## Xin Deng

List of Publications by Year in descending order

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		361413	414414
32	1,919	20	32
papers	citations	h-index	g-index
32	32	32	2656
all docs	docs citations	times ranked	citing authors

XIN DENC

#	Article	IF	CITATIONS
1	Comparative analysis of physiological, agronomic and transcriptional responses to drought stress in wheat local varieties from Mongolia and Northern China. Plant Physiology and Biochemistry, 2022, 170, 23-35.	5.8	5
2	DNA methylation-mediated modulation of rapid desiccation tolerance acquisition and dehydration stress memory in the resurrection plant Boea hygrometrica. PLoS Genetics, 2021, 17, e1009549.	3.5	22
3	Plant Sterol Clustering Correlates with Membrane Microdomains as Revealed by Optical and Computational Microscopy. Membranes, 2021, 11, 747.	3.0	4
4	A role of age-dependent DNA methylation reprogramming in regulating the regeneration capacity of Boea hygrometrica leaves. Functional and Integrative Genomics, 2020, 20, 133-149.	3.5	13
5	Weighted Gene Co-expression Network Analysis (WGCNA) Reveals the Hub Role of Protein Ubiquitination in the Acquisition of Desiccation Tolerance in Boea hygrometrica. Plant and Cell Physiology, 2019, 60, 2707-2719.	3.1	26
6	Common and Specific Mechanisms of Desiccation Tolerance in Two Gesneriaceae Resurrection Plants. Multiomics Evidences. Frontiers in Plant Science, 2019, 10, 1067.	3.6	16
7	Single-Molecule Imaging and Computational Microscopy Approaches Clarify the Mechanism of the Dimerization and Membrane Interactions of Green Fluorescent Protein. International Journal of Molecular Sciences, 2019, 20, 1410.	4.1	7
8	Acclimation-induced metabolic reprogramming contributes to rapid desiccation tolerance acquisition in Boea hygrometrica. Environmental and Experimental Botany, 2018, 148, 70-84.	4.2	23
9	Arabidopsis Blue Light Receptor Phototropin 1 Undergoes Blue Light-Induced Activation in Membrane Microdomains. Molecular Plant, 2018, 11, 846-859.	8.3	44
10	Transcriptome reprogramming during severe dehydration contributes to physiological and metabolic changes in the resurrection plant Haberlea rhodopensis. BMC Plant Biology, 2018, 18, 351.	3.6	40
11	A modified GFP facilitates counting membrane protein subunits by step-wise photobleaching in Arabidopsis. Journal of Plant Physiology, 2017, 213, 129-133.	3.5	9
12	BhbZIP60 from Resurrection Plant Boea hygrometrica Is an mRNA Splicing-Activated Endoplasmic Reticulum Stress Regulator Involved in Drought Tolerance. Frontiers in Plant Science, 2017, 8, 245.	3.6	22
13	An Effective and Inducible System of TAL Effector-Mediated Transcriptional Repression inÂArabidopsis. Molecular Plant, 2016, 9, 1546-1549.	8.3	5
14	Arabidopsis seed germination speed is controlled by SNL histone deacetylase-binding factor-mediated regulation of AUX1. Nature Communications, 2016, 7, 13412.	12.8	80
15	Transcriptome and Degradome Sequencing Reveals Dormancy Mechanisms of <i>Cunninghamia lanceolata</i> Seeds. Plant Physiology, 2016, 172, 2347-2362.	4.8	33
16	ABA receptor PYL9 promotes drought resistance and leaf senescence. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 1949-1954.	7.1	508
17	Global Transcriptome Analysis Reveals Acclimation-Primed Processes Involved in the Acquisition of Desiccation Tolerance in <i>Boea hygrometrica</i> . Plant and Cell Physiology, 2015, 56, 1429-1441.	3.1	54
18	The resurrection genome of <i>Boea hygrometrica</i> : A blueprint for survival of dehydration. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 5833-5837.	7.1	132

Xin Deng

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19	MicroRNA857 Is Involved in the Regulation of Secondary Growth of Vascular Tissues in Arabidopsis. Plant Physiology, 2015, 169, pp.01011.2015.	4.8	67
20	Single-molecule fluorescence imaging to quantify membrane protein dynamics and oligomerization in living plant cells. Nature Protocols, 2015, 10, 2054-2063.	12.0	60
21	Identification of a Retroelement from the Resurrection Plant Boea hygrometrica That Confers Osmotic and Alkaline Tolerance in Arabidopsis thaliana. PLoS ONE, 2014, 9, e98098.	2.5	19
22	A comparative study on Ca content and distribution in two Gesneriaceae species reveals distinctive mechanisms to cope with high rhizospheric soluble calcium. Frontiers in Plant Science, 2014, 5, 647.	3.6	14
23	Identification of Quantitative Trait Loci Controlling High Calcium Response in Arabidopsis thaliana. PLoS ONE, 2014, 9, e112511.	2.5	3
24	Molecular cloning and differential expression of sHSP gene family members from the resurrection plant Boea hygrometrica in response to abiotic stresses. Biologia (Poland), 2013, 68, 651-661.	1.5	14
25	<i>Arabidopsis</i> Paired Amphipathic Helix Proteins SNL1 and SNL2 Redundantly Regulate Primary Seed Dormancy via Abscisic Acid–Ethylene Antagonism Mediated by Histone Deacetylation. Plant Cell, 2013, 25, 149-166.	6.6	140
26	Understanding desiccation tolerance using the resurrection plant Boea hygrometrica as a model system. Frontiers in Plant Science, 2013, 4, 446.	3.6	52
27	A novel role for histone methyltransferase KYP/SUVH4 in the control of <i>Arabidopsis</i> primary seed dormancy. New Phytologist, 2012, 193, 605-616.	7.3	104
28	Cloning and expression analysis of a dirigent protein gene from the resurrection plant Boea hygrometrica. Progress in Natural Science: Materials International, 2009, 19, 347-352.	4.4	52
29	A WRKY transcription factor participates in dehydration tolerance in Boea hygrometrica by binding to the W-box elements of the galactinol synthase (BhGolS1) promoter. Planta, 2009, 230, 1155-1166.	3.2	174
30	Ectopic over-expression of BhHsf1, a heat shock factor from the resurrection plant Boea hygrometrica, leads to increased thermotolerance and retarded growth in transgenic Arabidopsis and tobacco. Plant Molecular Biology, 2009, 71, 451-467.	3.9	56
31	Proteome analysis of leaves from the resurrection plant Boea hygrometrica in response to dehydration and rehydration. Planta, 2007, 225, 1405-1420.	3.2	101
32	Title is missing!. Plant Molecular Biology Reporter, 1999, 17, 279-279.	1.8	20