

# Kashif Shahzad

## List of Publications by Year in descending order

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15  
papers

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citations

1039406

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1125271

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21  
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21  
docs citations

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times ranked

162  
citing authors

#	ARTICLE	IF	CITATIONS
1	Integrated analysis of small RNA, transcriptome and degradome sequencing reveals that micro-RNAs regulate anther development in CMS cotton. <i>Industrial Crops and Products</i> , 2022, 176, 114422.	2.5	3
2	Comparative performance of hybrid generations reveals the potential application of F2 hybrids in upland cotton. <i>Journal of Cotton Research</i> , 2022, 5, .	1.0	7
3	Single-base resolution methylomes of cotton CMS system reveal epigenomic changes in response to high-temperature stress during anther development. <i>Journal of Experimental Botany</i> , 2020, 71, 951-969.	2.4	31
4	Development and utilization of an InDel marker linked to the fertility restorer genes of CMS-D8 and CMS-D2 in cotton. <i>Molecular Biology Reports</i> , 2020, 47, 1275-1282.	1.0	10
5	Comparative transcriptome analysis between inbred and hybrids reveals molecular insights into yield heterosis of upland cotton. <i>BMC Plant Biology</i> , 2020, 20, 239.	1.6	28
6	Comparative transcriptome analysis of inbred lines and contrasting hybrids reveals overdominance mediate early biomass vigor in hybrid cotton. <i>BMC Genomics</i> , 2020, 21, 140.	1.2	22
7	Transcriptome Analysis Implicates Involvement of Long Noncoding RNAs in Cytoplasmic Male Sterility and Fertility Restoration in Cotton. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5530.	1.8	11
8	Adaptability and Stability Comparisons of Inbred and Hybrid Cotton in Yield and Fiber Quality Traits. <i>Agronomy</i> , 2019, 9, 516.	1.3	27
9	Genetic analysis of yield and fiber quality traits in upland cotton ( <i>Gossypium hirsutum</i> L.) cultivated in different ecological regions of China. <i>Journal of Cotton Research</i> , 2019, 2, .	1.0	22
10	Using yield quantitative trait locus targeted SSR markers to study the relationship between genetic distance and yield heterosis in upland cotton ( <i>Gossypium hirsutum</i> ). <i>Plant Breeding</i> , 2019, 138, 105-113.	1.0	18
11	Integrated Methylome and Transcriptome Analysis between the CMS-D2 Line ZBA and Its Maintainer Line ZB in Upland Cotton. <i>International Journal of Molecular Sciences</i> , 2019, 20, 6070.	1.8	17
12	Genome-wide analysis of Rf-PPR-like (RFL) genes and a new InDel marker development for Rf1 gene in cytoplasmic male sterile CMS-D2 Upland cotton. <i>Journal of Cotton Research</i> , 2018, 1, .	1.0	6
13	A combined small RNA and transcriptome sequencing analysis reveal regulatory roles of miRNAs during anther development of Upland cotton carrying cytoplasmic male sterile <i>Gossypium harknessii</i> (D2) cytoplasm. <i>BMC Plant Biology</i> , 2018, 18, 242.	1.6	25
14	Transcript Complexity and New Insights of Restorer Line in CMS-D8 Cotton Through Full-Length Transcriptomic Analysis. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
15	Homoeolog gene expression analysis reveals novel expression biases in upland hybrid cotton under intraspecific hybridization. <i>Functional and Integrative Genomics</i> , 0, , .	1.4	0