

Luciana Rossini Pinto

List of Publications by Year in descending order

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49
papers

1,303
citations

516215

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377514

34
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docs citations

56
times ranked

949
citing authors

#	ARTICLE	IF	CITATIONS
1	Marker-trait Association for Resistance to Sugarcane Mosaic Virus (SCMV) in a Sugarcane (<i>Saccharum</i>) Tj ETQq1 1 0,784314 rgBT /Over	0,9	14
2	Selection and validation of reference genes by RT-qPCR under photoperiodic induction of flowering in sugarcane (<i>Saccharum</i> spp.). <i>Scientific Reports</i> , 2021, 11, 4589.	1.6	7
3	Transcriptomic Analysis of Changes in Gene Expression During Flowering Induction in Sugarcane Under Controlled Photoperiodic Conditions. <i>Frontiers in Plant Science</i> , 2021, 12, 635784.	1.7	13
4	Screening of <i>Saccharum</i> spp. genotypes for sugarcane yellow leaf virus resistance by combining symptom phenotyping and highly precise virus titration. <i>Crop Protection</i> , 2021, 144, 105577.	1.0	8
5	The Wild Sugarcane and Sorghum Kinomes: Insights Into Expansion, Diversification, and Expression Patterns. <i>Frontiers in Plant Science</i> , 2021, 12, 668623.	1.7	18
6	Genome-wide approaches for the identification of markers and genes associated with sugarcane yellow leaf virus resistance. <i>Scientific Reports</i> , 2021, 11, 15730.	1.6	21
7	Effect of Sugarcane Cultivars Infected with Sugarcane Yellow Leaf Virus (ScYLV) on Feeding Behavior and Biological Performance of <i>Melanaphis sacchari</i> (Hemiptera: Aphididae). <i>Plants</i> , 2021, 10, 2122.	1.6	5
8	Machine learning approaches reveal genomic regions associated with sugarcane brown rust resistance. <i>Scientific Reports</i> , 2020, 10, 20057.	1.6	19
9	Epigenetic diversity of <i>Saccharum</i> spp. accessions assessed by methylation-sensitive amplification polymorphism (MSAP). <i>3 Biotech</i> , 2020, 10, 265.	1.1	3
10	Genetic Structure Analysis in Sugarcane (<i>Saccharum</i> spp.) Using Target Region Amplification Polymorphism (TRAP) Markers Based on Sugar- and Lignin-Related Genes and Potential Application in Core Collection Development. <i>Sugar Tech</i> , 2020, 22, 641-654.	0.9	11
11	Sugarcane mosaic virus mediated changes in cytosine methylation pattern and differentially transcribed fragments in resistance-contrasting sugarcane genotypes. <i>PLoS ONE</i> , 2020, 15, e0241493.	1.1	8
12	Gene Duplication in the Sugarcane Genome: A Case Study of Allele Interactions and Evolutionary Patterns in Two Genic Regions. <i>Frontiers in Plant Science</i> , 2019, 10, 553.	1.7	23
13	Reference genes for gene expression studies targeting sugarcane infected with Sugarcane mosaic virus (SCMV). <i>BMC Research Notes</i> , 2019, 12, 149.	0.6	8
14	Revisiting Meiosis in Sugarcane: Chromosomal Irregularities and the Prevalence of Bivalent Configurations. <i>Frontiers in Genetics</i> , 2018, 9, 213.	1.1	31
15	Unraveling the genetic structure of Brazilian commercial sugarcane cultivars through microsatellite markers. <i>PLoS ONE</i> , 2018, 13, e0195623.	1.1	30
16	New Sugarcane Microsatellites and Target Region Amplification Polymorphism Primers Designed from Candidate Genes Related to Disease Resistance. <i>Sugar Tech</i> , 2017, 19, 219-224.	0.9	3
17	Survey of the <i>Bru1</i> gene for brown rust resistance in Brazilian local and basic sugarcane germplasm. <i>Plant Breeding</i> , 2017, 136, 182-187.	1.0	10
18	DNA methylation in sugarcane somaclonal variants assessed through methylation-sensitive amplified polymorphism. <i>Genetics and Molecular Research</i> , 2017, 16, .	0.3	11

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19	Morphological analysis and DNA methylation in <i>Conyza bonariensis</i> L. cronquist (Asteraceae) phenotypes. <i>Bragantia</i> , 2017, 76, 480-491.	1.3	3
20	GENETIC VARIABILITY OF <i>Rottboellia cochinchinensis</i> POPULATIONS IN SUGARCANE FIELDS. <i>Planta Daninha</i> , 2016, 34, 475-484.	0.5	1
21	QTL mapping including codominant SNP markers with ploidy level information in a sugarcane progeny. <i>Euphytica</i> , 2016, 211, 1-16.	0.6	39
22	Efficiency of Different Antimitotics in Cytological Preparations of Sugarcane. <i>Sugar Tech</i> , 2016, 18, 222-228.	0.9	4
23	Screening Sugarcane Wild Accessions for Resistance to Sugarcane Mosaic Virus (SCMV). <i>Sugar Tech</i> , 2015, 17, 252-257.	0.9	9
24	Evaluation of Brazilian sugarcane genotypes for resistance to Sugarcane mosaic virus under greenhouse and field conditions. <i>Crop Protection</i> , 2015, 70, 15-20.	1.0	12
25	Marker-trait association and epistasis for brown rust resistance in sugarcane. <i>Euphytica</i> , 2015, 203, 533-547.	0.6	13
26	Flowering of Sugarcane Genotypes under Different Artificial Photoperiod Conditions. <i>American Journal of Plant Sciences</i> , 2015, 06, 456-463.	0.3	14
27	De Novo Assembly and Transcriptome Analysis of Contrasting Sugarcane Varieties. <i>PLoS ONE</i> , 2014, 9, e88462.	1.1	129
28	Selfing rate estimation in sugarcane under unfavorable natural conditions of crossing by using microsatellite markers. <i>Genetics and Molecular Research</i> , 2014, 13, 2278-2289.	0.3	4
29	Paternity identification in sugarcane polycrosses by using microsatellite markers. <i>Genetics and Molecular Research</i> , 2014, 13, 2268-2277.	0.3	7
30	Sugarcane Transcript Profiling Assessed by cDNA-AFLP Analysis during the Interaction with <i>Sugarcane Mosaic Virus</i>. <i>Advances in Microbiology</i> , 2014, 04, 511-520.	0.3	9
31	Phenotypic and biochemical responses of sugarcane cultivars to glyphosate application. <i>Sugar Tech</i> , 2013, 15, 127-135.	0.9	2
32	Comparison of Two Staining Methods for Pollen Viability Studies in Sugarcane. <i>Sugar Tech</i> , 2013, 15, 103-107.	0.9	13
33	SNP genotyping allows an in-depth characterisation of the genome of sugarcane and other complex autopolyploids. <i>Scientific Reports</i> , 2013, 3, 3399.	1.6	129
34	Characterization of the Genetic Variability of a Sugarcane Commercial Cross Through Yield Components and Quality Parameters. <i>Sugar Tech</i> , 2012, 14, 119-125.	0.9	15
35	A mixed model QTL analysis for sugarcane multiple-harvest-location trial data. <i>Theoretical and Applied Genetics</i> , 2012, 124, 835-849.	1.8	73
36	Functional markers for gene mapping and genetic diversity studies in sugarcane. <i>BMC Research Notes</i> , 2011, 4, 264.	0.6	51

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37	Comparison of AFLP, TRAP and SSRs in the estimation of genetic relationships in sugarcane. Sugar Tech, 2010, 12, 150-154.	0.9	24
38	Genetic variability among sugarcane genotypes based on polymorphisms in sucrose metabolism and drought tolerance genes. Euphytica, 2010, 172, 435-446.	0.6	21
39	Analysis of genomic and functional RFLP derived markers associated with sucrose content, fiber and yield QTLs in a sugarcane (Saccharum spp.) commercial cross. Euphytica, 2010, 172, 313-327.	0.6	46
40	Functional integrated genetic linkage map based on EST-markers for a sugarcane (Saccharum spp.) commercial cross. Molecular Breeding, 2007, 20, 189-208.	1.0	79
41	Characterization of novel sugarcane expressed sequence tag microsatellites and their comparison with genomic SSRs. Plant Breeding, 2006, 125, 378-384.	1.0	84
42	Development of an integrated genetic map of a sugarcane (Saccharum spp.) commercial cross, based on a maximum-likelihood approach for estimation of linkage and linkage phases. Theoretical and Applied Genetics, 2006, 112, 298-314.	1.8	101
43	Survey in the sugarcane expressed sequence tag database (SUCEST) for simple sequence repeats. Genome, 2004, 47, 795-804.	0.9	113
44	Genetic-diversity assessed by microsatellites in tropical maize populations submitted to a high-intensity reciprocal recurrent selection. Euphytica, 2003, 134, 277-286.	0.6	31
45	Reciprocal recurrent selection effects on the genetic structure of tropical maize populations assessed at microsatellite loci. Genetics and Molecular Biology, 2003, 26, 355-364.	0.6	18
46	Isoenzymatic variability in tropical maize populations under reciprocal recurrent selection. Scientia Agricola, 2003, 60, 291-297.	0.6	4
47	Influência de métodos de secagem na conservação de sementes de Ipê-branco. Revista Brasileira De Engenharia Agrícola E Ambiental, 2001, 5, 492-496.	0.4	14
48	Association Mapping for Sugarcane Quality Traits at Three Harvest Times. Sugar Tech, 0, , 1.	0.9	1
49	Taxonomically Restricted Genes Are Associated With Responses to Biotic and Abiotic Stresses in Sugarcane (Saccharum spp.). Frontiers in Plant Science, 0, 13, .	1.7	3