclAA27 in blueberry. <i>Plant Signaling and Behavior</i> , 2020, 15, 1700327.	2.4	20
7	A blueberry MIR156a "SPL12 module coordinates the accumulation of chlorophylls and anthocyanins during fruit ripening. <i>Journal of Experimental Botany</i> , 2020, 71, 5976-5989.	4.8	44
8	Characterization of the soybean R2R3-MYB transcription factor GmMYB81 and its functional roles under abiotic stresses. <i>Gene</i> , 2020, 753, 144803.	2.2	28
9	Genome-wide occupancy of histone H3K27 methyltransferases <i>CLIRLY LEAF</i> and <i>SWINGER</i> in <i>Arabidopsis</i> seedlings. <i>Plant Direct</i> , 2019, 3, e00100.	1.9	70
10	Soybean CCA1-like MYB transcription factor GmMYB133 modulates isoflavonoid biosynthesis. <i>Biochemical and Biophysical Research Communications</i> , 2018, 507, 324-329.	2.1	38
11	Functional roles of two 14-3-3s in response to salt stress in common bean. <i>Acta Physiologiae Plantarum</i> , 2018, 40, 1.	2.1	9
12	Conservation and diversification of the miR166 family in soybean and potential roles of newly identified miR166s. <i>BMC Plant Biology</i> , 2017, 17, 32.	3.6	66
13	Genome-Wide Analysis of CCA1-Like Proteins in Soybean and Functional Characterization of GmMYB138a. <i>International Journal of Molecular Sciences</i> , 2017, 18, 2040.	4.1	18
14	Comparative Analysis of Fruit Ripening-Related miRNAs and Their Targets in Blueberry Using Small RNA and Degradome Sequencing. <i>International Journal of Molecular Sciences</i> , 2017, 18, 2767.	4.1	36
15	Genome-wide analysis of DWD proteins in soybean ( <i>Glycine max</i> ): Significance of Gm08DWD and GmMYB176 interaction in isoflavonoid biosynthesis. <i>PLoS ONE</i> , 2017, 12, e0178947.	2.5	15
16	Combinatorial regulation of CLF and SDG8 during <i>Arabidopsis</i> shoot branching. <i>Acta Physiologiae Plantarum</i> , 2016, 38, 1.	2.1	2
17	Identification of 14-3-3 Family in Common Bean and Their Response to Abiotic Stress. <i>PLoS ONE</i> , 2015, 10, e0143280.	2.5	24
18	Computational identification of conserved microRNAs and their targets from expression sequence tags of blueberry ( <i>Vaccinium corybosum</i> ). <i>Plant Signaling and Behavior</i> , 2014, 9, e29462.	2.4	14

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19	MicroRNA-Mediated Repression of the Seed Maturation Program during Vegetative Development in <i>Arabidopsis</i> . <i>PLoS Genetics</i> , 2012, 8, e1003091.	3.5	68
20	Identification and characterization of microRNAs and their targets from expression sequence tags of <i>Ribes nigrum</i> . <i>Canadian Journal of Plant Science</i> , 0, , 1-7.	0.9	14