

Fan Wu

List of Publications by Year in descending order

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20
papers

444
citations

687363

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752698

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22
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22
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22
times ranked

380
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome and systems biology of <i>Melilotus albus</i> provides insights into coumarins biosynthesis. <i>Plant Biotechnology Journal</i> , 2022, 20, 592-609.	8.3	24
2	NAC and MYB Families and Lignin Biosynthesis-Related Members Identification and Expression Analysis in <i>Melilotus albus</i> . <i>Plants</i> , 2021, 10, 303.	3.5	19
3	Genome-Wide Identification and Development of LTR Retrotransposon-Based Molecular Markers for the <i>Melilotus</i> Genus. <i>Plants</i> , 2021, 10, 890.	3.5	7
4	Genome-Wide Analysis of the UDP-Glycosyltransferase Family Reveals Its Roles in Coumarin Biosynthesis and Abiotic Stress in <i>Melilotus albus</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 10826.	4.1	18
5	Genome-Wide Analysis of the Role of NAC Family in Flower Development and Abiotic Stress Responses in <i>Cleistogenes songorica</i> . <i>Genes</i> , 2020, 11, 927.	2.4	10
6	Analysis of Six Transcription Factor Families Explores Transcript Divergence of Cleistogamous and Chasmogamous Flowers in <i>Cleistogenes songorica</i> . <i>DNA and Cell Biology</i> , 2020, 39, 273-288.	1.9	4
7	Comprehensive analysis of bZIP transcription factors uncovers their roles during dimorphic floret differentiation and stress response in <i>Cleistogenes songorica</i> . <i>BMC Genomics</i> , 2019, 20, 760.	2.8	15
8	Genetic diversity, phylogenetic structure and development of core collections in <i>Melilotus</i> accessions from a Chinese gene bank. <i>Scientific Reports</i> , 2019, 9, 13017.	3.3	6
9	Differential co-expression networks of long non-coding RNAs and mRNAs in <i>Cleistogenes songorica</i> under water stress and during recovery. <i>BMC Plant Biology</i> , 2019, 19, 23.	3.6	70
10	Analysis of miRNAs and their target genes in five <i>Melilotus albus</i> NILs with different coumarin content. <i>Scientific Reports</i> , 2018, 8, 14138.	3.3	13
11	Coumarin Content, Morphological Variation, and Molecular Phylogenetics of <i>Melilotus</i> . <i>Molecules</i> , 2018, 23, 810.	3.8	18
12	Genetic variation and diversity in 199 <i>Melilotus</i> accessions based on a combination of 5 DNA sequences. <i>PLoS ONE</i> , 2018, 13, e0194172.	2.5	7
13	Transcriptomic profiling of <i>Melilotus albus</i> near-isogenic lines contrasting for coumarin content. <i>Scientific Reports</i> , 2017, 7, 4577.	3.3	21
14	Cross-species transferability of EST-SSR markers developed from the transcriptome of <i>Melilotus</i> and their application to population genetics research. <i>Scientific Reports</i> , 2017, 7, 17959.	3.3	53
15	Potential DNA barcodes for <i>Melilotus</i> species based on five single loci and their combinations. <i>PLoS ONE</i> , 2017, 12, e0182693.	2.5	15
16	Genotypic Variation in a Breeding Population of Yellow Sweet Clover (<i>Melilotus officinalis</i>). <i>Frontiers in Plant Science</i> , 2016, 7, 972.	3.6	23
17	Co-transforming bar and CsLEA enhanced tolerance to drought and salt stress in transgenic alfalfa (<i>Medicago sativa</i> L.). <i>Biochemical and Biophysical Research Communications</i> , 2016, 472, 75-82.	2.1	38
18	Analysis of genetic diversity and population structure in accessions of the genus <i>Melilotus</i> . <i>Industrial Crops and Products</i> , 2016, 85, 84-92.	5.2	25

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19	Interspecific Phylogenic Relationships within Genus <i>Melilotus</i> Based on Nuclear and Chloroplast DNA. PLoS ONE, 2015, 10, e0132596.	2.5	26
20	Co-transforming <i>bar</i> and <i>CsALDH</i> Genes Enhanced Resistance to Herbicide and Drought and Salt Stress in Transgenic Alfalfa (<i>Medicago sativa</i> L.). <i>Frontiers in Plant Science</i> , 2015, 6, 1115.	3.6	24