Dong-Hao Wang

List of Publications by Year in descending order

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18 papers	257 citations	933447 10 h-index	996975 15 g-index
18	18	18	182 citing authors
all docs	docs citations	times ranked	

#	Article	IF	CITATIONS
1	JA-Responsive Transcription Factor SmMYB97 Promotes Phenolic Acid and Tanshinone Accumulation in <i>Salvia miltiorrhiza (i). Journal of Agricultural and Food Chemistry, 2020, 68, 14850-14862.</i>	5.2	36
2	Molecular characterization and expression of three galactinol synthase genes that confer stress tolerance in Salvia miltiorrhiza. Journal of Plant Physiology, 2012, 169, 1838-1848.	3.5	30
3	Wholeâ€genome sequence data of <i>Hypericum perforatum</i> and functional characterization of melatonin biosynthesis by Nâ€acetylserotonin Oâ€methyltransferase. Journal of Pineal Research, 2021, 70, e12709.	7.4	30
4	Genome-Wide Identification and Characterization of the WRKY Gene Family in Scutellaria baicalensis Georgi under Diverse Abiotic Stress. International Journal of Molecular Sciences, 2022, 23, 4225.	4.1	22
5	Molecular Characterization and Overexpression of SmJMT Increases the Production of Phenolic Acids in Salvia miltiorrhiza. International Journal of Molecular Sciences, 2018, 19, 3788.	4.1	21
6	SmSPL6 Induces Phenolic Acid Biosynthesis and Affects Root Development in Salvia miltiorrhiza. International Journal of Molecular Sciences, 2021, 22, 7895.	4.1	16
7	R2R3-MYB Transcription Factor SmMYB52 Positively Regulates Biosynthesis of Salvianolic Acid B and Inhibits Root Growth in Salvia miltiorrhiza. International Journal of Molecular Sciences, 2021, 22, 9538.	4.1	13
8	Targeted mutagenesis of CYP76AK2 and CYP76AK3 in Salvia miltiorrhiza reveals their roles in tanshinones biosynthetic pathway. International Journal of Biological Macromolecules, 2021, 189, 455-463.	7.5	13
9	De novo sequencing of Bletilla striata (Orchidaceae) transcriptome and identification of genes involved in polysaccharide biosynthesis. Genetics and Molecular Biology, 2020, 43, e20190417.	1.3	13
10	Reference genes for qRT-PCR normalisation in different tissues, developmental stages, and stress conditions of <i>Hypericum perforatum</i>). PeerJ, 2019, 7, e7133.	2.0	11
11	MiR408-SmLAC3 Module Participates in Salvianolic Acid B Synthesis in Salvia miltiorrhiza. International Journal of Molecular Sciences, 2021, 22, 7541.	4.1	10
12	Transcription factor SmSPL7 promotes anthocyanin accumulation and negatively regulates phenolic acid biosynthesis in Salvia miltiorrhiza. Plant Science, 2021, 310, 110993.	3.6	10
13	Tweety-Homolog 1 Facilitates Pain via Enhancement of Nociceptor Excitability and Spinal Synaptic Transmission. Neuroscience Bulletin, 2021, 37, 478-496.	2.9	9
14	Genome-Wide Identification of the TIFY Family in Salvia miltiorrhiza Reveals That SmJAZ3 Interacts With SmWD40-170, a Relevant Protein That Modulates Secondary Metabolism and Development. Frontiers in Plant Science, 2021, 12, 630424.	3.6	8
15	Genome-wide identification, classification and expression profile analysis of the HSF gene family in <i>Hypericum perforatum</i> . PeerJ, 2021, 9, e11345.	2.0	6
16	Functional Characterization of Serotonin N-Acetyltransferase Genes (SNAT1/2) in Melatonin Biosynthesis of Hypericum perforatum. Frontiers in Plant Science, 2021, 12, 781717.	3.6	5
17	Genome-Wide Analysis and the Expression Pattern of the ERF Gene Family in Hypericum perforatum. Plants, 2021, 10, 133.	3.5	3
18	The cytosolic protein GRP1 facilitates abscisic acid- and darkness-induced stomatal closure in Salvia miltiorrhiza. Journal of Plant Physiology, 2020, 245, 153112.	3.5	1