

# Mãrcio de Carvalho Moretzsohn

## List of Publications by Year in descending order

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Version: 2024-02-01

33  
papers

2,926  
citations

304602

22  
h-index

454834

30  
g-index

35  
all docs

35  
docs citations

35  
times ranked

2111  
citing authors

#	ARTICLE	IF	CITATIONS
1	Spontaneous generation of diversity in <i>Arachis neopolyploids</i> ( <i>Arachis ipaensis</i> – <i>Arachis</i> ) Tj ETQq1 1 0.784314 0.08 / Overlock 10		
2	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, .	3.3	18
3	Introgressão assistida por marcadores de genes de resistência às cercosporioses em linhagens de amendoim. <i>South American Sciences</i> , 2021, 2, e21149.	0.0	0
4	Presence of resveratrol in wild <i>Arachis</i> species adds new value to this overlooked genetic resource. <i>Scientific Reports</i> , 2020, 10, 12787.	1.6	5
5	Broadening the Variability for Peanut Breeding with a Wild Species-Derived Induced Allotetraploid. <i>Agronomy</i> , 2020, 10, 1917.	1.3	7
6	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
7	Resistência múltipla a doenças foliares e potencial agrônomico de famílias RC3F2 descendentes de <i>Arachis hypogaea</i> x ( <i>A. magnaxA.stenosperma</i> )4x. <i>South American Sciences</i> , 2020, 1, e2061.	0.0	0
8	Uso de espécies silvestres como fontes de resistências às cercosporioses no amendoim. <i>South American Sciences</i> , 2020, 1, e2025.	0.0	0
9	The genome sequence of segmental allotetraploid peanut <i>Arachis hypogaea</i> . <i>Nature Genetics</i> , 2019, 51, 877-884.	9.4	439
10	BRS 425: the first runner peanut cultivar related to wild ancestral species. <i>Crop Breeding and Applied Biotechnology</i> , 2019, 19, 373-377.	0.1	4
11	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
12	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
13	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
14	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
15	<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
16	Tetrasomic Recombination Is Surprisingly Frequent in Allotetraploid <i>Arachis</i> . <i>Genetics</i> , 2015, 199, 1093-1105.	1.2	52
17	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
18	Yield, market quality, and leaf spots partial resistance of interspecific peanut progenies. <i>Crop Breeding and Applied Biotechnology</i> , 2015, 15, 175-180.	0.1	7

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19	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
20	A study of the relationships of cultivated peanut ( <i>Arachis hypogaea</i> ) and its most closely related wild species using intron sequences and microsatellite markers. <i>Annals of Botany</i> , 2013, 111, 113-126.	1.4	166
21	Integrated Consensus Map of Cultivated Peanut and Wild Relatives Reveals Structures of the A and B Genomes of <i>Arachis</i> and Divergence of the Legume Genomes. <i>DNA Research</i> , 2013, 20, 173-184.	1.5	113
22	Global transcriptome analysis of two wild relatives of peanut under drought and fungi infection. <i>BMC Genomics</i> , 2012, 13, 387.	1.2	83
23	Fostered and left behind alleles in peanut: interspecific QTL mapping reveals footprints of domestication and useful natural variation for breeding. <i>BMC Plant Biology</i> , 2012, 12, 26.	1.6	114
24	An International Reference Consensus Genetic Map with 897 Marker Loci Based on 11 Mapping Populations for Tetraploid Groundnut ( <i>Arachis hypogaea</i> L.). <i>PLoS ONE</i> , 2012, 7, e41213.	1.1	89
25	An overview of peanut and its wild relatives. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2011, 9, 134-149.	0.4	116
26	Phylogenetic relationships in genus <i>Arachis</i> based on ITS and 5.8S rDNA sequences. <i>BMC Plant Biology</i> , 2010, 10, 255.	1.6	51
27	An analysis of synteny of <i>Arachis</i> with <i>Lotus</i> and <i>Medicago</i> sheds new light on the structure, stability and evolution of legume genomes.. <i>BMC Genomics</i> , 2009, 10, 45.	1.2	125
28	A linkage map for the B-genome of <i>Arachis</i> (Fabaceae) and its synteny to the A-genome. <i>BMC Plant Biology</i> , 2009, 9, 40.	1.6	97
29	Identification of candidate genome regions controlling disease resistance in <i>Arachis</i> . <i>BMC Plant Biology</i> , 2009, 9, 112.	1.6	118
30	Genetic relationships among <i>Arachis hypogaea</i> L. (AABB) and diploid <i>Arachis</i> species with AA and BB genomes. <i>Genetic Resources and Crop Evolution</i> , 2008, 55, 15-20.	0.8	19
31	Legume Anchor Markers Link Syntenic Regions Between <i>Phaseolus vulgaris</i> , <i>Lotus japonicus</i> , <i>Medicago truncatula</i> and <i>Arachis</i> . <i>Genetics</i> , 2008, 179, 2299-2312.	1.2	85
32	ESTs from a wild <i>Arachis</i> species for gene discovery and marker development. <i>BMC Plant Biology</i> , 2007, 7, 7.	1.6	112
33	New softwares for automated microsatellite marker development. <i>Nucleic Acids Research</i> , 2006, 34, e31-e31.	6.5	43