

# Monalisa Carneiro

## List of Publications by Year in descending order

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Version: 2024-02-01

50  
papers

1,406  
citations

430442

18  
h-index

360668

35  
g-index

57  
all docs

57  
docs citations

57  
times ranked

1215  
citing authors

#	ARTICLE	IF	CITATIONS
1	Building the sugarcane genome for biotechnology and identifying evolutionary trends. BMC Genomics, 2014, 15, 540.	1.2	136
2	SNP genotyping allows an in-depth characterisation of the genome of sugarcane and other complex autopolyploids. Scientific Reports, 2013, 3, 3399.	1.6	129
3	De Novo Assembly and Transcriptome Analysis of Contrasting Sugarcane Varieties. PLoS ONE, 2014, 9, e88462.	1.1	129
4	Assembly of the 373k gene space of the polyploid sugarcane genome reveals reservoirs of functional diversity in the world's leading biomass crop. GigaScience, 2019, 8, .	3.3	106
5	Co-expression network analysis reveals transcription factors associated to cell wall biosynthesis in sugarcane. Plant Molecular Biology, 2016, 91, 15-35.	2.0	99
6	Sugarcane improvement: how far can we go?. Current Opinion in Biotechnology, 2012, 23, 265-270.	3.3	92
7	GBS-based single dosage markers for linkage and QTL mapping allow gene mining for yield-related traits in sugarcane. BMC Genomics, 2017, 18, 72.	1.2	91
8	Effects of drought on the microtranscriptome of field-grown sugarcane plants. Planta, 2013, 237, 783-798.	1.6	59
9	A genome-wide association study identified loci for yield component traits in sugarcane ( <i>Saccharum</i> ) Tj ETQq1 1 0.784314 rgBT /Over	1.1	54
10	History and Current Status of Sugarcane Breeding, Germplasm Development and Molecular Genetics in Brazil. Sugar Tech, 2022, 24, 112-133.	0.9	48
11	The characterization of a new set of EST-derived simple sequence repeat (SSR) markers as a resource for the genetic analysis of <i>Phaseolus vulgaris</i> . BMC Genetics, 2011, 12, 41.	2.7	38
12	Genomic resources for energy cane breeding in the post genomics era. Computational and Structural Biotechnology Journal, 2019, 17, 1404-1414.	1.9	38
13	RAPD-based genetic linkage maps of yellow passion fruit ( <i>Passiflora edulis</i> Sims. f. <i>flavicarpa</i> Deg.). Genome, 2002, 45, 670-678.	0.9	35
14	Mixed Modeling of Yield Components and Brown Rust Resistance in Sugarcane Families. Agronomy Journal, 2016, 108, 1824-1837.	0.9	34
15	Linkage and mapping of resistance genes to <i>Xanthomonas axonopodis</i> pv. <i>passiflorae</i> in yellow passion fruit. Genome, 2006, 49, 17-29.	0.9	26
16	Time-series expression profiling of sugarcane leaves infected with <i>Puccinia kuehnii</i> reveals an ineffective defense system leading to susceptibility. Plant Cell Reports, 2020, 39, 873-889.	2.8	25
17	Gene Duplication in the Sugarcane Genome: A Case Study of Allele Interactions and Evolutionary Patterns in Two Genic Regions. Frontiers in Plant Science, 2019, 10, 553.	1.7	23
18	Metabolite Profiles of Sugarcane Culm Reveal the Relationship Among Metabolism and Axillary Bud Outgrowth in Genetically Related Sugarcane Commercial Cultivars. Frontiers in Plant Science, 2018, 9, 857.	1.7	21

#	ARTICLE	IF	CITATIONS
19	Breeding of Sugarcane. Handbook of Plant Breeding, 2015, , 29-42.	0.1	20
20	Alternative Splicing of Circadian Clock Genes Correlates With Temperature in Field-Grown Sugarcane. Frontiers in Plant Science, 2019, 10, 1614.	1.7	20
21	The Wild Sugarcane and Sorghum Kinomes: Insights Into Expansion, Diversification, and Expression Patterns. Frontiers in Plant Science, 2021, 12, 668623.	1.7	18
22	Rhythms of Transcription in Field-Grown Sugarcane Are Highly Organ Specific. Scientific Reports, 2020, 10, 6565.	1.6	16
23	Molecular diversity and genetic structure of Saccharum complex accessions. PLoS ONE, 2020, 15, e0233211.	1.1	16
24	Field microenvironments regulate crop diel transcript and metabolite rhythms. New Phytologist, 2021, 232, 1738-1749.	3.5	13
25	Using quantitative PCR with retrotransposon-based insertion polymorphisms as markers in sugarcane. Journal of Experimental Botany, 2015, 66, 4239-4250.	2.4	10
26	Differential expression in leaves of Saccharum genotypes contrasting in biomass production provides evidence of genes involved in carbon partitioning. BMC Genomics, 2020, 21, 673.	1.2	10
27	Genetic Variability, Correlation among Agronomic Traits, and Genetic Progress in a Sugarcane Diversity Panel. Agriculture (Switzerland), 2021, 11, 533.	1.4	9
28	Adaptabilidade e estabilidade de clones de cana-de-açúcar. Bragantia, 2013, 72, 208-216.	1.3	8
29	Validação de marcadores moleculares associados à resistência à ferrugem marrom em cana-de-açúcar. Summa Phytopathologica, 2017, 43, 36-40.	0.3	8
30	RB975952 - Early maturing sugarcane cultivar. Crop Breeding and Applied Biotechnology, 2015, 15, 193-196.	0.1	7
31	Assessment of Gene Flow to Wild Relatives and Nutritional Composition of Sugarcane in Brazil. Frontiers in Bioengineering and Biotechnology, 2020, 8, 598.	2.0	6
32	Field resistance and molecular detection of the orange rust resistance gene linked to G1 marker in Brazilian cultivars of sugarcane. Summa Phytopathologica, 2020, 46, 92-97.	0.3	6
33	Planting Season Impacts Sugarcane Stem Development, Secondary Metabolite Levels, and Natural Antisense Transcription. Cells, 2021, 10, 3451.	1.8	6
34	RB975242 and RB975201 - Late maturation sugarcane varieties. Crop Breeding and Applied Biotechnology, 2016, 16, 365-370.	0.1	5
35	Reação de cultivares de feijoeiro comum à mancha angular em casa de vegetação. Tropical Plant Pathology, 2006, 31, 306-309.	0.3	5
36	RB005014 - a sugarcane cultivar with high tillering and agroindustrial yield. Crop Breeding and Applied Biotechnology, 2019, 19, 230-234.	0.1	4

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37	Origin, Genetic Diversity, Conservation, and Traditional and Molecular Breeding Approaches in Sugarcane. , 2022, , 83-116.		4
38	Valida��o de marcadores moleculares associados � pung�ncia em pimenta. Horticultura Brasileira, 2015, 33, 189-195.	0.1	3
39	Characterization of pepper accessions using molecular markers linked to pungency and SSR. Horticultura Brasileira, 2019, 37, 152-160.	0.1	3
40	RB965902 and RB965917 Early/medium maturing sugarcane varieties. Crop Breeding and Applied Biotechnology, 2011, 11, 280-285.	0.1	2
41	Genetic map of the common bean using a breeding population derived from the Mesoamerican gene pool. Crop Breeding and Applied Biotechnology, 2010, 10, 1-8.	0.1	2
42	RB985476 - a sugarcane cultivar with high agro-industrial yield and disease resistance. Crop Breeding and Applied Biotechnology, 2020, 20, .	0.1	1
43	Temporal Gene Expression in Apical Culms Shows Early Changes in Cell Wall Biosynthesis Genes in Sugarcane. Frontiers in Plant Science, 2021, 12, 736797.	1.7	1
44	Differential Gene Expression Among Genotypes of the Genus Saccharum Contrasting in Biomass Production. Proceedings (mdpi), 2019, 36, .	0.2	0
45	M�todo r�pido para extra�o de DNA de Puccinia kuehnii. Summa Phytopathologica, 2013, 39, 198-200.	0.3	0
46	Root growth and antioxidant enzyme responses to aluminium stress in sugarcane. Semina:Ciencias Agrarias, 2020, 41, 3449-3456.	0.1	0
47	Molecular diversity and genetic structure of Saccharum complex accessions. , 2020, 15, e0233211.		0
48	Molecular diversity and genetic structure of Saccharum complex accessions. , 2020, 15, e0233211.		0
49	Molecular diversity and genetic structure of Saccharum complex accessions. , 2020, 15, e0233211.		0
50	Molecular diversity and genetic structure of Saccharum complex accessions. , 2020, 15, e0233211.		0