

Dung Tien Le

List of Publications by Year in descending order

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46
papers

2,653
citations

331538

21
h-index

233338

45
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49
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49
docs citations

49
times ranked

3370
citing authors

#	ARTICLE	IF	CITATIONS
1	The Drought-Mediated Soybean GmNAC085 Functions as a Positive Regulator of Plant Response to Salinity. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8986.	1.8	10
2	Synthesis and Photocatalytic Activity of ZnO - Ga_2O_3 Nanostructures for Decomposition of Formaldehyde under Deep Ultraviolet Irradiation. <i>Catalysts</i> , 2020, 10, 1105.	1.6	7
3	The GATA Gene Family in Chickpea: Structure Analysis and Transcriptional Responses to Abscisic Acid and Dehydration Treatments Revealed Potential Genes Involved in Drought Adaptation. <i>Journal of Plant Growth Regulation</i> , 2020, 39, 1647-1660.	2.8	15
4	Strategies for the Regeneration of <i>Paphiopedilum callosum</i> through Internode Tissue Cultures Using Dark-Light Cycles. <i>Hortscience: A Publication of the American Society for Horticultural Science</i> , 2019, 54, 920-925.	0.5	3
5	A system for large scale production of chrysanthemum using microponics with the supplement of silver nanoparticles under light-emitting diodes. <i>Scientia Horticulturae</i> , 2018, 232, 153-161.	1.7	25
6	The soybean transcription factor GmNAC085 enhances drought tolerance in Arabidopsis. <i>Environmental and Experimental Botany</i> , 2018, 151, 12-20.	2.0	58
7	Identification, Structural Characterization and Gene Expression Analysis of Members of the Nuclear Factor-Y Family in Chickpea (<i>Cicer arietinum</i> L.) under Dehydration and Abscisic Acid Treatments. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3290.	1.8	14
8	Function of the evolutionarily conserved plant methionine-S-sulfoxide reductase without the catalytic residue. <i>Protoplasma</i> , 2018, 255, 1741-1750.	1.0	7
9	Progress of loop-mediated isothermal amplification technique in molecular diagnosis of plant diseases. <i>Applied Biological Chemistry</i> , 2017, 60, 169-180.	0.7	39
10	Genome-Wide Analysis of Genes Encoding Methionine-Rich Proteins in <i>Arabidopsis</i> and Soybean Suggesting Their Roles in the Adaptation of Plants to Abiotic Stress. <i>International Journal of Genomics</i> , 2016, 2016, 1-8.	0.8	11
11	Expression analyses of soybean genes encoding methionine-R-sulfoxide reductase under various conditions suggest a possible role in the adaptation to stress. <i>Applied Biological Chemistry</i> , 2016, 59, 681-687.	0.7	10
12	Establishment of a loop-mediated isothermal amplification (LAMP) assay for the detection of phytoplasma-associated cassava witches' broom disease. <i>Applied Biological Chemistry</i> , 2016, 59, 151-156.	0.7	25
13	Improving Nutritional Quality of Plant Proteins Through Genetic Engineering. <i>Current Genomics</i> , 2016, 17, 220-229.	0.7	51
14	Comparative analysis of root transcriptomes from two contrasting drought-responsive Williams 82 and DT2008 soybean cultivars under normal and dehydration conditions. <i>Frontiers in Plant Science</i> , 2015, 6, 551.	1.7	37
15	Creation of transgenic rice plants producing small interfering RNA of Rice tungro spherical virus. <i>GM Crops and Food</i> , 2015, 6, 47-53.	2.0	12
16	Comments on "Long term toxicity of a Roundup herbicide and a Roundup-tolerant genetically modified maize". <i>Food and Chemical Toxicology</i> , 2013, 53, 443-444.	1.8	3
17	Characterization of the Newly Developed Soybean Cultivar DT2008 in Relation to the Model Variety W82 Reveals a New Genetic Resource for Comparative and Functional Genomics for Improved Drought Tolerance. <i>BioMed Research International</i> , 2013, 2013, 1-8.	0.9	20
18	The Auxin Response Factor Transcription Factor Family in Soybean: Genome-Wide Identification and Expression Analyses During Development and Water Stress. <i>DNA Research</i> , 2013, 20, 511-524.	1.5	151

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19	Diversity of Plant Methionine Sulfoxide Reductases B and Evolution of a Form Specific for Free Methionine Sulfoxide. PLoS ONE, 2013, 8, e65637.	1.1	26
20	Evaluation of Candidate Reference Genes for Normalization of Quantitative RT-PCR in Soybean Tissues under Various Abiotic Stress Conditions. PLoS ONE, 2012, 7, e46487.	1.1	115
21	Characterization of methionine oxidation and methionine sulfoxide reduction using methionine-rich cysteine-free proteins. BMC Biochemistry, 2012, 13, 21.	4.4	48
22	Differential Gene Expression in Soybean Leaf Tissues at Late Developmental Stages under Drought Stress Revealed by Genome-Wide Transcriptome Analysis. PLoS ONE, 2012, 7, e49522.	1.1	162
23	Transcriptome Analyses of a Salt-Tolerant Cytokinin-Deficient Mutant Reveal Differential Regulation of Salt Stress Response by Cytokinin Deficiency. PLoS ONE, 2012, 7, e32124.	1.1	146
24	Identification and Expression Analysis of Cytokinin Metabolic Genes in Soybean under Normal and Drought Conditions in Relation to Cytokinin Levels. PLoS ONE, 2012, 7, e42411.	1.1	132
25	Analysis of Cytokinin Mutants and Regulation of Cytokinin Metabolic Genes Reveals Important Regulatory Roles of Cytokinins in Drought, Salt and Abscisic Acid Responses, and Abscisic Acid Biosynthesis. Plant Cell, 2011, 23, 2169-2183.	3.1	647
26	Genome-Wide Survey and Expression Analysis of the Plant-Specific NAC Transcription Factor Family in Soybean During Development and Dehydration Stress. DNA Research, 2011, 18, 263-276.	1.5	362
27	Development and Evaluation of a Rapid Diagnostic Test for Plasmodium falciparum, P. vivax, and Mixed-Species Malaria Antigens. American Journal of Tropical Medicine and Hygiene, 2011, 85, 989-993.	0.6	22
28	Genome-Wide Expression Profiling of Soybean Two-Component System Genes in Soybean Root and Shoot Tissues under Dehydration Stress. DNA Research, 2011, 18, 17-29.	1.5	113
29	Molecular detection of nine rice viruses by a reverse-transcription loop-mediated isothermal amplification assay. Journal of Virological Methods, 2010, 170, 90-93.	1.0	62
30	Amino acids conferring herbicide resistance in tobacco acetohydroxyacid synthase. GM Crops, 2010, 1, 62-67.	1.8	7
31	Evaluation of a rapid diagnostic test, NanoSign [®] Influenza A/B Antigen, for detection of the 2009 pandemic influenza A/H1N1 viruses. Virology Journal, 2010, 7, 244.	1.4	23
32	Functional Analysis of Free Methionine-R-sulfoxide Reductase from Saccharomyces cerevisiae. Journal of Biological Chemistry, 2009, 284, 4354-4364.	1.6	83
33	Cloning and characterization of phosphoglucose isomerase from Sphingomonas chungbukensis DJ77. BMB Reports, 2009, 42, 172-177.	1.1	8
34	Cloning and characterization of phosphomannose isomerase from sphingomonas chungbukensis DJ77. BMB Reports, 2009, 42, 523-528.	1.1	4
35	Characterization of peptide Methionine oxidation and Methionine sulfoxide reduction using Methionine-rich proteins. FASEB Journal, 2009, 23, 855.8.	0.2	0
36	Functional analysis of yeast fRMs _r and its role in the reduction of free methionine-sulfoxides in yeast and mammalian cells. FASEB Journal, 2009, 23, 861.3.	0.2	0

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37	Inhibitors of Bacillus anthracis acetohydroxyacid synthase. Enzyme and Microbial Technology, 2008, 43, 270-275.	1.6	7
38	Analysis of Methionine/Selenomethionine Oxidation and Methionine Sulfoxide Reductase Function Using Methionine-Rich Proteins and Antibodies against Their Oxidized Forms. Biochemistry, 2008, 47, 6685-6694.	1.2	50
39	Mammals Reduce Methionine-S-sulfoxide with MsrA and Are Unable to Reduce Methionine-R-sulfoxide, and This Function Can Be Restored with a Yeast Reductase. Journal of Biological Chemistry, 2008, 283, 28361-28369.	1.6	49
40	Virtual Screening of Tubercular Acetohydroxy Acid Synthase Inhibitors through Analysis of Structural Models. Bulletin of the Korean Chemical Society, 2007, 28, 947-952.	1.0	2
41	Two consecutive aspartic acid residues conferring herbicide resistance in tobacco acetohydroxy acid synthase. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2005, 1749, 103-112.	1.1	16
42	Roles of Three Well-Conserved Arginine Residues in Mediating the Catalytic Activity of Tobacco Acetohydroxy Acid Synthase. Journal of Biochemistry, 2005, 138, 35-40.	0.9	11
43	FAD-independent and Herbicide-resistant Mutants of Tobacco Acetohydroxy Acid Synthase. Bulletin of the Korean Chemical Society, 2005, 26, 916-920.	1.0	1
44	Homology modeling of the structure of tobacco acetohydroxy acid synthase and examination of the active site by site-directed mutagenesis. Biochemical and Biophysical Research Communications, 2004, 317, 930-938.	1.0	14
45	Amino acid residues conferring herbicide resistance in tobacco acetohydroxy acid synthase. Biochemical Journal, 2004, 383, 53-61.	1.7	13
46	Roles of conserved methionine residues in tobacco acetolactate synthase. Biochemical and Biophysical Research Communications, 2003, 306, 1075-1082.	1.0	13