

# Yi Xu

## List of Publications by Year in descending order

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21  
papers

592  
citations

687363

13  
h-index

752698

20  
g-index

21  
all docs

21  
docs citations

21  
times ranked

925  
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparative transcriptomics and gene network analysis revealed secondary metabolism as preeminent metabolic pathways for heat tolerance in hard fescue. <i>Grass Research</i> , 2021, 1, 1-10.	1.7	1
2	Lipidomic reprogramming associated with drought stress priming enhanced heat tolerance in tall fescue ( <i>Festuca arundinacea</i> ). <i>Plant, Cell and Environment</i> , 2019, 42, 947-958.	5.7	75
3	Comparative transcriptomic analysis reveals common molecular factors responsive to heat and drought stress in <i>Agrostis stolonifera</i> . <i>Scientific Reports</i> , 2018, 8, 15181.	3.3	32
4	Transcriptomic analysis reveals unique molecular factors for lipid hydrolysis, secondary cell-walls and oxidative protection associated with thermotolerance in perennial grass. <i>BMC Genomics</i> , 2018, 19, 70.	2.8	15
5	Candidate Genes and Molecular Markers Correlated to Physiological Traits for Heat Tolerance in Fine Fescue Cultivars. <i>International Journal of Molecular Sciences</i> , 2018, 19, 116.	4.1	30
6	Transcriptional regulation of hormone synthesis and signaling pathways by overexpressing cytokinin synthesis contributes to improved drought tolerance in creeping bentgrass. <i>Physiologia Plantarum</i> , 2017, 161, 235-256.	5.2	22
7	Transcriptional factors for stress signaling, oxidative protection, and protein modification in <i>ipt</i> -transgenic creeping bentgrass exposed to drought stress. <i>Environmental and Experimental Botany</i> , 2017, 144, 49-60.	4.2	13
8	Exogenous Ascorbic Acid Mediated Abiotic Stress Tolerance in Plants. , 2017, , 233-253.		2
9	The green ash transcriptome and identification of genes responding to abiotic and biotic stresses. <i>BMC Genomics</i> , 2016, 17, 702.	2.8	32
10	Physiological and iTRAQ-Based Proteomic Analyses Reveal the Function of Spermidine on Improving Drought Tolerance in White Clover. <i>Journal of Proteome Research</i> , 2016, 15, 1563-1579.	3.7	28
11	Enhancing cytokinin synthesis by overexpressing <i>ipt</i> alleviated drought inhibition of root growth through activating ROS-scavenging systems in <i>Agrostis stolonifera</i> . <i>Journal of Experimental Botany</i> , 2016, 67, 1979-1992.	4.8	137
12	Differentially Expressed Genes Associated with Improved Drought Tolerance in Creeping Bentgrass Overexpressing a Gene for Cytokinin Biosynthesis. <i>PLoS ONE</i> , 2016, 11, e0166676.	2.5	23
13	Cellular and Molecular Mechanisms for Elevated CO <sub>2</sub> Regulation of Plant Growth and Stress Adaptation. <i>Crop Science</i> , 2015, 55, 1405-1424.	1.8	48
14	Ascorbic acid mitigation of water stress-inhibition of root growth in association with oxidative defense in tall fescue ( <i>Festuca arundinacea</i> Schreb.). <i>Frontiers in Plant Science</i> , 2015, 6, 807.	3.6	48
15	Root Antioxidant Mechanisms in Relation to Root Thermotolerance in Perennial Grass Species Contrasting in Heat Tolerance. <i>PLoS ONE</i> , 2015, 10, e0138268.	2.5	12
16	Preliminary Genomic Characterization of Ten Hardwood Tree Species from Multiplexed Low Coverage Whole Genome Sequencing. <i>PLoS ONE</i> , 2015, 10, e0145031.	2.5	28
17	Comparative expression analysis of resistant and susceptible <i>Populus</i> clones inoculated with <i>Septoria musiva</i> . <i>Plant Science</i> , 2014, 223, 69-78.	3.6	21
18	LtuCAD1 Is a Cinnamyl Alcohol Dehydrogenase Ortholog Involved in Lignin Biosynthesis in <i>Liriodendron tulipifera</i> L., a Basal Angiosperm Timber Species. <i>Plant Molecular Biology Reporter</i> , 2013, 31, 1089-1099.	1.8	5

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19	Wood chemistry analysis and expression profiling of a poplar clone expressing a tyrosine-rich peptide. <i>Plant Cell Reports</i> , 2013, 32, 1827-1841.	5.6	5
20	Investigation of genome structure of a cinnamyl alcohol dehydrogenase locus in a basal angiosperm hardwood species, <i>Liriodendron tulipifera</i> L., reveals low synteny. <i>Journal of Systematics and Evolution</i> , 2011, 49, 396-405.	3.1	2
21	Generation of a large-scale genomic resource for functional and comparative genomics in <i>Liriodendron tulipifera</i> L.. <i>Tree Genetics and Genomes</i> , 2011, 7, 941-954.	1.6	13