

# Qiong Wang

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1841731/publications.pdf>

Version: 2024-02-01

11  
papers

2,996  
citations

1040056

9  
h-index

1474206

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g-index

11  
all docs

11  
docs citations

11  
times ranked

2017  
citing authors

#	ARTICLE	IF	CITATIONS
1	Divergence of two cultivated allotetraploid cottons unveiled by single-molecule long-read expression sequencing. , 2022, 1, 100002.		1
2	Gossypium barbadense and Gossypium hirsutum genomes provide insights into the origin and evolution of allotetraploid cotton. Nature Genetics, 2019, 51, 739-748.	21.4	568
3	Mutation of SELF-PRUNING homologs in cotton promotes short-branching plant architecture. Journal of Experimental Botany, 2018, 69, 2543-2553.	4.8	49
4	Genomic insights into divergence and dual domestication of cultivated allotetraploid cottons. Genome Biology, 2017, 18, 33.	8.8	128
5	Genomic analyses in cotton identify signatures of selection and loci associated with fiber quality and yield traits. Nature Genetics, 2017, 49, 1089-1098.	21.4	384
6	Small interfering <scp>RNA</scp>s from bidirectional transcripts of <i>Gh<scp>MML</scp>3_A12</i> regulate cotton fiber development. New Phytologist, 2016, 210, 1298-1310.	7.3	124
7	Sequence-based ultra-dense genetic and physical maps reveal structural variations of allopolyploid cotton genomes. Genome Biology, 2015, 16, 108.	9.6	108
8	Genome-Wide Mining, Characterization and Development of Microsatellite Markers in Gossypium Species. Scientific Reports, 2015, 5, 10638.	3.3	58
9	Sequencing of allotetraploid cotton (Gossypium hirsutum L. acc. TM-1) provides a resource for fiber improvement. Nature Biotechnology, 2015, 33, 531-537.	17.5	1,560
10	Identification of centromeric regions on the linkage map of cotton using centromere-related repeats. Genomics, 2014, 104, 587-593.	2.9	15
11	Gossypium barbadense and Gossypium hirsutum genomes provide insights into the origin and evolution of allotetraploid cotton. , 0, .		1