

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

9
g-index

11
all docs

11
docs citations

11
times ranked

2017
citing authors

#	ARTICLE	IF	CITATIONS
1	Sequencing of allotetraploid cotton (<i>Gossypium hirsutum</i> L. acc. TM-1) provides a resource for fiber improvement. <i>Nature Biotechnology</i> , 2015, 33, 531-537.	17.5	1,560
2	<i>Gossypium barbadense</i> and <i>Gossypium hirsutum</i> genomes provide insights into the origin and evolution of allotetraploid cotton. <i>Nature Genetics</i> , 2019, 51, 739-748.	21.4	568
3	Genomic analyses in cotton identify signatures of selection and loci associated with fiber quality and yield traits. <i>Nature Genetics</i> , 2017, 49, 1089-1098.	21.4	384
4	Genomic insights into divergence and dual domestication of cultivated allotetraploid cottons. <i>Genome Biology</i> , 2017, 18, 33.	8.8	128
5	Small interfering <i>scnRNA</i> s from bidirectional transcripts of <i>GhMML3_A12</i> regulate cotton fiber development. <i>New Phytologist</i> , 2016, 210, 1298-1310.	7.3	124
6	Sequence-based ultra-dense genetic and physical maps reveal structural variations of allopolyploid cotton genomes. <i>Genome Biology</i> , 2015, 16, 108.	9.6	108
7	Genome-Wide Mining, Characterization and Development of Microsatellite Markers in <i>Gossypium</i> Species. <i>Scientific Reports</i> , 2015, 5, 10638.	3.3	58
8	Mutation of SELF-PRUNING homologs in cotton promotes short-branching plant architecture. <i>Journal of Experimental Botany</i> , 2018, 69, 2543-2553.	4.8	49
9	Identification of centromeric regions on the linkage map of cotton using centromere-related repeats. <i>Genomics</i> , 2014, 104, 587-593.	2.9	15
10	<i>Gossypium barbadense</i> and <i>Gossypium hirsutum</i> genomes provide insights into the origin and evolution of allotetraploid cotton. , 0, .		1
11	Divergence of two cultivated allotetraploid cottons unveiled by single-molecule long-read expression sequencing. , 2022, 1, 100002.		1