

Boshou Liao

List of Publications by Year in descending order

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Version: 2024-02-01

43
papers

1,493
citations

279798

23
h-index

345221

36
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43
all docs

43
docs citations

43
times ranked

1177
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide analysis of the basic leucine zipper (bZIP) transcription factor gene family in six legume genomes. <i>BMC Genomics</i> , 2015, 16, 1053.	2.8	93
2	Development and deployment of a high-density linkage map identified quantitative trait loci for plant height in peanut (<i>Arachis hypogaea</i> L.). <i>Scientific Reports</i> , 2016, 6, 39478.	3.3	76
3	Mitigating Aflatoxin Contamination in Groundnut through A Combination of Genetic Resistance and Post-Harvest Management Practices. <i>Toxins</i> , 2019, 11, 315.	3.4	73
4	Quantitative trait locus analysis for pod- and kernel-related traits in the cultivated peanut (<i>Arachis</i>) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	2.7	70
5	Transcriptomic, biochemical and physio-anatomical investigations shed more light on responses to drought stress in two contrasting sesame genotypes. <i>Scientific Reports</i> , 2017, 7, 8755.	3.3	62
6	Development of a High-Density Genetic Map Based on Specific Length Amplified Fragment Sequencing and Its Application in Quantitative Trait Loci Analysis for Yield-Related Traits in Cultivated Peanut. <i>Frontiers in Plant Science</i> , 2018, 9, 827.	3.6	56
7	Co-localization of major quantitative trait loci for pod size and weight to a 3.7ÂcM interval on chromosome A05 in cultivated peanut (<i>Arachis hypogaea</i> L.). <i>BMC Genomics</i> , 2017, 18, 58.	2.8	54
8	Analysis of Genetic Diversity and Population Structure of Sesame Accessions from Africa and Asia as Major Centers of Its Cultivation. <i>Genes</i> , 2016, 7, 14.	2.4	51
9	Discovery of genomic regions and candidate genes controlling shelling percentage using <scp>QTL</scp>â€seq approach in cultivated peanut (<i>Arachis hypogaea</i> L.). <i>Plant Biotechnology Journal</i> , 2019, 17, 1248-1260.	8.3	51
10	Quantitative Trait Locus Analysis of Late Leaf Spot Resistance and Plant-Type-Related Traits in Cultivated Peanut (<i>Arachis hypogaea</i> L.) under Multi-Environments. <i>PLoS ONE</i> , 2016, 11, e0166873.	2.5	51
11	Chromosomes A07 and A05 associated with stable and major QTLs for pod weight and size in cultivated peanut (<i>Arachis hypogaea</i> L.). <i>Theoretical and Applied Genetics</i> , 2018, 131, 267-282.	3.6	49
12	Development of SSR markers and identification of major quantitative trait loci controlling shelling percentage in cultivated peanut (<i>Arachis hypogaea</i> L.). <i>Theoretical and Applied Genetics</i> , 2017, 130, 1635-1648.	3.6	48
13	PTGBase: an integrated database to study tandem duplicated genes in plants. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, .	3.0	46
14	PMDBase: a database for studying microsatellite DNA and marker development in plants. <i>Nucleic Acids Research</i> , 2017, 45, D1046-D1053.	14.5	46
15	Genome-wide systematic characterization of bZIP transcription factors and their expression profiles during seed development and in response to salt stress in peanut. <i>BMC Genomics</i> , 2019, 20, 51.	2.8	42
16	Nextâ€generation sequencing identified genomic region and diagnostic markers for resistance to bacterial wilt on chromosome B02 in peanut (<i>Arachis hypogaea</i> L.). <i>Plant Biotechnology Journal</i> , 2019, 17, 2356-2369.	8.3	41
17	Transcriptome Analysis of a New Peanut Seed Coat Mutant for the Physiological Regulatory Mechanism Involved in Seed Coat Cracking and Pigmentation. <i>Frontiers in Plant Science</i> , 2016, 7, 1491.	3.6	39
18	Evolutionary history and functional divergence of the cytochrome P450 gene superfamily between <i>Arabidopsis thaliana</i> and <i>Brassica</i> species uncover effects of whole genome and tandem duplications. <i>BMC Genomics</i> , 2017, 18, 733.	2.8	37

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19	Identification of genomic regions and diagnostic markers for resistance to aflatoxin contamination in peanut (<i>Arachis hypogaea</i> L.). <i>BMC Genetics</i> , 2019, 20, 32.	2.7	37
20	Genomic survey sequencing for development and validation of single-locus SSR markers in peanut (<i>Arachis hypogaea</i> L.). <i>BMC Genomics</i> , 2016, 17, 420.	2.8	33
21	High-resolution mapping of a major and consensus quantitative trait locus for oil content to a ~0.8-Mb region on chromosome A08 in peanut (<i>Arachis hypogaea</i> L.). <i>Theoretical and Applied Genetics</i> , 2020, 133, 37-49.	3.6	33
22	Comprehensive Screening of Some West and Central African Sesame Genotypes for Drought Resistance Probing by Agromorphological, Physiological, Biochemical and Seed Quality Traits. <i>Agronomy</i> , 2017, 7, 83.	3.0	29
23	Transcriptome and metabolome reveal redirection of flavonoids in a white testa peanut mutant. <i>BMC Plant Biology</i> , 2020, 20, 161.	3.6	28
24	Genetic Variation and Association Mapping of Seed-Related Traits in Cultivated Peanut (<i>Arachis</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 5 2105.	3.6	27
25	A Major and Stable QTL for Bacterial Wilt Resistance on Chromosome B02 Identified Using a High-Density SNP-Based Genetic Linkage Map in Cultivated Peanut Yuanza 9102 Derived Population. <i>Frontiers in Genetics</i> , 2018, 9, 652.	2.3	27
26	Dynamic transcriptome landscape of sesame (<i>Sesamum indicum</i> L.) under progressive drought and after rewatering. <i>Genomics Data</i> , 2017, 11, 122-124.	1.3	24
27	Mutant Transcriptome Sequencing Provides Insights into Pod Development in Peanut (<i>Arachis</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 5 2105.	3.6	23
28	Characterization and Transferable Utility of Microsatellite Markers in the Wild and Cultivated <i>Arachis</i> Species. <i>PLoS ONE</i> , 2016, 11, e0156633.	2.5	21
29	Stable QTLs for Plant Height on Chromosome A09 Identified From Two Mapping Populations in Peanut (<i>Arachis hypogaea</i> L.). <i>Frontiers in Plant Science</i> , 2018, 9, 684.	3.6	21
30	Dissection of the Genetic Basis of Yield-Related Traits in the Chinese Peanut Mini-Core Collection Through Genome-Wide Association Studies. <i>Frontiers in Plant Science</i> , 2021, 12, 637284.	3.6	18
31	Genome evolutionary dynamics followed by diversifying selection explains the complexity of the <i>Sesamum indicum</i> genome. <i>BMC Genomics</i> , 2017, 18, 257.	2.8	17
32	Four QTL clusters containing major and stable QTLs for saturated fatty acid contents in a dense genetic map of cultivated peanut (<i>Arachis hypogaea</i> L.). <i>Molecular Breeding</i> , 2019, 39, 1.	2.1	17
33	Optimization of extraction of total trans resveratrol from peanut seeds and its determination by HPLC. <i>Journal of Separation Science</i> , 2020, 43, 1024-1031.	2.5	17
34	Genomic affinities of <i>Arachis</i> genus and interspecific hybrids were revealed by SRAP markers. <i>Genetic Resources and Crop Evolution</i> , 2010, 57, 903-913.	1.6	15
35	The Peanut (<i>Arachis hypogaea</i> L.) Gene AhLPAT2 Increases the Lipid Content of Transgenic <i>Arabidopsis</i> Seeds. <i>PLoS ONE</i> , 2015, 10, e0136170.	2.5	15
36	Transcriptomic profiling reveals pigment regulation during peanut testa development. <i>Plant Physiology and Biochemistry</i> , 2018, 125, 116-125.	5.8	15

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37	Identification of Two Novel Peanut Genotypes Resistant to Aflatoxin Production and Their SNP Markers Associated with Resistance. <i>Toxins</i> , 2020, 12, 156.	3.4	15
38	Genome-wide expression quantitative trait locus analysis in a recombinant inbred line population for trait dissection in peanut. <i>Plant Biotechnology Journal</i> , 2020, 18, 779-790.	8.3	14
39	Discovery of two novel and adjacent QTLs on chromosome B02 controlling resistance against bacterial wilt in peanut variety Zhonghua 6. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1133-1148.	3.6	14
40	Construction of ddRADseq-Based High-Density Genetic Map and Identification of Quantitative Trait Loci for Trans-resveratrol Content in Peanut Seeds. <i>Frontiers in Plant Science</i> , 2021, 12, 644402.	3.6	14
41	Key Regulators of Sucrose Metabolism Identified through Comprehensive Comparative Transcriptome Analysis in Peanuts. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7266.	4.1	14
42	Phenotypic evaluation of the Chinese mini-mini core collection of peanut (<i>Arachis hypogaea</i> L.) and assessment for resistance to bacterial wilt disease caused by <i>Ralstonia solanacearum</i> . <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2013, 11, 77-83.	0.8	11
43	High-Density Genetic Linkage Map Construction Using Whole-Genome Resequencing for Mapping QTLs of Resistance to <i>Aspergillus flavus</i> Infection in Peanut. <i>Frontiers in Plant Science</i> , 2021, 12, 745408.	3.6	9