

Jun Tang

List of Publications by Year in descending order

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41
papers

993
citations

471371
17
h-index

454834
30
g-index

41
all docs

41
docs citations

41
times ranked

1235
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide analysis of Dof family transcription factors and their responses to abiotic stresses in Chinese cabbage. <i>BMC Genomics</i> , 2015, 16, 33.	1.2	103
2	Genome-wide analysis of the R2R3-MYB transcription factor genes in Chinese cabbage (<i>Brassica rapa</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.2	71
3	Genome-Wide Fractionation and Identification of WRKY Transcription Factors in Chinese Cabbage (<i>Brassica rapa</i> ssp. <i>pekinensis</i>) Reveals Collinearity and Their Expression Patterns Under Abiotic and Biotic Stresses. <i>Plant Molecular Biology Reporter</i> , 2014, 32, 781-795.	1.0	69
4	A novel cold-inducible gene from Pak-choi (<i>Brassica campestris</i> ssp. <i>chinensis</i>), BcWRKY46, enhances the cold, salt and dehydration stress tolerance in transgenic tobacco. <i>Molecular Biology Reports</i> , 2012, 39, 4553-4564.	1.0	68
5	Isolation and characterization of cytotoxic cyclotides from <i>Viola tricolor</i> . <i>Peptides</i> , 2010, 31, 1434-1440.	1.2	65
6	Genome-wide characterization and expression profiling of SWEET genes in cabbage (<i>Brassica oleracea</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T 93.	1.2	51
7	Characterization and co-expression analysis of WRKY orthologs involved in responses to multiple abiotic stresses in Pak-choi (<i>Brassica campestris</i> ssp. <i>chinensis</i>). <i>BMC Plant Biology</i> , 2013, 13, 188.	1.6	46
8	Genome-wide analysis of auxin transport genes identifies the hormone responsive patterns associated with leafy head formation in Chinese cabbage. <i>Scientific Reports</i> , 2017, 7, 42229.	1.6	36
9	Retention, Molecular Evolution, and Expression Divergence of the Auxin/Indole Acetic Acid and Auxin Response Factor Gene Families in <i>Brassica Rapa</i> Shed Light on Their Evolution Patterns in Plants. <i>Genome Biology and Evolution</i> , 2016, 8, 302-316.	1.1	35
10	The grapevine kinome: annotation, classification and expression patterns in developmental processes and stress responses. <i>Horticulture Research</i> , 2018, 5, 19.	2.9	30
11	Molecular evolution, characterization, and expression analysis of SnRK2 gene family in Pak-choi (<i>Brassica rapa</i> ssp. <i>chinensis</i>). <i>Frontiers in Plant Science</i> , 2015, 6, 879.	1.7	29
12	Genome-Wide Identification and Expression Profiling of Sugar Transporter Protein (STP) Family Genes in Cabbage (<i>Brassica oleracea</i> var. <i>capitata</i> L.) Reveals their Involvement in Clubroot Disease Responses. <i>Genes</i> , 2019, 10, 71.	1.0	29
13	Characterization of CIPK Family in Asian Pear (<i>Pyrus bretschneideri</i> Rehd) and Co-expression Analysis Related to Salt and Osmotic Stress Responses. <i>Frontiers in Plant Science</i> , 2016, 7, 1361.	1.7	26
14	Genome-wide analysis and identification of TIR-NBS-LRR genes in Chinese cabbage (<i>Brassica rapa</i> ssp.) Tj ETQq0 0 0 rgBT /Overlock 10 T Pathology, 2015, 90, 89-97.	1.3	25
15	Isolation and Characterization of Bioactive Cyclotides from <i>Viola labridorica</i> . <i>Helvetica Chimica Acta</i> , 2010, 93, 2287-2295.	1.0	24
16	Transcriptome Sequencing of the Sweet Potato Progenitor (<i>Ipomoea Trifida</i> (H.B.K.) G. Don.) and Discovery of Drought Tolerance Genes. <i>Tropical Plant Biology</i> , 2016, 9, 63-72.	1.0	21
17	Fine-Mapping and Analysis of Cgl1, a Gene Conferring Glossy Trait in Cabbage (<i>Brassica oleracea</i> L. var.) Tj ETQq1 1,0,784314 rgBT /O	1.7	20
18	Transcriptome analysis reveals complex response of the medicinal/ornamental halophyte <i>Iris halophila</i> Pall. to high environmental salinity. <i>Ecotoxicology and Environmental Safety</i> , 2018, 165, 250-260.	2.9	19

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19	Molecular cloning and characterization of BcCSP1, a Pak-choi (<i>Brassica rapa</i> ssp. <i>chinensis</i>) cold shock protein gene highly co-expressed under ABA and cold stimulation. <i>Acta Physiologiae Plantarum</i> , 2016, 38, 1.	1.0	17
20	Comparative transcriptomic analysis reveals gene expression changes during early stages of <i>Plasmodiophora brassicae</i> infection in cabbage (<i>Brassica oleracea</i> var. <i>capitata</i> L.). <i>Canadian Journal of Plant Pathology</i> , 2019, 41, 188-199.	0.8	17
21	Antibacterial Pentacyclic Polyketides from a Soil-Derived <i>Streptomyces</i> . <i>Journal of Natural Products</i> , 2020, 83, 1919-1924.	1.5	16
22	Molecular cloning and characterization of a novel salt-specific responsive WRKY transcription factor gene IlWRKY2 from the halophyte <i>Iris lactea</i> var. <i>chinensis</i> . <i>Genes and Genomics</i> , 2018, 40, 893-903.	0.5	15
23	Fine Mapping and Candidate Gene Identification for Wax Biosynthesis Locus, BoWax1 in <i>Brassica oleracea</i> L. var. <i>capitata</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 309.	1.7	15
24	Genome-wide identification of genes encoding putative secreted E3 ubiquitin ligases and functional characterization of PbRING1 in the biotrophic protist <i>Plasmodiophora brassicae</i> . <i>Current Genetics</i> , 2019, 65, 1355-1365.	0.8	15
25	BcMAF2 activates BcTEM1 and represses flowering in Pak-choi (<i>Brassica rapa</i> ssp. <i>chinensis</i>). <i>Plant Molecular Biology</i> , 2019, 100, 19-32.	2.0	15
26	Growth, physiological adaptation, and NHX gene expression analysis of <i>Iris halophila</i> under salt stress. <i>Environmental Science and Pollution Research</i> , 2018, 25, 25207-25216.	2.7	14
27	Benwamycins A-G, Trialkyl-Substituted Benzene Derivatives from a Soil-Derived <i>Streptomyces</i> . <i>Journal of Natural Products</i> , 2020, 83, 111-117.	1.5	14
28	Molecular analysis of a novel alkaline metal salt (NaCl)-responsive WRKY transcription factor gene IlWRKY1 from the halophyte <i>Iris lactea</i> var. <i>chinensis</i> . <i>International Biodeterioration and Biodegradation</i> , 2018, 127, 139-145.	1.9	13
29	Fine-mapping and transcriptome analysis of BoGL-3, a wax-less gene in cabbage (<i>Brassica oleracea</i> L. var. Tj ETQq1_1.0.784314 rgBT MO	1.0	12
30	An in vitro system to study cyclopeptide heterophyllin B biosynthesis in the medicinal plant <i>Pseudostellaria heterophylla</i> . <i>Plant Cell, Tissue and Organ Culture</i> , 2012, 108, 137-145.	1.2	10
31	C-repeat binding factor gene family identified in non-heading Chinese cabbage is functional in abiotic and biotic stress response but different from that in <i>Arabidopsis</i> . <i>Acta Physiologiae Plantarum</i> , 2014, 36, 3217-3229.	1.0	9
32	Genome-Wide Analysis of Basic Helix-Loop-Helix Superfamily Members Reveals Organization and Chilling-Responsive Patterns in Cabbage (<i>Brassica oleracea</i> var. <i>capitata</i> L.). <i>Genes</i> , 2019, 10, 914.	1.0	8
33	High resistance of transgenic cabbage plants with a synthetic cry1Ia8 gene from <i>Bacillus thuringiensis</i> against two lepidopteran species under field conditions. <i>Pest Management Science</i> , 2016, 72, 315-321.	1.7	7
34	Identification, evolution and functional inference on the cold-shock domain protein family in Pak-choi (<i>Brassica rapa</i> ssp. <i>chinensis</i>) and Chinese cabbage (<i>Brassica rapa</i> ssp. <i>pekinensis</i>). <i>Journal of Plant Interactions</i> , 2019, 14, 232-241.	1.0	7
35	Transcriptomic analysis of resistant and susceptible cabbage lines reveals differential expressions and candidate genes involved in cabbage early responses to black rot. <i>3 Biotech</i> , 2020, 10, 308.	1.1	7
36	Boron promotes phosphate remobilization in <i>Arabidopsis thaliana</i> and <i>Brassica oleracea</i> under phosphate deficiency. <i>Plant and Soil</i> , 2018, 431, 191-202.	1.8	5

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37	Characterization and Expression Profiling Analysis of Calmodulin Genes in Response to Salt and Osmotic Stresses in Pear (<i>Pyrus bretschneideri</i> Rehd.) and in Comparison with <i>Arabidopsis</i> . <i>BioMed Research International</i> , 2017, 2017, 1-13.	0.9	3
38	Mono-/Bis-Alkenoic Acid Derivatives From an Endophytic Fungus <i>Scopulariopsis candelabrum</i> and Their Antifungal Activity. <i>Frontiers in Chemistry</i> , 2021, 9, 812564.	1.8	3
39	Characterization of inthomycin biosynthetic gene cluster revealing new insights into carboxamide formation. <i>Chinese Journal of Natural Medicines</i> , 2020, 18, 677-683.	0.7	2
40	Preferential retention, expression profile and potential functional diversity analysis of HD-Zip gene family in <i>Brassica rapa</i> . <i>Plant Growth Regulation</i> , 2017, 82, 421-430.	1.8	1
41	Evolution of Acyl-CoA-binding protein gene family in plants provides insights into potential functions of grapevine (<i>Vitis vinifera</i> L.). <i>Journal of Berry Research</i> , 2020, 10, 677-696.	0.7	1