

# Sarah Muniz Nardeli

## List of Publications by Year in descending order

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Version: 2024-02-01

12  
papers

470  
citations

1163117

8  
h-index

1199594

12  
g-index

12  
all docs

12  
docs citations

12  
times ranked

779  
citing authors

#	ARTICLE	IF	CITATIONS
1	Insights into the role of alternative splicing in plant temperature response. <i>Journal of Experimental Botany</i> , 2021, , .	4.8	17
2	Overexpression of the CaHB12 transcription factor in cotton ( <i>Gossypium hirsutum</i> ) improves drought tolerance. <i>Plant Physiology and Biochemistry</i> , 2021, 165, 80-93.	5.8	11
3	Genome-wide analysis of the MADS-box gene family in polyploid cotton ( <i>Gossypium hirsutum</i> ) and in its diploid parental species ( <i>Gossypium arboreum</i> and <i>Gossypium raimondii</i> ). <i>Plant Physiology and Biochemistry</i> , 2018, 127, 169-184.	5.8	30
4	Functional characterization of AGAMOUS-subfamily members from cotton during reproductive development and in response to plant hormones. <i>Plant Reproduction</i> , 2017, 30, 19-39.	2.2	12
5	Early Heat Shock Protein Response and Selection of Reference Genes in <i>Arabidopsis thaliana</i> Seedlings Subjected to Marine Fuel Contamination. <i>Water, Air, and Soil Pollution</i> , 2017, 228, 1.	2.4	9
6	Promoter isolation and characterization of GhAO-like1, a <i>Gossypium hirsutum</i> gene similar to multicopper oxidases that is highly expressed in reproductive organs. <i>Genome</i> , 2016, 59, 23-36.	2.0	4
7	Transcriptional responses of <i>Arabidopsis thaliana</i> to oil contamination. <i>Environmental and Experimental Botany</i> , 2016, 127, 63-72.	4.2	13
8	Evaluation of Reference Genes for RT-qPCR Normalization in Cowpea under Drought Stress during Biological Nitrogen Fixation. <i>Crop Science</i> , 2015, 55, 1660-1672.	1.8	6
9	Isolation and Characterization of Three New Promoters from <i>Gossypium hirsutum</i> that Show High Activity in Reproductive Tissues. <i>Plant Molecular Biology Reporter</i> , 2014, 32, 630-643.	1.8	12
10	Analysis of the <i>Arabidopsis</i> REM gene family predicts functions during flower development. <i>Annals of Botany</i> , 2014, 114, 1507-1515.	2.9	55
11	Isolation and functional characterization of a cotton ubiquitination-related promoter and 5'UTR that drives high levels of expression in root and flower tissues. <i>BMC Biotechnology</i> , 2011, 11, 115.	3.3	18
12	Identification and evaluation of new reference genes in <i>Gossypium hirsutum</i> for accurate normalization of real-time quantitative RT-PCR data. <i>BMC Plant Biology</i> , 2010, 10, 49.	3.6	283