

Douglas S Domingues

List of Publications by Year in descending order

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Version: 2024-02-01

60
papers

1,856
citations

331670

21
h-index

289244

40
g-index

65
all docs

65
docs citations

65
times ranked

2503
citing authors

#	ARTICLE	IF	CITATIONS
1	RNA-Seq differential expression analysis: An extended review and a software tool. <i>PLoS ONE</i> , 2017, 12, e0190152.	2.5	451
2	Physiological Responses to Drought, Salinity, and Heat Stress in Plants: A Review. <i>Stresses</i> , 2022, 2, 113-135.	4.8	149
3	The accumulation of endogenous proline induces changes in gene expression of several antioxidant enzymes in leaves of transgenic Swingle citrumelo. <i>Molecular Biology Reports</i> , 2013, 40, 3269-3279.	2.3	134
4	Nitric Oxide Mediates the Hormonal Control of Crassulacean Acid Metabolism Expression in Young Pineapple Plants. <i>Plant Physiology</i> , 2010, 152, 1971-1985.	4.8	80
5	The Biotechnology Roadmap for Sugarcane Improvement. <i>Tropical Plant Biology</i> , 2010, 3, 75-87.	1.9	62
6	Analysis of plant LTR-retrotransposons at the fine-scale family level reveals individual molecular patterns. <i>BMC Genomics</i> , 2012, 13, 137.	2.8	57
7	Genome-wide association study reveals candidate genes influencing lipids and diterpenes contents in <i>Coffea arabica</i> L. <i>Scientific Reports</i> , 2018, 8, 465.	3.3	53
8	Pattern recognition analysis on long noncoding RNAs: a tool for prediction in plants. <i>Briefings in Bioinformatics</i> , 2019, 20, 682-689.	6.5	53
9	Stress-induced γ -1-pyrroline-5-carboxylate synthetase (P5CS) gene confers tolerance to salt stress in transgenic sugarcane. <i>Acta Physiologiae Plantarum</i> , 2014, 36, 2309-2319.	2.1	52
10	Nitrogen Starvation, Salt and Heat Stress in Coffee (<i>Coffea arabica</i> L.): Identification and Validation of New Genes for qPCR Normalization. <i>Molecular Biotechnology</i> , 2013, 53, 315-325.	2.4	42
11	Galactinol synthase transcriptional profile in two genotypes of <i>Coffea canephora</i> with contrasting tolerance to drought. <i>Genetics and Molecular Biology</i> , 2015, 38, 182-190.	1.3	40
12	Transcriptome Analysis of Leaves, Flowers and Fruits Perisperm of <i>Coffea arabica</i> L. Reveals the Differential Expression of Genes Involved in Raffinose Biosynthesis. <i>PLoS ONE</i> , 2017, 12, e0169595.	2.5	35
13	A novel linkage map of sugarcane with evidence for clustering of retrotransposon-based markers. <i>BMC Genetics</i> , 2012, 13, 51.	2.7	34
14	NCED expression is related to increased ABA biosynthesis and stomatal closure under aluminum stress. <i>Environmental and Experimental Botany</i> , 2021, 185, 104404.	4.2	33
15	Homeologous genes involved in mannitol synthesis reveal unequal contributions in response to abiotic stress in <i>Coffea arabica</i> . <i>Molecular Genetics and Genomics</i> , 2014, 289, 951-963.	2.1	30
16	The Terrestrial Carnivorous Plant <i>Utricularia reniformis</i> Sheds Light on Environmental and Life-Form Genome Plasticity. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3.	4.1	30
17	MathFeature: feature extraction package for DNA, RNA and protein sequences based on mathematical descriptors. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	30
18	PlanTE-MIR DB: a database for transposable element-related microRNAs in plant genomes. <i>Functional and Integrative Genomics</i> , 2016, 16, 235-242.	3.5	29

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19	Transcriptionally active LTR retrotransposons in Eucalyptus genus are differentially expressed and insertionally polymorphic. <i>BMC Plant Biology</i> , 2015, 15, 198.	3.6	28
20	An integrated analysis of mRNA and sRNA transcriptional profiles in <i>Coffea arabica</i> L. roots: insights on nitrogen starvation responses. <i>Functional and Integrative Genomics</i> , 2019, 19, 151-169.	3.5	28
21	Transcriptome analysis in <i>Coffea eugenioides</i> , an Arabica coffee ancestor, reveals differentially expressed genes in leaves and fruits. <i>Molecular Genetics and Genomics</i> , 2016, 291, 323-336.	2.1	26
22	Thermoperiod affects the diurnal cycle of nitrate reductase expression and activity in pineapple plants by modulating the endogenous levels of cytokinins. <i>Physiologia Plantarum</i> , 2009, 137, 201-212.	5.2	23
23	Terminal-Repeat Retrotransposons with GAG Domain in Plant Genomes: A New Testimony on the Complex World of Transposable Elements. <i>Genome Biology and Evolution</i> , 2015, 7, 493-504.	2.5	23
24	TERL: classification of transposable elements by convolutional neural networks. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	22
25	Feature extraction approaches for biological sequences: a comparative study of mathematical features. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	22
26	Inpactor, Integrated and Parallel Analyzer and Classifier of LTR Retrotransposons and Its Application for Pineapple LTR Retrotransposons Diversity and Dynamics. <i>Biology</i> , 2018, 7, 32.	2.8	21
27	Diterpenes biochemical profile and transcriptional analysis of cytochrome P450s genes in leaves, roots, flowers, and during <i>Coffea arabica</i> L. fruit development. <i>Plant Physiology and Biochemistry</i> , 2017, 111, 340-347.	5.8	19
28	PlaNC-TE: a comprehensive knowledgebase of non-coding RNAs and transposable elements in plants. Database: the Journal of Biological Databases and Curation, 2018, 2018, 1-7.	3.0	19
29	Low root PIP1-1 and PIP2 aquaporins expression could be related to reduced hydration in "Rangpur"™ lime plants exposed to aluminium. <i>Functional Plant Biology</i> , 2020, 47, 112.	2.1	18
30	ceRNAs in plants: computational approaches and associated challenges for target mimic research. <i>Briefings in Bioinformatics</i> , 2017, 19, 1273-1289.	6.5	16
31	mirtronDB: a mirtron knowledge base. <i>Bioinformatics</i> , 2019, 35, 3873-3874.	4.1	16
32	Population structure and genetic relationships between Ethiopian and Brazilian <i>Coffea arabica</i> genotypes revealed by SSR markers. <i>Genetica</i> , 2019, 147, 205-216.	1.1	14
33	Functional annotation and distribution overview of RNA families in 27 <i>Streptococcus agalactiae</i> genomes. <i>BMC Genomics</i> , 2018, 19, 556.	2.8	11
34	Decarboxylation mechanisms of C4 photosynthesis in <i>Saccharum</i> spp.: increased PEPC activity under water-limiting conditions. <i>BMC Plant Biology</i> , 2019, 19, 144.	3.6	11
35	Boron transport in Eucalyptus. 2. Identification in silico of a putative boron transporter for xylem loading in eucalypt. <i>Genetics and Molecular Biology</i> , 2005, 28, 625-629.	1.3	11
36	An Atlas of Plant Transposable Elements. <i>F1000Research</i> , 2021, 10, 1194.	1.6	11

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37	Genome-wide identification, classification and transcriptional analysis of nitrate and ammonium transporters in <i>Coffea</i> . <i>Genetics and Molecular Biology</i> , 2017, 40, 346-359.	1.3	10
38	Hexanoic acid: a new potential substitute for copper-based agrochemicals against citrus canker. <i>Journal of Applied Microbiology</i> , 2021, 131, 2488-2499.	3.1	10
39	Differentially Accumulated Proteins in <i>Coffea arabica</i> Seeds during Perisperm Tissue Development and Their Relationship to Coffee Grain Size. <i>Journal of Agricultural and Food Chemistry</i> , 2016, 64, 1635-1647.	5.2	9
40	A Novel Decomposing Model With Evolutionary Algorithms for Feature Selection in Long Non-Coding RNAs. <i>IEEE Access</i> , 2020, 8, 181683-181697.	4.2	9
41	Gene expression and enzymatic activity of pectin methylesterase during fruit development and ripening in <i>Coffea arabica</i> L.. <i>Genetics and Molecular Research</i> , 2012, 11, 3186-3197.	0.2	9
42	Construction and characterization of a BAC library from the <i>Coffea arabica</i> genotype Timor Hybrid CFC 832/2. <i>Genetica</i> , 2013, 141, 217-226.	1.1	8
43	Genome-wide analysis of EgEVE_1, a transcriptionally active endogenous viral element associated to small RNAs in <i>Eucalyptus</i> genomes. <i>Genetics and Molecular Biology</i> , 2017, 40, 217-225.	1.3	8
44	Transcriptional patterns of <i>Coffea arabica</i> L. nitrate reductase, glutamine and asparagine synthetase genes are modulated under nitrogen suppression and coffee leaf rust. <i>PeerJ</i> , 2020, 8, e8320.	2.0	8
45	Mutator System Derivatives Isolated from Sugarcane Genome Sequence. <i>Tropical Plant Biology</i> , 2012, 5, 233-243.	1.9	7
46	Distribution of Divo in <i>Coffea</i> genomes, a poorly described family of angiosperm LTR-Retrotransposons. <i>Molecular Genetics and Genomics</i> , 2017, 292, 741-754.	2.1	7
47	Low-Copy Genes in Terpenoid Metabolism: The Evolution and Expression of MVK and DXR Genes in Angiosperms. <i>Plants</i> , 2020, 9, 525.	3.5	6
48	Genome-Wide Screening and Characterization of Non-Coding RNAs in <i>Coffea canephora</i> . <i>Non-coding RNA</i> , 2020, 6, 39.	2.6	5
49	Identification of the transcriptionally active cytochrome P450 repertoire in <i>Coffea arabica</i> . <i>Genetics and Molecular Research</i> , 2015, 14, 2399-2412.	0.2	4
50	Elevated [CO ₂] Mitigates Drought Effects and Increases Leaf 5-O-Caffeoylquinic Acid and Caffeine Concentrations During the Early Growth of <i>Coffea Arabica</i> Plants. <i>Frontiers in Sustainable Food Systems</i> , 2021, 5, .	3.9	4
51	The urea transporter DUR3 is differentially regulated by abiotic and biotic stresses in coffee plants. <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 203-212.	3.1	3
52	Identificação de marcador RAPD e SCAR relacionados ao caractere florescimento precoce em <i>Eucalyptus grandis</i> . <i>Ciencia Florestal</i> , 2010, 16, 251-260.	0.3	3
53	Identification of potential transcriptionally active Copia LTR retrotransposons in <i>Eucalyptus</i> . <i>BMC Proceedings</i> , 2011, 5, .	1.6	1
54	Computational Analysis of and CircRNAs in. <i>Methods in Molecular Biology</i> , 2021, 2362, 147-172.	0.9	1

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55	Identificação e Caracterização de Microsatélites de Coffea arabica a partir de dados de sequenciamento de RNA e de BACs. BBR - Biochemistry and Biotechnology Reports, 2013, 2, 186.	0.0	1
56	Transcriptome Analyses of Leaves Reveal That Hexanoic Acid Priming Differentially Regulate Gene Expression in Contrasting Coffea arabica Cultivars. Frontiers in Sustainable Food Systems, 2021, 5, .	3.9	1
57	How candidate genes respond to aluminum toxicity in Citrus x limonia Osbeck?. Theoretical and Experimental Plant Physiology, 0, , .	2.4	1
58	Structure analyses and expression pattern of the ERF transcription factor family in Coffea arabica. Journal of Botanical Research, 2021, 3, .	0.2	0
59	CoffeebEST: an integrated resource for Coffea spp expressed sequence tags. Genetics and Molecular Research, 2014, 13, 10913-10920.	0.2	0
60	mirtronDB: a mirtron knowledge base. , 0, , .		0