

# Huijun Duan

## List of Publications by Year in descending order

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14  
papers

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citations

1307594

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#	ARTICLE	IF	CITATIONS
1	Cotton <i>ChSSI2</i> isoforms from the stearyl acyl carrier protein fatty acid desaturase family regulate Verticillium wilt resistance. <i>Molecular Plant Pathology</i> , 2021, 22, 1041-1056.	4.2	16
2	Comparative transcriptomic analysis of contrasting hybrid cultivars reveal key drought-responsive genes and metabolic pathways regulating drought stress tolerance in maize at various stages. <i>PLoS ONE</i> , 2020, 15, e0240468.	2.5	7
3	Comparative proteomics analysis of two maize hybrids revealed drought-stress tolerance mechanisms. <i>Biotechnology and Biotechnological Equipment</i> , 2020, 34, 763-780.	1.3	16
4	DIA (Data Independent Acquisition) proteomic based study on maize filling-kernel stage drought stress-responsive proteins and metabolic pathways. <i>Biotechnology and Biotechnological Equipment</i> , 2020, 34, 1198-1214.	1.3	2
5	Comparative transcriptomic and physiological analyses of contrasting hybrid cultivars ND476 and ZX978 identify important differentially expressed genes and pathways regulating drought stress tolerance in maize. <i>Genes and Genomics</i> , 2020, 42, 937-955.	1.4	5
6	Comparative Proteomics and Physiological Analyses Reveal Important Maize Filling-Kernel Drought-Responsive Genes and Metabolic Pathways. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3743.	4.1	36
7	Maize leaves drought-responsive genes revealed by comparative transcriptome of two cultivars during the filling stage. <i>PLoS ONE</i> , 2019, 14, e0223786.	2.5	13
8	Differentially Expressed Genes and Enriched Pathways During Drought-Sensitive Period Under Field Conditions in Bread Wheat. <i>Plant Molecular Biology Reporter</i> , 2019, 37, 389-400.	1.8	8
9	Key Maize Drought-Responsive Genes and Pathways Revealed by Comparative Transcriptome and Physiological Analyses of Contrasting Inbred Lines. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1268.	4.1	78
10	Comparative Proteomic and Morpho-Physiological Analyses of Maize Wild-Type Vp16 and Mutant vp16 Germinating Seed Responses to PEG-Induced Drought Stress. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5586.	4.1	14
11	Analysis of sulphur and chlorine induced DNA cytosine methylation alterations in fresh corn ( <i>Zea mays</i> ) using MSAP approach. <i>Genes and Genomics</i> , 2018, 40, 913-925.	1.4	5
12	Effects of ethephon on DNA methylation and gene expressions associated with shortened internodes in maize. <i>Biotechnology and Biotechnological Equipment</i> , 2018, 32, 30-40.	1.3	3
13	Comparative Proteomic and Physiological Analyses of Two Divergent Maize Inbred Lines Provide More Insights into Drought-Stress Tolerance Mechanisms. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3225.	4.1	41
14	Molecular cloning and characterization of ClZE, a zeaxanthin epoxidase gene in watermelon ( <i>Citrullus lanatus</i> ). <i>Biotechnology and Biotechnological Equipment</i> , 2017, 31, 259-269.	1.3	2