Agnelo Furtado

List of Publications by Year
in descending order

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100 papers	3,404 citations	136950 32 h-index	168389 53 g-index
109 all docs	109 docs citations	109 times ranked	4283 citing authors

#	Article	IF	Citations
1	Protocol: a simple method for extracting next-generation sequencing quality genomic DNA from recalcitrant plant species. Plant Methods, 2014, 10, 21.	4.3	339
2	Genomics of crop wild relatives: expanding the gene pool for crop improvement. Plant Biotechnology Journal, 2016, 14, 1070-1085.	8.3	303
3	A survey of the complex transcriptome from the highly polyploid sugarcane genome using full-length isoform sequencing and de novo assembly from short read sequencing. BMC Genomics, 2017, 18, 395.	2.8	180
4	Influence of genotype and environment on coffee quality. Trends in Food Science and Technology, 2016, 57, 20-30.	15.1	150
5	Relationships of wild and domesticated rices (Oryza AA genome species) based upon whole chloroplast genome sequences. Scientific Reports, 2015, 5, 13957.	3.3	148
6	Potential for Genetic Improvement of Sugarcane as a Source of Biomass for Biofuels. Frontiers in Bioengineering and Biotechnology, 2015, 3, 182.	4.1	109
7	Transcriptome analysis highlights key differentially expressed genes involved in cellulose and lignin biosynthesis of sugarcane genotypes varying in fiber content. Scientific Reports, 2018, 8, 11612.	3.3	91
8	Long-read sequencing of the coffee bean transcriptome reveals the diversity of full-length transcripts. GigaScience, 2017, 6, 1-13.	6.4	90
9	Wild Sorghum as a Promising Resource for Crop Improvement. Frontiers in Plant Science, 2020, 11, 1108.	3.6	87
10	Modifying plants for biofuel and biomaterial production. Plant Biotechnology Journal, 2014, 12, 1246-1258.	8.3	82
11	Effects of genotype and temperature on accumulation of plant secondary metabolites in Canadian and Australian wheat grown under controlled environments. Scientific Reports, 2017, 7, 9133.	3.3	76
12	New evidence for grain specific C4 photosynthesis in wheat. Scientific Reports, 2016, 6, 31721.	3.3	62
13	Comparison of long-read methods for sequencing and assembly of a plant genome. GigaScience, 2020, 9, .	6.4	62
14	Comparison of promoters in transgenic rice. Plant Biotechnology Journal, 2008, 6, 679-693.	8.3	61
15	Analysis of promoters in transgenic barley and wheat. Plant Biotechnology Journal, 2009, 7, 240-253.	8.3	58
16	Sequencing of bulks of segregants allows dissection of genetic control of amylose content in rice. Plant Biotechnology Journal, 2018, 16, 100-110.	8.3	52
17	Sequencing of Australian wild rice genomes reveals ancestral relationships with domesticated rice. Plant Biotechnology Journal, 2017, 15, 765-774.	8.3	51
18	Use of a draft genome of coffee (Coffea arabica) to identify <scp>SNP</scp>s associated with caffeine content. Plant Biotechnology Journal, 2018, 16, 1756-1766.	8.3	48

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19	The transcriptome of the developing grain: a resource for understanding seed development and the molecular control of the functional and nutritional properties of wheat. BMC Genomics, 2017, 18, 766.	2.8	46
20	Conservation and utilization of African Oryza genetic resources. Rice, 2013, 6, 29.	4.0	45
21	Genome and transcriptome sequencing characterises the gene space of Macadamia integrifolia (Proteaceae). BMC Genomics, 2016, 17, 937.	2.8	45
22	Chloroplast Genome of Novel Rice Germplasm Identified in Northern Australia. Tropical Plant Biology, 2014, 7, 111-120.	1.9	43
23	High-Throughput Profiling of the Fiber and Sugar Composition of Sugarcane Biomass. Bioenergy Research, 2017, 10, 400-416.	3.9	42
24	Association of variation in the sugarcane transcriptome with sugar content. BMC Genomics, 2017, 18, 909.	2.8	41
25	The wheat Em promoter drives reporter gene expression in embryo and aleurone tissue of transgenic barley and rice. Plant Biotechnology Journal, 2005, 3, 421-434.	8.3	40
26	Advances in genomics for the improvement of quality in coffee. Journal of the Science of Food and Agriculture, 2016, 96, 3300-3312.	3.5	40
27	Molecular structures and properties of starches of Australian wild rice. Carbohydrate Polymers, 2017, 172, 213-222.	10.2	39
28	Structural elements that modulate the substrate specificity of plant purple acid phosphatases: Avenues for improved phosphorus acquisition in crops. Plant Science, 2020, 294, 110445.	3.6	37
29	Analysis of the diversity and tissue specificity of sucrose synthase genes in the long read transcriptome of sugarcane. BMC Plant Biology, 2019, 19, 160.	3.6	36
30	Measurement of green fluorescent protein concentration in single cells by image analysis. Analytical Biochemistry, 2002, 310, 84-92.	2.4	35
31	Randomly Amplified DNA Fingerprinting: A Culmination of DNA Marker Technologies Based on Arbitrarily-Primed PCR Amplification. Journal of Biomedicine and Biotechnology, 2002, 2, 141-150.	3.0	34
32	Functional cereals for production in new and variable climates. Current Opinion in Plant Biology, 2016, 30, 11-18.	7.1	33
33	Diversity and evolution of rice progenitors in Australia. Ecology and Evolution, 2018, 8, 4360-4366.	1.9	32
34	Transcriptome profiling of wheat genotypes under heat stress during grain-filling. Journal of Cereal Science, 2020, 91, 102895.	3.7	32
35	DNA Extraction from Vegetative Tissue for Next-Generation Sequencing. Methods in Molecular Biology, 2014, 1099, 1-5.	0.9	32
36	Evaluation of chloroplast genome annotation tools and application to analysis of the evolution of coffee species. PLoS ONE, 2019, 14, e0216347.	2.5	31

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37	Pathways of Photosynthesis in Non-Leaf Tissues. Biology, 2020, 9, 438.	2.8	31
38	The promoter of the asi gene directs expression in the maternal tissues of the seed in transgenic barley. Plant Molecular Biology, 2003, 52, 787-800.	3.9	26
39	RNA Extraction from Developing or Mature Wheat Seeds. Methods in Molecular Biology, 2014, 1099, 23-28.	0.9	26
40	Chromosome-Scale Assembly and Annotation of the Macadamia Genome (Macadamia integrifolia) Tj ETQq0 0 0 rgBT /Overlock 1	1.8	26
41	Association of gene expression with biomass content and composition in sugarcane. PLoS ONE, 2017, 12, e0183417.	2.5	26
42	Influence of Gene Expression on Hardness in Wheat. PLoS ONE, 2016, 11, e0164746.	2.5	24
43	Next generation sequencing of total DNA from sugarcane provides no evidence for chloroplast heteroplasmy. New Negatives in Plant Science, 2015, 1-2, 33-45.	0.9	23
44	The coffee bean transcriptome explains the accumulation of the major bean components through ripening. Scientific Reports, 2018, 8, 11414.	3.3	23
45	Direct Chloroplast Sequencing: Comparison of Sequencing Platforms and Analysis Tools for Whole Chloroplast Barcoding. PLoS ONE, 2014, 9, e110387.	2.5	22
46	Wheat seed transcriptome reveals genes controlling key traits for human preference and crop adaptation. Current Opinion in Plant Biology, 2018, 45, 231-236.	7.1	22
47	Variation in bean morphology and biochemical composition measured in different genetic groups of arabica coffee (Coffea arabica L.). Tree Genetics and Genomes, 2017, 13, 1.	1.6	21
48	Pests, diseases, and aridity have shaped the genome of Corymbia citriodora. Communications Biology, 2021, 4, 537.	4.4	21
49	Deâ€‰novo chromosome level assembly of a plant genome from long read sequence data. Plant Journal, 2022, 109, 727-736.	5.7	20
50	SNP in the Coffea arabica genome associated with coffee quality. Tree Genetics and Genomes, 2018, 14, 1.	1.6	19
51	Chloroplast phylogeography of AA genome rice species. Molecular Phylogenetics and Evolution, 2018, 127, 475-487.	2.7	19
52	Efficient Eucalypt Cell Wall Deconstruction and Conversion for Sustainable Lignocellulosic Biofuels. Frontiers in Bioengineering and Biotechnology, 2015, 3, 190.	4.1	18
53	Fasciclin-like arabinogalactan protein gene expression is associated with yield of flour in the milling of wheat. Scientific Reports, 2017, 7, 12539.	3.3	18
54	Does C₄ Photosynthesis Occur in Wheat Seeds?. Plant Physiology, 2017, 174, 1992-1995.	4.8	18

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55	Two divergent chloroplast genome sequence clades captured in the domesticated rice gene pool may have significance for rice production. BMC Plant Biology, 2020, 20, 472.	3.6	18
56	Improvements in the sequencing and assembly of plant genomes. GigaByte, 0, 2021, 1-10.	0.0	15
57	Phylogenetic relationships in the Sorghum genus based on sequencing of the chloroplast and nuclear genes. Plant Genome, 2021, 14, e20123.	2.8	13
58	Commentary: New evidence for grain specific C4 photosynthesis in wheat. Frontiers in Plant Science, 2016, 7, 1537.	3.6	12
59	De novo assembly and characterizing of the culm-derived meta-transcriptome from the polyploid sugarcane genome based on coding transcripts. Heliyon, 2018, 4, e00583.	3.2	12
60	Metabolic changes in the developing sugarcane culm associated with high yield and early high sugar content. Plant Direct, 2020, 4, e00276.	1.9	12
61	DNA banks and their role in facilitating the application of genomics to plant germplasm. Plant Genetic Resources: Characterisation and Utilisation, 2006, 4, 64-70.	0.8	11
62	Evidence of inter-sectional chloroplast capture in Corymbia among sections Torellianae and Maculatae. Australian Journal of Botany, 2018, 66, 369.	0.6	11
63	Variation in sugarcane biomass composition and enzymatic saccharification of leaves, internodes and roots. Biotechnology for Biofuels, 2020, 13, 201.	6.2	11
64	Grain physical characteristic of the Australian wild rices. Plant Genetic Resources: Characterisation and Utilisation, 2017, 15, 409-420.	0.8	10
65	Differential expression in leaves of Saccharum genotypes contrasting in biomass production provides evidence of genes involved in carbon partitioning. BMC Genomics, 2020, 21, 673.	2.8	10
66	Slower development of lower canopy beans produces better coffee. Journal of Experimental Botany, 2020, 71, 4201-4214.	4.8	10
67	The jojoba genome reveals wide divergence of the sex chromosomes in a dioecious plant. Plant Journal, 2021, 108, 1283-1294.	5.7	9
68	A Comprehensive High-Quality DNA and RNA Extraction Protocol for a Range of Cultivars and Tissue Types of the Woody Crop Avocado. Plants, 2022, 11, 242.	3.5	9
69	Breeding for improved blanchability in peanut: phenotyping, genotype Ã— environment interaction and selection. Crop and Pasture Science, 2018, 69, 1237.	1.5	8
70	The Impact of cDNA Normalization on Long-Read Sequencing of a Complex Transcriptome. Frontiers in Genetics, 2019, 10, 654.	2.3	8
71	Limited allele-specific gene expression in highly polyploid sugarcane. Genome Research, 2022, 32, 297-308.	5.5	8
72	Cyanogenesis in the Sorghum Genus: From Genotype to Phenotype. Genes, 2022, 13, 140.	2.4	7

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73	The genome of the endangered Macadamia jansenii displays little diversity but represents an important genetic resource for plant breeding. Plant Direct, 2021, 5, e364.	1.9	7
74	Phylogeny and Molecular Evolution of miR820 and miR396 microRNA Families in Oryza AA Genomes. Tropical Plant Biology, 2018, 11, 1-16.	1.9	6
75	DIFFERENTIAL RESPONSE OF WHEAT GENOTYPES TO HEAT STRESS DURING GRAIN FILLING. Experimental Agriculture, 2019, 55, 818-827.	0.9	6
76	Comparison of Chapatti and Breadmaking Quality of Wheat Genotypes. Cereal Chemistry, 2017, 94, 409-416.	2.2	5
77	Relationships between Iraqi Rice Varieties at the Nuclear and Plastid Genome Levels. Plants, 2019, 8, 481.	3.5	5
78	Fragrance in Pandanus amaryllifolius Roxb. Despite the Presence of a Betaine Aldehyde Dehydrogenase 2. International Journal of Molecular Sciences, 2021, 22, 6968.	4.1	4
79	Analysis of the expression of transcription factors and other genes associated with aleurone layer development in wheat endosperm. Journal of Cereal Science, 2019, 85, 62-69.	3.7	3
80	Secondary genepool of Australian Cajanus species contains sources of resistance to Helicoverpa armigera (HÃ¼bner). Annals of Applied Biology, 2022, 180, 259-272.	2.5	3
81	Potential of Genome Editing to Capture Diversity From Australian Wild Rice Relatives. Frontiers in Genome Editing, 2022, 4, 875243.	5.2	3
82	Development of Transcriptome Analysis Methods. , 2021, , 462-471.		2
83	Transcript profiles of wild and domesticated sorghum under water-stressed conditions and the differential impact on dhurrin metabolism. Planta, 2022, 255, 51.	3.2	2
84	Comparison of the root, leaf and internode transcriptomes in sugarcane (Saccharum spp. hybrids). Current Research in Biotechnology, 2022, 4, 167-178.	3.7	2
85	Reticulate Evolution in AA-Genome Wild Rice in Australia. Frontiers in Plant Science, 2022, 13, 767635.	3.6	2
86	The Long Read Transcriptome of Rice (Oryza sativa ssp. japonica var. Nipponbare) Reveals Novel Transcripts. Rice, 2022, 15, .	4.0	2
87	Determination of Phylogenetic Relationships of the Genus Sorghum Using Nuclear and Chloroplast Genome Assembly. Proceedings (mdpi), 2019, 36, 17.	0.2	1
88	Sequence Variants Linked to Key Traits in Interspecific Crosses between African and Asian Rice. Plants, 2020, 9, 1653.	3.5	1
89	RNA Extraction From Plant Seeds. , 2021, , 451-461.		1
90	RNA-Seq to Understand Transcriptomes and Application in Improving Crop Quality. , 2021, , 472-485.		1

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91	Transcriptome changes in the developing sugarcane culm associated with high yield and early-season high sugar content. Theoretical and Applied Genetics, 2022, 135, 1619-1636.	3.6	1
92	Allele expression biases in mixed-ploid sugarcane accessions. Scientific Reports, 2022, 12, .	3.3	1
93	Cloning of DNA Fragments: Ligation Reactions in Agarose Gel. Methods in Molecular Biology, 2014, 1099, 117-121.	0.9	0
94	Relationships between Iraqi Rice Varieties at the Nuclear and Plastid Genome Levels. Proceedings (mdpi), 2019, 36, .	0.2	0
95	Analysis of Differences in Gene Expression Associated with Variation in Biomass Composition in Sugarcane. Proceedings (mdpi), 2019, 36, 164.	0.2	0
96	SNPs Linked to Key Traits in Hybrids between African and Asian Rice. Proceedings (mdpi), 2019, 36, .	0.2	0
97	Re-sequencing Resources to Improve Starch and Grain Quality in Rice. Methods in Molecular Biology, 2019, 1892, 201-240.	0.9	0
98	Wheat Grain Transcriptome. , 2021, , 501-512.		0
99	Identification of genes associated with chapatti quality using transcriptome analysis. Journal of Cereal Science, 2021, 101, 103276.	3.7	0
100	RNA Extraction for Transcriptome Analysis. , 2021, , 440-450.		0