

Ye Chu

List of Publications by Year in descending order

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Version: 2024-02-01

60
papers

2,905
citations

331670

21
h-index

182427

51
g-index

60
all docs

60
docs citations

60
times ranked

1842
citing authors

#	ARTICLE	IF	CITATIONS
1	The genome sequences of <i>Arachis duranensis</i> and <i>Arachis ipaensis</i> , the diploid ancestors of cultivated peanut. <i>Nature Genetics</i> , 2016, 48, 438-446.	21.4	761
2	The genome sequence of segmental allotetraploid peanut <i>Arachis hypogaea</i> . <i>Nature Genetics</i> , 2019, 51, 877-884.	21.4	439
3	Marker-Assisted Selection to Pyramid Nematode Resistance and the High Oleic Trait in Peanut. <i>Plant Genome</i> , 2011, 4, 110-117.	2.8	160
4	Mapping Late Leaf Spot Resistance in Peanut (<i>Arachis hypogaea</i>) Using QTL-seq Reveals Markers for Marker-Assisted Selection. <i>Frontiers in Plant Science</i> , 2018, 9, 83.	3.6	118
5	Genome-wide SNP Genotyping Resolves Signatures of Selection and Tetrasomic Recombination in Peanut. <i>Molecular Plant</i> , 2017, 10, 309-322.	8.3	114
6	Two Alleles of <i>FAD2B</i> Control the High Oleic Acid Trait in Cultivated Peanut. <i>Crop Science</i> , 2009, 49, 2029-2036.	1.8	109
7	Recombination is suppressed in an alien introgression in peanut harboring <i>Rma</i> , a dominant root-knot nematode resistance gene. <i>Molecular Breeding</i> , 2010, 26, 357-370.	2.1	109
8	High-density genetic map using whole-genome resequencing for fine mapping and candidate gene discovery for disease resistance in peanut. <i>Plant Biotechnology Journal</i> , 2018, 16, 1954-1967.	8.3	90
9	Frequency of a Loss-of-Function Mutation in Oleoyl-PC Desaturase (<i>FAD2A</i>) in the Mini-Core of the U.S. Peanut Germplasm Collection. <i>Crop Science</i> , 2007, 47, 2372-2378.	1.8	78
10	Reduction of IgE Binding and Nonpromotion of <i>Aspergillus flavus</i> Fungal Growth by Simultaneously Silencing <i>Ara h 2</i> and <i>Ara h 6</i> in Peanut. <i>Journal of Agricultural and Food Chemistry</i> , 2008, 56, 11225-11233.	5.2	68
11	Nested-association mapping (NAM)-based genetic dissection uncovers candidate genes for seed and pod weights in peanut (<i>Arachis hypogaea</i>). <i>Plant Biotechnology Journal</i> , 2020, 18, 1457-1471.	8.3	65
12	Development of a PCR-based Molecular Marker to Select for Nematode Resistance in Peanut. <i>Crop Science</i> , 2007, 47, 841-845.	1.8	59
13	QTL identification for seed weight and size based on a high-density SLAF-seq genetic map in peanut (<i>Arachis hypogaea</i> L.). <i>BMC Plant Biology</i> , 2019, 19, 537.	3.6	54
14	Machine Learning as an Effective Method for Identifying True Single Nucleotide Polymorphisms in Polyploid Plants. <i>Plant Genome</i> , 2019, 12, 180023.	2.8	50
15	Horizontal Transfer of Non-LTR Retrotransposons from Arthropods to Flowering Plants. <i>Molecular Biology and Evolution</i> , 2018, 35, 354-364.	8.9	41
16	Development and Phenotyping of Recombinant Inbred Line (RIL) Populations for Peanut (<i>Arachis</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	9.1	40
17	Major QTLs for Resistance to Early and Late Leaf Spot Diseases Are Identified on Chromosomes 3 and 5 in Peanut (<i>Arachis hypogaea</i>). <i>Frontiers in Plant Science</i> , 2019, 10, 883.	3.6	40
18	Registration of 'TifNV' High O/L™ Peanut. <i>Journal of Plant Registrations</i> , 2017, 11, 228-230.	0.5	34

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19	Gene expression profiling describes the genetic regulation of <i>Meloidogyne arenaria</i> resistance in <i>Arachis hypogaea</i> and reveals a candidate gene for resistance. <i>Scientific Reports</i> , 2017, 7, 1317.	3.3	32
20	Impact of Molecular Genetic Research on Peanut Cultivar Development. <i>Agronomy</i> , 2011, 1, 3-17.	3.0	26
21	Mapping quantitative trait loci (QTLs) and estimating the epistasis controlling stem rot resistance in cultivated peanut (<i>Arachis hypogaea</i>). <i>Theoretical and Applied Genetics</i> , 2020, 133, 1201-1212.	3.6	24
22	IntroMap: A Pipeline and Set of Diagnostic Diploid <i>Arachis</i> SNPs as a Tool for Mapping Alien Introgressions in <i>Arachis hypogaea</i> . <i>Peanut Science</i> , 2017, 44, 66-73.	0.1	23
23	Insight into Genes Regulating Postharvest Aflatoxin Contamination of Tetraploid Peanut from Transcriptional Profiling. <i>Genetics</i> , 2018, 209, 143-156.	2.9	23
24	Pod and Seed Trait QTL Identification To Assist Breeding for Peanut Market Preferences. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2297-2315.	1.8	22
25	Bcl-xL transformed peanut (<i>Arachis hypogaea</i> L.) exhibits paraquat tolerance. <i>Plant Cell Reports</i> , 2007, 27, 85-92.	5.6	21
26	Genotypic Regulation of Aflatoxin Accumulation but Not <i>Aspergillus</i> Fungal Growth upon Post-Harvest Infection of Peanut (<i>Arachis hypogaea</i> L.) Seeds. <i>Toxins</i> , 2017, 9, 218.	3.4	20
27	A new source of root-knot nematode resistance from <i>Arachis stenosperma</i> incorporated into allotetraploid peanut (<i>Arachis hypogaea</i>). <i>Scientific Reports</i> , 2019, 9, 17702.	3.3	20
28	Major seed size QTL on chromosome A05 of peanut (<i>Arachis hypogaea</i>) is conserved in the US mini core germplasm collection. <i>Molecular Breeding</i> , 2020, 40, 1.	2.1	19
29	Improvement of peanut (<i>Arachis hypogaea</i> L.) transformation efficiency and determination of transgene copy number by relative quantitative real-time PCR. <i>In Vitro Cellular and Developmental Biology - Plant</i> , 2013, 49, 266-275.	2.1	18
30	A Technique to Study <i>Meloidogyne arenaria</i> Resistance in <i>Agrobacterium rhizogenes</i> -Transformed Peanut. <i>Plant Disease</i> , 2014, 98, 1292-1299.	1.4	18
31	Legacy genetics of <i>Arachis cardenasii</i> in the peanut crop shows the profound benefits of international seed exchange. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	18
32	Two New <i>Aspergillus flavus</i> Reference Genomes Reveal a Large Insertion Potentially Contributing to Isolate Stress Tolerance and Aflatoxin Production. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3515-3531.	1.8	15
33	Use of green fluorescent protein as A non-destructive marker for peanut genetic transformation. <i>In Vitro Cellular and Developmental Biology - Plant</i> , 2005, 41, 437-445.	2.1	14
34	Genotypic Characterization of the U.S. Peanut Core Collection. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 4013-4026.	1.8	14
35	Characterization of peanut lines with interspecific introgressions conferring late leaf spot resistance. <i>Crop Science</i> , 2021, 61, 1724-1738.	1.8	13
36	Expression of the limited transpiration trait under high vapour pressure deficit in peanut populations: Runner and virginia types. <i>Journal of Agronomy and Crop Science</i> , 2017, 203, 295-300.	3.5	12

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37	Quantitative trait loci sequencing-derived molecular markers for selection of stem rot resistance in peanut. <i>Crop Science</i> , 2020, 60, 2008-2018.	1.8	12
38	Phenotyping and genotyping parents of sixteen recombinant inbred peanut populations. <i>Peanut Science</i> , 2018, 45, 1-11.	0.1	11
39	Resistance in Peanut Cultivars and Breeding Lines to Three Root-Knot Nematode Species. <i>Plant Disease</i> , 2008, 92, 631-638.	1.4	10
40	Genetic insight and mapping of the pod constriction trait in Virginia-type peanut. <i>BMC Genetics</i> , 2018, 19, 93.	2.7	9
41	Registration of GA-BatSten1 and GA-MagSten1, two induced allotetraploids derived from peanut wild relatives with superior resistance to leaf spots, rust, and root-knot nematode. <i>Journal of Plant Registrations</i> , 2021, 15, 372-378.	0.5	9
42	Comparison of SNP Calling Pipelines and NGS Platforms to Predict the Genomic Regions Harboring Candidate Genes for Nodulation in Cultivated Peanut. <i>Frontiers in Genetics</i> , 2020, 11, 222.	2.3	7
43	Identification of consistent QTL for time to maturation in Virginia-type Peanut (<i>Arachis hypogaea</i> L.). <i>BMC Plant Biology</i> , 2021, 21, 186.	3.6	7
44	Validation of resistance to root-knot nematode incorporated in peanut from the wild relative <i>Arachis stenosperma</i> . <i>Agronomy Journal</i> , 2021, 113, 2293-2302.	1.8	7
45	Registration of three peanut allotetraploid interspecific hybrids resistant to late leaf spot disease and tomato spotted wilt. <i>Journal of Plant Registrations</i> , 2021, 15, 562-572.	0.5	7
46	Fine Phenotyping of Pod and Seed Traits in <i>Arachis</i> Germplasm Accessions Using Digital Image Analysis. <i>Peanut Science</i> , 2015, 42, 65-73.	0.1	6
47	De novo QTL-seq Identifies Loci Linked to Blanchability in Peanut (<i>Arachis hypogaea</i>) and Refines Previously Identified QTL with Low Coverage Sequence. <i>Agronomy</i> , 2021, 11, 2201.	3.0	6
48	Development and Genetic Characterization of Peanut Advanced Backcross Lines That Incorporate Root-Knot Nematode Resistance From <i>Arachis stenosperma</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 785358.	3.6	5
49	Introgression Analysis and Morphological Characterization of an <i>Arachis hypogaea</i> – <i>A. diogenii</i> Interspecific Hybrid Derived Population. <i>Crop Science</i> , 2019, 59, 640-649.	1.8	4
50	Image-based phenotyping accelerated QTL mapping and qtl-environment interaction analysis of testa colour in peanut (<i>Arachis hypogaea</i>). <i>Plant Breeding</i> , 2021, 140, 884-895.	1.9	4
51	Identification of a major locus for flowering pattern sheds light on plant architecture diversification in cultivated peanut. <i>Theoretical and Applied Genetics</i> , 2022, 135, 1767-1777.	3.6	4
52	Registration of TifGP-3 and TifGP-4 peanut germplasm lines. <i>Journal of Plant Registrations</i> , 0, , .	0.5	3
53	Influence of Temperature on Susceptibility of CVS. Tifguard and Georgia-06G Peanut to <i>Meloidogyne arenaria</i> . <i>Journal of Nematology</i> , 2017, 50, 33-40.	0.9	3
54	Homoeologous recombination is recurrent in the nascent synthetic allotetraploid <i>Arachis ipaensis</i> – <i>Arachis correntina</i> 4x and its derivatives. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	2

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55	Morphological and reproductive characterization of nascent allotetraploids cross-compatible with cultivated peanut (<i>Arachis hypogaea</i> L.). <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 2883-2896.	1.6	2
56	Hypoallergenic Foods beyond Infant Formulas. , 0, , 285-308.		2
57	Resistance to rust (<i>Puccinia arachidis</i> Speg.) identified in nascent allotetraploids cross-compatible with cultivated peanut (<i>Arachis hypogaea</i> L.). <i>Peanut Science</i> , 0, , .	0.1	1
58	Development and applications of KASP markers distinguishing A- and B/K-genomes of <i>Arachis</i> . <i>Euphytica</i> , 2021, 217, 1.	1.2	1
59	Anatomical characteristics correlated to peg strength in <i>Arachis</i> . <i>Peanut Science</i> , 2021, 48, 97-112.	0.1	1
60	Registration of two peanut recombinant inbred lines (TifGPâ€5 and TifGPâ€6) resistant to late leaf spot disease. <i>Journal of Plant Registrations</i> , 0, , .	0.5	1