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List of Publications by Year in descending order

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43
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2,382
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236612

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1851
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptome Responses of Wild Arachis to UV-C Exposure Reveal Genes Involved in General Plant Defense and Priming. <i>Plants</i> , 2022, 11, 408.	1.6	4
2	Overexpression of DUF538 from Wild Arachis Enhances Plant Resistance to Meloidogyne spp.. <i>Agronomy</i> , 2021, 11, 559.	1.3	6
3	Defining the combined stress response in wild Arachis. <i>Scientific Reports</i> , 2021, 11, 11097.	1.6	13
4	Ectopic expression of an expansin-like B gene from wild Arachis enhances tolerance to both abiotic and biotic stresses. <i>Plant Journal</i> , 2021, 107, 1681-1696.	2.8	17
5	Characterization of raffinose metabolism genes uncovers a wild Arachis galactinol synthase conferring tolerance to abiotic stresses. <i>Scientific Reports</i> , 2020, 10, 15258.	1.6	37
6	Comparative Genomics Reveals Novel Target Genes towards Specific Control of Plant-Parasitic Nematodes. <i>Genes</i> , 2020, 11, 1347.	1.0	29
7	Presence of resveratrol in wild Arachis species adds new value to this overlooked genetic resource. <i>Scientific Reports</i> , 2020, 10, 12787.	1.6	5
8	Proteomics unravels new candidate genes for Meloidogyne resistance in wild Arachis. <i>Journal of Proteomics</i> , 2020, 217, 103690.	1.2	12
9	Evolutionarily conserved plant genes responsive to root-knot nematodes identified by comparative genomics. <i>Molecular Genetics and Genomics</i> , 2020, 295, 1063-1078.	1.0	14
10	Brazilian Kayabi Indian accessions of peanut, <i>Arachis hypogaea</i> (Fabales, Fabaceae): origin, diversity and evolution. <i>Genetics and Molecular Biology</i> , 2020, 43, e20190418.	0.6	1
11	Contrasting Effects of Wild Arachis Dehydrin Under Abiotic and Biotic Stresses. <i>Frontiers in Plant Science</i> , 2019, 10, 497.	1.7	18
12	Overexpression of Wild Arachis Lipocalin Enhances Root-Knot Nematode Resistance in Peanut Hairy Roots. <i>Plant Molecular Biology Reporter</i> , 2019, 37, 74-86.	1.0	6
13	Comparative proteomics and gene expression analysis in <i>Arachis duranensis</i> reveal stress response proteins associated to drought tolerance. <i>Journal of Proteomics</i> , 2019, 192, 299-310.	1.2	39
14	The genome structure of <i>Arachis hypogaea</i> (Linnaeus, 1753) and an induced <i>Arachis</i> allotetraploid revealed by molecular cytogenetics. <i>Comparative Cytogenetics</i> , 2018, 12, 111-140.	0.3	15
15	Segmental allopolyploidy in action: Increasing diversity through polyploid hybridization and homoeologous recombination. <i>American Journal of Botany</i> , 2018, 105, 1053-1066.	0.8	42
16	Comparative root transcriptome of wild Arachis reveals NBS-LRR genes related to nematode resistance. <i>BMC Plant Biology</i> , 2018, 18, 159.	1.6	27
17	Early responses to dehydration in contrasting wild Arachis species. <i>PLoS ONE</i> , 2018, 13, e0198191.	1.1	24
18	Genome-wide analysis of expansin superfamily in wild Arachis discloses a stress-responsive expansin-like B gene. <i>Plant Molecular Biology</i> , 2017, 94, 79-96.	2.0	43

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19	Ex vitro hairy root induction in detached peanut leaves for plant-nematode interaction studies. <i>Plant Methods</i> , 2017, 13, 25.	1.9	26
20	Phenotypic effects of allotetraploidization of wild <i>Arachis</i> and their implications for peanut domestication. <i>American Journal of Botany</i> , 2017, 104, 379-388.	0.8	34
21	Functional Genomics in Peanut Wild Relatives. <i>Compendium of Plant Genomes</i> , 2017, , 149-164.	0.3	6
22	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.	9.4	761
23	Genetic Mapping of Resistance to <i>Meloidogyne arenaria</i> in <i>Arachis stenosperma</i> : A New Source of Nematode Resistance for Peanut. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 377-390.	0.8	46
24	<i>Arachis batizocoi</i> : a study of its relationship to cultivated peanut (<i>A. hypogaea</i>) and its potential for introgression of wild genes into the peanut crop using induced allotetraploids. <i>Annals of Botany</i> , 2015, 115, 237-249.	1.4	51
25	Identification of QTLs for Rust Resistance in the Peanut Wild Species <i>Arachis magna</i> and the Development of KASP Markers for Marker-Assisted Selection. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1403-1413.	0.8	57
26	Transcriptome Profiling of Wild <i>Arachis</i> from Water-Limited Environments Uncovers Drought Tolerance Candidate Genes. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 1876-1892.	1.0	59
27	Root Transcriptome Analysis of Wild Peanut Reveals Candidate Genes for Nematode Resistance. <i>PLoS ONE</i> , 2015, 10, e0140937.	1.1	52
28	The Use of SNP Markers for Linkage Mapping in Diploid and Tetraploid Peanuts. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 89-96.	0.8	67
29	The repetitive component of the A genome of peanut (<i>Arachis hypogaea</i>) and its role in remodelling intergenic sequence space since its evolutionary divergence from the B genome. <i>Annals of Botany</i> , 2013, 112, 545-559.	1.4	30
30	A survey of genes involved in <i>Arachis stenosperma</i> resistance to <i>Meloidogyne arenaria</i> race 1. <i>Functional Plant Biology</i> , 2013, 40, 1298.	1.1	30
31	The effect of tetraploidization of wild <i>Arachis</i> on leaf morphology and other drought-related traits. <i>Environmental and Experimental Botany</i> , 2012, 84, 17-24.	2.0	52
32	Global transcriptome analysis of two wild relatives of peanut under drought and fungi infection. <i>BMC Genomics</i> , 2012, 13, 387.	1.2	83
33	Matita, a new retroelement from peanut: characterization and evolutionary context in the light of the <i>Arachis</i> B genome divergence. <i>Molecular Genetics and Genomics</i> , 2012, 287, 21-38.	1.0	43
34	Reference genes for quantitative reverse transcription-polymerase chain reaction expression studies in wild and cultivated peanut. <i>BMC Research Notes</i> , 2011, 4, 339.	0.6	63
35	A Study of Gene Expression in the Nematode Resistant Wild Peanut Relative, <i>Arachis stenosperma</i> , in Response to Challenge with <i>Meloidogyne arenaria</i> . <i>Tropical Plant Biology</i> , 2010, 3, 183-192.	1.0	30
36	Ultrastructure of the Initial Interaction of <i>Puccinia arachidis</i> and <i>Cercosporidium personatum</i> with Leaves of <i>Arachis hypogaea</i> and <i>Arachis stenosperma</i> . <i>Journal of Phytopathology</i> , 2010, 158, 792-796.	0.5	25

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37	An analysis of synteny of Arachis with Lotus and Medicago sheds new light on the structure, stability and evolution of legume genomes.. BMC Genomics, 2009, 10, 45.	1.2	125
38	A linkage map for the B-genome of Arachis (Fabaceae) and its synteny to the A-genome. BMC Plant Biology, 2009, 9, 40.	1.6	97
39	Identification of candidate genome regions controlling disease resistance in Arachis. BMC Plant Biology, 2009, 9, 112.	1.6	118
40	BAC libraries construction from the ancestral diploid genomes of the allotetraploid cultivated peanut. BMC Plant Biology, 2008, 8, 14.	1.6	28
41	ESTs from a wild Arachis species for gene discovery and marker development. BMC Plant Biology, 2007, 7, 7.	1.6	112
42	Transgenic tobacco plants expressing Tarin 1 inhibit the growth of Pseudomonas syringae pv. tomato and the development of Spodoptera frugiperda. Annals of Applied Biology, 2003, 143, 349-357.	1.3	6
43	Development of a PCR test for the detection of Curtobacterium flaccumfaciens pv. flaccumfaciens. Antonie Van Leeuwenhoek, 2001, 80, 1-10.	0.7	29