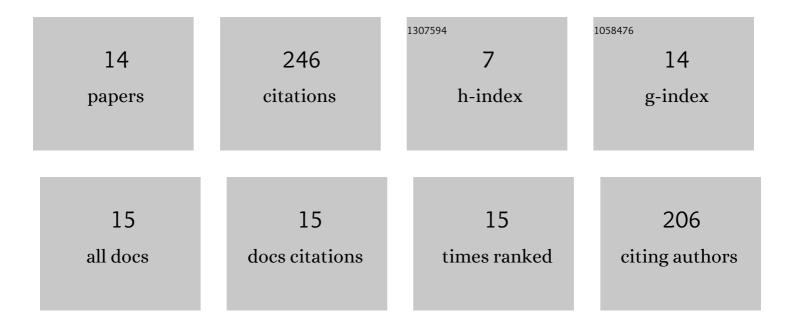
## Huijun Duan

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7612452/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Key Maize Drought-Responsive Genes and Pathways Revealed by Comparative Transcriptome and Physiological Analyses of Contrasting Inbred Lines. International Journal of Molecular Sciences, 2019, 20, 1268.	4.1	78
2	Comparative Proteomic and Physiological Analyses of Two Divergent Maize Inbred Lines Provide More Insights into Drought-Stress Tolerance Mechanisms. International Journal of Molecular Sciences, 2018, 19, 3225.	4.1	41
3	Comparative Proteomics and Physiological Analyses Reveal Important Maize Filling-Kernel Drought-Responsive Genes and Metabolic Pathways. International Journal of Molecular Sciences, 2019, 20, 3743.	4.1	36
4	Comparative proteomics analysis of two maize hybrids revealed drought-stress tolerance mechanisms. Biotechnology and Biotechnological Equipment, 2020, 34, 763-780.	1.3	16
5	Cotton <i>GhSSI2</i> isoforms from the stearoyl acyl carrier protein fatty acid desaturase family regulate Verticillium wilt resistance. Molecular Plant Pathology, 2021, 22, 1041-1056.	4.2	16
6	Comparative Proteomic and Morpho-Physiological Analyses of Maize Wild-Type Vp16 and Mutant vp16 Germinating Seed Responses to PEC-Induced Drought Stress. International Journal of Molecular Sciences, 2019, 20, 5586.	4.1	14
7	Maize leaves drought-responsive genes revealed by comparative transcriptome of two cultivars during the filling stage. PLoS ONE, 2019, 14, e0223786.	2.5	13
8	Differentially Expressed Genes and Enriched Pathways During Drought-Sensitive Period Under Field Conditions in Bread Wheat. Plant Molecular Biology Reporter, 2019, 37, 389-400.	1.8	8
9	Comparative transcriptomic analysis of contrasting hybrid cultivars reveal key drought-responsive genes and metabolic pathways regulating drought stress tolerance in maize at various stages. PLoS ONE, 2020, 15, e0240468.	2.5	7
10	Analysis of sulphur and chlorine induced DNA cytosine methylation alterations in fresh corn (Zea) Tj ETQqO 0 0 rg (MSAP) approach. Genes and Genomics, 2018, 40, 913-925.	gBT /Over 1.4	ock 10 Tf 50 5
11	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. Genes and Genomics, 2020, 42, 937-955.	1.4	5
12	Effects of ethephon on DNA methylation and gene expressions associated with shortened internodes in maize. Biotechnology and Biotechnological Equipment, 2018, 32, 30-40.	1.3	3
13	Molecular cloning and characterization of ClZE, a zeaxanthin epoxidase gene in watermelon (Citrullus lanatus). Biotechnology and Biotechnological Equipment, 2017, 31, 259-269.	1.3	2
14	DIA (Data Independent Acquisition) proteomic based study on maize filling-kernel stage drought stress-responsive proteins and metabolic pathways. Biotechnology and Biotechnological Equipment, 2020, 34, 1198-1214.	1.3	2