

# Peng He

## List of Publications by Year in descending order

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Version: 2024-02-01

11  
papers

324  
citations

933447

10  
h-index

1281871

11  
g-index

11  
all docs

11  
docs citations

11  
times ranked

383  
citing authors

#	ARTICLE	IF	CITATIONS
1	Auxin promotes fiber elongation by enhancing gibberellic acid biosynthesis in cotton. <i>Plant Biotechnology Journal</i> , 2022, 20, 423-425.	8.3	19
2	GhARF16 modulates leaf development by transcriptionally regulating the <i>GhKNOX2</i> gene in cotton. <i>Plant Biotechnology Journal</i> , 2021, 19, 548-562.	8.3	15
3	Origin of a Subgenome and Genome Evolution of Allotetraploid Cotton Species. <i>Molecular Plant</i> , 2020, 13, 1238-1240.	8.3	11
4	GhYGL1d, a pentatricopeptide repeat protein, is required for chloroplast development in cotton. <i>BMC Plant Biology</i> , 2019, 19, 350.	3.6	10
5	Comprehensive analysis of WOX genes uncovers that WOX13 is involved in phytohormone-mediated fiber development in cotton. <i>BMC Plant Biology</i> , 2019, 19, 312.	3.6	28
6	Comprehensive analyses of ZFP gene family and characterization of expression profiles during plant hormone response in cotton. <i>BMC Plant Biology</i> , 2019, 19, 329.	3.6	12
7	Auxin-mediated statolith production for root gravitropism. <i>New Phytologist</i> , 2019, 224, 761-774.	7.3	55
8	Two pivotal RNA editing sites in the mitochondrial <i>atp1</i> mRNA are required for ATP synthase to produce sufficient ATP for cotton fiber cell elongation. <i>New Phytologist</i> , 2018, 218, 167-182.	7.3	36
9	Genome-wide identification of the GhARF gene family reveals that GhARF2 and GhARF18 are involved in cotton fibre cell initiation. <i>Journal of Experimental Botany</i> , 2018, 69, 4323-4337.	4.8	43
10	The PIN gene family in cotton ( <i>Gossypium hirsutum</i> ): genome-wide identification and gene expression analyses during root development and abiotic stress responses. <i>BMC Genomics</i> , 2017, 18, 507.	2.8	46
11	Abundant RNA editing sites of chloroplast protein-coding genes in <i>Ginkgo biloba</i> and an evolutionary pattern analysis. <i>BMC Plant Biology</i> , 2016, 16, 257.	3.6	49