## Mingying Liu

List of Publications by Year in descending order

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623734 839539 18 657 14 18 citations g-index h-index papers 18 18 18 891 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Identification and functional characterization of ABCC transporters for Cd tolerance and accumulation in Sedum alfredii Hance. Scientific Reports, 2020, 10, 20928.	3.3	14
2	SaHsfA4c From Sedum alfredii Hance Enhances Cadmium Tolerance by Regulating ROS-Scavenger Activities and Heat Shock Proteins Expression. Frontiers in Plant Science, 2020, 11, 142.	3.6	28
3	cDNA Library for Mining Functional Genes in <i>Sedum alfredii</i> Hance Related to Cadmium Tolerance and Characterization of the Roles of a Novel <i>SaCTP2</i> Gene in Enhancing Cadmium Hyperaccumulation. Environmental Science & Eamp; Technology, 2019, 53, 10926-10940.	10.0	21
4	Identification and comprehensive analysis of the characteristics and roles of leucine-rich repeat receptor-like protein kinase (LRR-RLK) genes in Sedum alfredii Hance responding to cadmium stress. Ecotoxicology and Environmental Safety, 2019, 167, 95-106.	6.0	16
5	Sedum alfredii SaNramp6 Metal Transporter Contributes to Cadmium Accumulation in Transgenic Arabidopsis thaliana. Scientific Reports, 2017, 7, 13318.	3.3	60
6	Overexpressing the Sedum alfredii Cu/Zn Superoxide Dismutase Increased Resistance to Oxidative Stress in Transgenic Arabidopsis. Frontiers in Plant Science, 2017, 8, 1010.	3.6	73
7	Phenotypic and Comparative Transcriptome Analysis of Different Ploidy Plants in Dendrocalamus latiflorus Munro. Frontiers in Plant Science, 2017, 8, 1371.	3.6	14
8	Functional Characterization of a Gene in Sedum alfredii Hance Resembling Rubber Elongation Factor Endowed with Functions Associated with Cadmium Tolerance. Frontiers in Plant Science, 2016, 7, 965.	3.6	13
9	Integration of small <scp>RNA</scp> s, degradome and transcriptome sequencing in hyperaccumulator <i>Sedum alfredii</i> uncovers a complex regulatory network and provides insights into cadmium phytoremediation. Plant Biotechnology Journal, 2016, 14, 1470-1483.	8.3	96
10	Validation of Reference Genes Aiming Accurate Normalization of qRT-PCR Data in Dendrocalamus latiflorus Munro. PLoS ONE, 2014, 9, e87417.	2.5	17
11	Enhanced cold stress tolerance of transgenic Dendrocalamus latiflorus Munro (Ma bamboo) plants expressing a bacterial CodA gene. In Vitro Cellular and Developmental Biology - Plant, 2014, 50, 385-391.	2.1	23
12	Identification and expression analysis of salt-responsive genes using a comparative microarray approach in Salix matsudana. Molecular Biology Reports, 2014, 41, 6555-6568.	2.3	10
13	Callus induction and plant regeneration from anthers of Dendrocalamus latiflorus Munro. In Vitro Cellular and Developmental Biology - Plant, 2013, 49, 375-382.	2.1	22
14	Selection and Validation of Reference Genes for Real-Time Quantitative PCR in Hyperaccumulating Ecotype of Sedum alfredii under Different Heavy Metals Stresses. PLoS ONE, 2013, 8, e82927.	2.5	39
15	Expression profile of miRNAs in Populus cathayana L. and Salix matsudana Koidz under salt stress. Molecular Biology Reports, 2012, 39, 8645-8654.	2.3	37
16	Transcriptome Sequencing and De Novo Analysis for Ma Bamboo (Dendrocalamus latiflorus Munro) Using the Illumina Platform. PLoS ONE, 2012, 7, e46766.	2.5	104
17	Amphioxus IGF-like peptide induces mouse muscle cell development via binding to IGF receptors and activating MAPK and PI3K/Akt signaling pathways. Molecular and Cellular Endocrinology, 2011, 343, 45-54.	3.2	19
18	A kringle-containing protease with plasminogen-like activity in the basal chordate <i>Branchiostoma belcheri</i> . Bioscience Reports, 2009, 29, 385-395.	2.4	51