

Agnelo Furtado

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/541219/publications.pdf>

Version: 2024-02-01

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	Secondary gene pool of Australian <i>Cajanus</i> species contains sources of resistance to <i>Helicoverpa armigera</i> (H&A4bner). <i>Annals of Applied Biology</i> , 2022, 180, 259-272.	2.5	3
2	<i>Deâ€%onovo</i> chromosome level assembly of a plant genome from long read sequence data. <i>Plant Journal</i> , 2022, 109, 727-736.	5.7	20
3	Cyanogenesis in the Sorghum Genus: From Genotype to Phenotype. <i>Genes</i> , 2022, 13, 140.	2.4	7
4	A Comprehensive High-Quality DNA and RNA Extraction Protocol for a Range of Cultivars and Tissue Types of the Woody Crop Avocado. <i>Plants</i> , 2022, 11, 242.	3.5	9
5	Transcript profiles of wild and domesticated sorghum under water-stressed conditions and the differential impact on dhurrin metabolism. <i>Planta</i> , 2022, 255, 51.	3.2	2
6	Comparison of the root, leaf and internode transcriptomes in sugarcane (<i>Saccharum</i> spp. hybrids). <i>Current Research in Biotechnology</i> , 2022, 4, 167-178.	3.7	2
7	Transcriptome changes in the developing sugarcane culm associated with high yield and early-season high sugar content. <i>Theoretical and Applied Genetics</i> , 2022, 135, 1619-1636.	3.6	1
8	Reticulate Evolution in AA-Genome Wild Rice in Australia. <i>Frontiers in Plant Science</i> , 2022, 13, 767635.	3.6	2
9	Limited allele-specific gene expression in highly polyploid sugarcane. <i>Genome Research</i> , 2022, 32, 297-308.	5.5	8
10	Potential of Genome Editing to Capture Diversity From Australian Wild Rice Relatives. <i>Frontiers in Genome Editing</i> , 2022, 4, 875243.	5.2	3
11	Allele expression biases in mixed-ploid sugarcane accessions. <i>Scientific Reports</i> , 2022, 12, .	3.3	1
12	The Long Read Transcriptome of Rice (<i>Oryza sativa</i> ssp. japonica var. Nipponbare) Reveals Novel Transcripts. <i>Rice</i> , 2022, 15, .	4.0	2
13	RNA Extraction From Plant Seeds. , 2021, , 451-461.		1
14	Development of Transcriptome Analysis Methods. , 2021, , 462-471.		2
15	RNA-Seq to Understand Transcriptomes and Application in Improving Crop Quality. , 2021, , 472-485.		1
16	Wheat Grain Transcriptome. , 2021, , 501-512.		0
17	Pests, diseases, and aridity have shaped the genome of <i>Corymbia citriodora</i> . <i>Communications Biology</i> , 2021, 4, 537.	4.4	21
18	Fragrance in <i>Pandanus amaryllifolius</i> Roxb. Despite the Presence of a Betaine Aldehyde Dehydrogenase 2. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6968.	4.1	4

#	ARTICLE	IF	CITATIONS
19	Phylogenetic relationships in the <i>Sorghum</i> genus based on sequencing of the chloroplast and nuclear genes. <i>Plant Genome</i> , 2021, 14, e20123.	2.8	13
20	Identification of genes associated with chapatti quality using transcriptome analysis. <i>Journal of Cereal Science</i> , 2021, 101, 103276.	3.7	0
21	The jojoba genome reveals wide divergence of the sex chromosomes in a dioecious plant. <i>Plant Journal</i> , 2021, 108, 1283-1294.	5.7	9
22	RNA Extraction for Transcriptome Analysis. , 2021, , 440-450.		0
23	The genome of the endangered <i>Macadamia janseni</i> displays little diversity but represents an important genetic resource for plant breeding. <i>Plant Direct</i> , 2021, 5, e364.	1.9	7
24	Transcriptome profiling of wheat genotypes under heat stress during grain-filling. <i>Journal of Cereal Science</i> , 2020, 91, 102895.	3.7	32
25	Differential expression in leaves of <i>Saccharum</i> genotypes contrasting in biomass production provides evidence of genes involved in carbon partitioning. <i>BMC Genomics</i> , 2020, 21, 673.	2.8	10
26	Wild Sorghum as a Promising Resource for Crop Improvement. <i>Frontiers in Plant Science</i> , 2020, 11, 1108.	3.6	87
27	Chromosome-Scale Assembly and Annotation of the Macadamia Genome (<i>Macadamia integrifolia</i>) Tj ETQq1_1.0.784314 rgBT / 1.8 26		
28	Metabolic changes in the developing sugarcane culm associated with high yield and early high sugar content. <i>Plant Direct</i> , 2020, 4, e00276.	1.9	12
29	Two divergent chloroplast genome sequence clades captured in the domesticated rice gene pool may have significance for rice production. <i>BMC Plant Biology</i> , 2020, 20, 472.	3.6	18
30	Variation in sugarcane biomass composition and enzymatic saccharification of leaves, internodes and roots. <i>Biotechnology for Biofuels</i> , 2020, 13, 201.	6.2	11
31	Sequence Variants Linked to Key Traits in Interspecific Crosses between African and Asian Rice. <i>Plants</i> , 2020, 9, 1653.	3.5	1
32	Pathways of Photosynthesis in Non-Leaf Tissues. <i>Biology</i> , 2020, 9, 438.	2.8	31
33	Slower development of lower canopy beans produces better coffee. <i>Journal of Experimental Botany</i> , 2020, 71, 4201-4214.	4.8	10
34	Structural elements that modulate the substrate specificity of plant purple acid phosphatases: Avenues for improved phosphorus acquisition in crops. <i>Plant Science</i> , 2020, 294, 110445.	3.6	37
35	Comparison of long-read methods for sequencing and assembly of a plant genome. <i>GigaScience</i> , 2020, 9, .	6.4	62
36	The Impact of cDNA Normalization on Long-Read Sequencing of a Complex Transcriptome. <i>Frontiers in Genetics</i> , 2019, 10, 654.	2.3	8

#	ARTICLE	IF	CITATIONS
37	Evaluation of chloroplast genome annotation tools and application to analysis of the evolution of coffee species. PLoS ONE, 2019, 14, e0216347.	2.5	31
38	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
39	Relationships between Iraqi Rice Varieties at the Nuclear and Plastid Genome Levels. Proceedings (mdpi), 2019, 36, .	0.2	0
40	Analysis of Differences in Gene Expression Associated with Variation in Biomass Composition in Sugarcane. Proceedings (mdpi), 2019, 36, 164.	0.2	0
41	SNPs Linked to Key Traits in Hybrids between African and Asian Rice. Proceedings (mdpi), 2019, 36, .	0.2	0
42	Relationships between Iraqi Rice Varieties at the Nuclear and Plastid Genome Levels. Plants, 2019, 8, 481.	3.5	5
43	Determination of Phylogenetic Relationships of the Genus Sorghum Using Nuclear and Chloroplast Genome Assembly. Proceedings (mdpi), 2019, 36, 17.	0.2	1
44	DIFFERENTIAL RESPONSE OF WHEAT GENOTYPES TO HEAT STRESS DURING GRAIN FILLING. Experimental Agriculture, 2019, 55, 818-827.	0.9	6
45	Re-sequencing Resources to Improve Starch and Grain Quality in Rice. Methods in Molecular Biology, 2019, 1892, 201-240.	0.9	0
46	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
47	Use of a draft genome of coffee (<i>Coffea arabica</i>) to identify SNPs associated with caffeine content. Plant Biotechnology Journal, 2018, 16, 1756-1766.	8.3	48
48	Phylogeny and Molecular Evolution of miR820 and miR396 microRNA Families in Oryza AA Genomes. Tropical Plant Biology, 2018, 11, 1-16.	1.9	6
49	Diversity and evolution of rice progenitors in Australia. Ecology and Evolution, 2018, 8, 4360-4366.	1.9	32
50	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
51	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
52	Breeding for improved blanchability in peanut: phenotyping, genotype × environment interaction and selection. Crop and Pasture Science, 2018, 69, 1237.	1.5	8
53	Evidence of inter-sectional chloroplast capture in <i>Corymbia</i> among sections <i>Torellianae</i> and <i>Maculatae</i> . Australian Journal of Botany, 2018, 66, 369.	0.6	11
54	SNP in the <i>Coffea arabica</i> genome associated with coffee quality. Tree Genetics and Genomes, 2018, 14, 1.	1.6	19

#	ARTICLE	IF	CITATIONS
55	Wheat seed transcriptome reveals genes controlling key traits for human preference and crop adaptation. <i>Current Opinion in Plant Biology</i> , 2018, 45, 231-236.	7.1	22
56	Chloroplast phylogeography of AA genome rice species. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 475-487.	2.7	19
57	Transcriptome analysis highlights key differentially expressed genes involved in cellulose and lignin biosynthesis of sugarcane genotypes varying in fiber content. <i>Scientific Reports</i> , 2018, 8, 11612.	3.3	91
58	The coffee bean transcriptome explains the accumulation of the major bean components through ripening. <i>Scientific Reports</i> , 2018, 8, 11414.	3.3	23
59	Variation in bean morphology and biochemical composition measured in different genetic groups of arabica coffee (<i>Coffea arabica</i> L.). <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	1.6	21
60	Grain physical characteristic of the Australian wild rices. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2017, 15, 409-420.	0.8	10
61	Comparison of Chapatti and Breadmaking Quality of Wheat Genotypes. <i>Cereal Chemistry</i> , 2017, 94, 409-416.	2.2	5
62	High-Throughput Profiling of the Fiber and Sugar Composition of Sugarcane Biomass. <i>Bioenergy Research</i> , 2017, 10, 400-416.	3.9	42
63	Molecular structures and properties of starches of Australian wild rice. <i>Carbohydrate Polymers</i> , 2017, 172, 213-222.	10.2	39
64	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. <i>BMC Genomics</i> , 2017, 18, 395.	2.8	180
65	Fasciclin-like arabinogalactan protein gene expression is associated with yield of flour in the milling of wheat. <i>Scientific Reports</i> , 2017, 7, 12539.	3.3	18
66	Effects of genotype and temperature on accumulation of plant secondary metabolites in Canadian and Australian wheat grown under controlled environments. <i>Scientific Reports</i> , 2017, 7, 9133.	3.3	76
67	Long-read sequencing of the coffee bean transcriptome reveals the diversity of full-length transcripts. <i>GigaScience</i> , 2017, 6, 1-13.	6.4	90
68	Does C ₄ Photosynthesis Occur in Wheat Seeds?. <i>Plant Physiology</i> , 2017, 174, 1992-1995.	4.8	18
69	Sequencing of Australian wild rice genomes reveals ancestral relationships with domesticated rice. <i>Plant Biotechnology Journal</i> , 2017, 15, 765-774.	8.3	51
70	The transcriptome of the developing grain: a resource for understanding seed development and the molecular control of the functional and nutritional properties of wheat. <i>BMC Genomics</i> , 2017, 18, 766.	2.8	46
71	Association of variation in the sugarcane transcriptome with sugar content. <i>BMC Genomics</i> , 2017, 18, 909.	2.8	41
72	Association of gene expression with biomass content and composition in sugarcane. <i>PLoS ONE</i> , 2017, 12, e0183417.	2.5	26

#	ARTICLE	IF	CITATIONS
73	Commentary: New evidence for grain specific C4 photosynthesis in wheat. <i>Frontiers in Plant Science</i> , 2016, 7, 1537.	3.6	12
74	Advances in genomics for the improvement of quality in coffee. <i>Journal of the Science of Food and Agriculture</i> , 2016, 96, 3300-3312.	3.5	40
75	Influence of genotype and environment on coffee quality. <i>Trends in Food Science and Technology</i> , 2016, 57, 20-30.	15.1	150
76	New evidence for grain specific C4 photosynthesis in wheat. <i>Scientific Reports</i> , 2016, 6, 31721.	3.3	62
77	Genome and transcriptome sequencing characterises the gene space of <i>Macadamia integrifolia</i> (Proteaceae). <i>BMC Genomics</i> , 2016, 17, 937.	2.8	45
78	Functional cereals for production in new and variable climates. <i>Current Opinion in Plant Biology</i> , 2016, 30, 11-18.	7.1	33
79	Genomics of crop wild relatives: expanding the gene pool for crop improvement. <i>Plant Biotechnology Journal</i> , 2016, 14, 1070-1085.	8.3	303
80	Influence of Gene Expression on Hardness in Wheat. <i>PLoS ONE</i> , 2016, 11, e0164746.	2.5	24
81	Next generation sequencing of total DNA from sugarcane provides no evidence for chloroplast heteroplasmy. <i>New Negatives in Plant Science</i> , 2015, 1-2, 33-45.	0.9	23
82	Relationships of wild and domesticated rices (<i>Oryza</i> AA genome species) based upon whole chloroplast genome sequences. <i>Scientific Reports</i> , 2015, 5, 13957.	3.3	148
83	Potential for Genetic Improvement of Sugarcane as a Source of Biomass for Biofuels. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 182.	4.1	109
84	Efficient Eucalypt Cell Wall Deconstruction and Conversion for Sustainable Lignocellulosic Biofuels. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 190.	4.1	18
85	Direct Chloroplast Sequencing: Comparison of Sequencing Platforms and Analysis Tools for Whole Chloroplast Barcoding. <i>PLoS ONE</i> , 2014, 9, e110387.	2.5	22
86	Chloroplast Genome of Novel Rice Germplasm Identified in Northern Australia. <i>Tropical Plant Biology</i> , 2014, 7, 111-120.	1.9	43
87	Modifying plants for biofuel and biomaterial production. <i>Plant Biotechnology Journal</i> , 2014, 12, 1246-1258.	8.3	82
88	RNA Extraction from Developing or Mature Wheat Seeds. <i>Methods in Molecular Biology</i> , 2014, 1099, 23-28.	0.9	26
89	Cloning of DNA Fragments: Ligation Reactions in Agarose Gel. <i>Methods in Molecular Biology</i> , 2014, 1099, 117-121.	0.9	0
90	Protocol: a simple method for extracting next-generation sequencing quality genomic DNA from recalcitrant plant species. <i>Plant Methods</i> , 2014, 10, 21.	4.3	339

#	ARTICLE	IF	CITATIONS
91	DNA Extraction from Vegetative Tissue for Next-Generation Sequencing. <i>Methods in Molecular Biology</i> , 2014, 1099, 1-5.	0.9	32
92	Conservation and utilization of African <i>Oryza</i> genetic resources. <i>Rice</i> , 2013, 6, 29.	4.0	45
93	Analysis of promoters in transgenic barley and wheat. <i>Plant Biotechnology Journal</i> , 2009, 7, 240-253.	8.3	58
94	Comparison of promoters in transgenic rice. <i>Plant Biotechnology Journal</i> , 2008, 6, 679-693.	8.3	61
95	DNA banks and their role in facilitating the application of genomics to plant germplasm. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2006, 4, 64-70.	0.8	11
96	The wheat Em promoter drives reporter gene expression in embryo and aleurone tissue of transgenic barley and rice. <i>Plant Biotechnology Journal</i> , 2005, 3, 421-434.	8.3	40
97	The promoter of the <i>asi</i> gene directs expression in the maternal tissues of the seed in transgenic barley. <i>Plant Molecular Biology</i> , 2003, 52, 787-800.	3.9	26
98	Randomly Amplified DNA Fingerprinting: A Culmination of DNA Marker Technologies Based on Arbitrarily-Primed PCR Amplification. <i>Journal of Biomedicine and Biotechnology</i> , 2002, 2, 141-150.	3.0	34
99	Measurement of green fluorescent protein concentration in single cells by image analysis. <i>Analytical Biochemistry</i> , 2002, 310, 84-92.	2.4	35
100	Improvements in the sequencing and assembly of plant genomes. <i>GigaByte</i> , 0, 2021, 1-10.	0.0	15