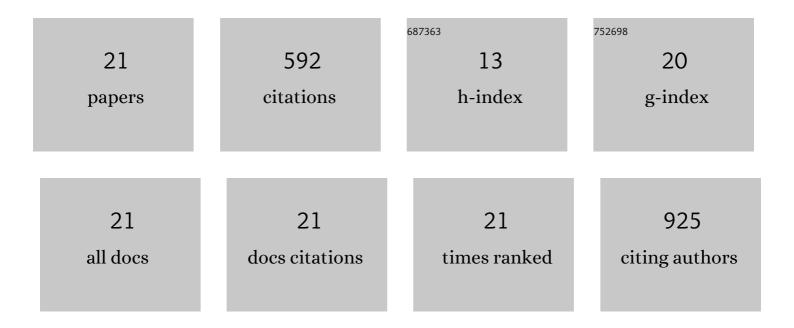


List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Comparative transcriptomics and gene network analysis revealed secondary metabolism as preeminent metabolic pathways for heat tolerance in hard fescue. Grass Research, 2021, 1, 1-10.	1.7	1
2	Lipidomic reprogramming associated with drought stress primingâ€enhanced heat tolerance in tall fescue (<scp><i>Festuca arundinacea</i></scp>). Plant, Cell and Environment, 2019, 42, 947-958.	5.7	75
3	Comparative transcriptomic analysis reveals common molecular factors responsive to heat and drought stress in Agrostis stolonifera. Scientific Reports, 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. BMC Genomics, 2018, 19, 70.	2.8	15
5	Candidate Genes and Molecular Markers Correlated to Physiological Traits for Heat Tolerance in Fine Fescue Cultivars. International Journal of Molecular Sciences, 2018, 19, 116.	4.1	30
6	Transcriptional regulation of hormoneâ€synthesis and signaling pathways by overexpressing cytokininâ€synthesis contributes to improved drought tolerance in creeping bentgrass. Physiologia Plantarum, 2017, 161, 235-256.	5.2	22
7	Transcriptional factors for stress signaling, oxidative protection, and protein modification in ipt-transgenic creeping bentgrass exposed to drought stress. Environmental and Experimental Botany, 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. BMC Genomics, 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. Journal of Proteome Research, 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> . Journal of Experimental Botany, 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. PLoS ONE, 2016, 11, e0166676.	2.5	23
13	Cellular and Molecular Mechanisms for Elevated CO ₂ –Regulation of Plant Growth and Stress Adaptation. Crop Science, 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 (Festuca arundinacea Schreb.). Frontiers in Plant Science, 2015, 6, 807.	3.6	48
15	Root Antioxidant Mechanisms in Relation to Root Thermotolerance in Perennial Grass Species Contrasting in Heat Tolerance. PLoS ONE, 2015, 10, e0138268.	2.5	12
16	Preliminary Genomic Characterization of Ten Hardwood Tree Species from Multiplexed Low Coverage Whole Genome Sequencing. PLoS ONE, 2015, 10, e0145031.	2.5	28
17	Comparative expression analysis of resistant and susceptible Populus clones inoculated with Septoria musiva. Plant Science, 2014, 223, 69-78.	3.6	21
18	LtuCAD1 Is a Cinnamyl Alcohol Dehydrogenase Ortholog Involved in Lignin Biosynthesis in Liriodendron tulipifera L., a Basal Angiosperm Timber Species. Plant Molecular Biology Reporter, 2013, 31, 1089-1099.	1.8	5

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#	Article	IF	CITATIONS
19	Wood chemistry analysis and expression profiling of a poplar clone expressing a tyrosine-rich peptide. Plant Cell Reports, 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. Journal of Systematics and Evolution, 2011, 49, 396-405.	3.1	2
21	Generation of a large-scale genomic resource for functional and comparative genomics in Liriodendron tulipifera L Tree Genetics and Genomes, 2011, 7, 941-954.	1.6	13