

# Sarfraz Shafiq

## List of Publications by Year in descending order

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14  
papers

675  
citations

858243

12  
h-index

1181555

14  
g-index

16  
all docs

16  
docs citations

16  
times ranked

1162  
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptional cascades in the regulation of 2â€AP biosynthesis under Zn supply in fragrant rice. <i>Physiologia Plantarum</i> , 2022, 174, .	2.6	7
2	Eco-Environmental Aspects of COVID-19 Pandemic and Potential Control Strategies. <i>International Journal of Environmental Research and Public Health</i> , 2021, 18, 3488.	1.2	15
3	The Interplay between Toxic and Essential Metals for Their Uptake and Translocation Is Likely Governed by DNA Methylation and Histone Deacetylation in Maize. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6959.	1.8	17
4	Histone Deacetylase (HDAC) Gene Family in Allotetraploid Cotton and Its Diploid Progenitors: In Silico Identification, Molecular Characterization, and Gene Expression Analysis under Multiple Abiotic Stresses, DNA Damage and Phytohormone Treatments. <i>International Journal of Molecular Sciences</i> , 2020, 21, 321.	1.8	26
5	Lead, Cadmium and Zinc Phytotoxicity Alter DNA Methylation Levels to Confer Heavy Metal Tolerance in Wheat. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4676.	1.8	70
6	Comparative Genome-wide Analysis and Expression Profiling of Histone Acetyltransferase (HAT) Gene Family in Response to Hormonal Applications, Metal and Abiotic Stresses in Cotton. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5311.	1.8	26
7	EARLY FLOWERING IN SHORT DAYS (EFS) regulates the seed size in Arabidopsis. <i>Science China Life Sciences</i> , 2018, 61, 214-224.	2.3	17
8	DNA Topoisomerase 1 Prevents R-loop Accumulation to Modulate Auxin-Regulated Root Development in Rice. <i>Molecular Plant</i> , 2017, 10, 821-833.	3.9	43
9	Functions of plants long non-coding RNAs. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2016, 1859, 155-162.	0.9	72
10	Genome-wide gene expression profiling to investigate molecular phenotypes of Arabidopsis mutants deprived in distinct histone methyltransferases and demethylases. <i>Genomics Data</i> , 2015, 4, 143-145.	1.3	18
11	The <i>trxG</i> family histone methyltransferase <i>SET DOMAIN GROUP</i> 26 promotes flowering via a distinctive genetic pathway. <i>Plant Journal</i> , 2015, 81, 316-328.	2.8	61
12	Combinatorial functions of diverse histone methylations in <i>Arabidopsis thaliana</i> flowering time regulation. <i>New Phytologist</i> , 2014, 201, 312-322.	3.5	66
13	The self-incompatibility mating system of the olive ( <i>Olea europaea</i> L.) functions with dominance between S-alleles. <i>Tree Genetics and Genomes</i> , 2014, 10, 1055-1067.	0.6	39
14	Histone modifications in transcriptional activation during plant development. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2011, 1809, 567-576.	0.9	195