RogÃ©rio Margis

List of Publications by Year
in descending order

163 papers	7,293 citations	66343 42 h-index	66911 78 g-index
165 all docs	165 docs citations	165 times ranked	9893 citing authors

#	Article	IF	Citations
1	Circular RNAs are miRNA sponges and can be used as a new class of biomarker. Journal of Biotechnology, 2016, 238, 42-51.	3.8	645
2	Glutathione peroxidase family â€“ an evolutionary overview. FEBS Journal, 2008, 275, 3959-3970.	4.7	400
3	Identification of novel soybean microRNAs involved in abiotic and biotic stresses. BMC Genomics, 2011, 12, 307.	2.8	313
4	The evolution and diversification of Dicers in plants. FEBS Letters, 2006, 580, 2442-2450.	2.8	283
5	Identification of blood microRNAs associated to ParkinsoÅ„s disease. Journal of Biotechnology, 2011, 152, 96-101.	3.8	244
6	Rice ascorbate peroxidase gene family encodes functionally diverse isoforms localized in different subcellular compartments. Planta, 2006, 224, 300-314.	3.2	199
7	Structural and Phylogenetic Relationships among Plant and Animal Cystatins. Archives of Biochemistry and Biophysics, 1998, 359, 24-30.	3.0	176
8	Evolutionary view of acyl-CoA diacylglycerol acyltransferase (DGAT), a key enzyme in neutral lipid biosynthesis. BMC Evolutionary Biology, 2011, 11, 263.	3.2	174
9	Analysis of the Molecular Evolutionary History of the Ascorbate Peroxidase Gene Family: Inferences from the Rice Genome. Journal of Molecular Evolution, 2004, 59, 761-770.	1.8	158
10	Posttranscriptional Gene Silencing Is Not Compromised in the Arabidopsis CARPEL FACTORY (DICER-LIKE1) Mutant, a Homolog of Dicer-1 from Drosophila. Current Biology, 2003, 13, 236-240.	3.9	142
11	The use of microRNAs as reference genes for quantitative polymerase chain reaction in soybean. Analytical Biochemistry, 2010, 406, 185-192.	2.4	138
12	Description of plant tRNA-derived RNA fragments (tRFs) associated with argonaute and identification of their putative targets. Biology Direct, 2013, 8, 6.	4.6	121
13	New Insights into Aluminum Tolerance in Rice: The ASR5 Protein Binds the STAR1 Promoter and Other Aluminum-Responsive Genes. Molecular Plant, 2014, 7, 709-721.	8.3	117
14	Cytosolic APx knockdown indicates an ambiguous redox responses in rice. Phytochemistry, 2010, 71, 548-558.	2.9	115
15	The mitochondrial glutathione peroxidase GPX3 is essential for H2O2 homeostasis and root and shoot development in rice. Plant Science, 2013, 208, 93-101.	3.6	110
16	Complete nucleotide sequence and genetic organization of grapevine fanleaf nepovirus RNA1. Journal of General Virology, 1991, 72, 2357-2365.	2.9	108
17	MicroRNAs play critical roles during plant development and in response to abiotic stresses. Genetics and Molecular Biology, 2012, 35, 1069-1077.	1.3	108
18	Optimal sampling strategy for estimation of spatial genetic structure in tree populations. Heredity, 2005, 95, 281-289.	2.6	100

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19	SIRT1 Transcription Is Decreased in Visceral Adipose Tissue of Morbidly Obese Patients with Severe Hepatic Steatosis. Obesity Surgery, 2010, 20, 633-639.	2.1	91
20	Involvement of ASR genes in aluminium tolerance mechanisms in rice. Plant, Cell and Environment, 2013, 36, 52-67.	5.7	86
21	Aluminum triggers broad changes in microRNA expression in rice roots. Genetics and Molecular Research, 2011, 10, 2817-2832.	0.2	85
22	Resveratrol Upregulated SIRT1, FOXO1, and Adiponectin and Downregulated PPARÎ³1â€“3 mRNA Expression in Human Visceral Adipocytes. Obesity Surgery, 2011, 21, 356-361.	2.1	84
23	Biosynthesis of Triacylglycerols (TAGs) in Plants and algae. International Journal of Plant Biology, 2011, 2, e10.	2.6	81
24	The knockdown of chloroplastic ascorbate peroxidases reveals its regulatory role in the photosynthesis and protection under photo-oxidative stress in rice. Plant Science, 2014, 214, 74-87.	3.6	81
25	Rice ASR1 and ASR5 are complementary transcription factors regulating aluminium responsive genes. Plant, Cell and Environment, 2016, 39, 645-651.	5.7	75
26	Survey of glycine-rich proteins (GRPs) in the Eucalyptus expressed sequence tag database (ForEST). Genetics and Molecular Biology, 2005, 28, 608-624.	1.3	70
27	Reference Genes for the Normalization of Gene Expression in Eucalyptus Species. Plant and Cell Physiology, 2012, 53, 405-422.	3.1	69
28	The evolution of pyrroline-5-carboxylate synthase in plants: a key enzyme in proline synthesis. Molecular Genetics and Genomics, 2009, 281, 87-97.	2.1	68
29	Identifying Conserved and Novel MicroRNAs in Developing Seeds of Brassica napus Using Deep Sequencing. PLoS ONE, 2012, 7, e50663.	2.5	61
30	The Wall-associated Kinase gene family in rice genomes. Plant Science, 2014, 229, 181-192.	3.6	59
31	Ascorbate peroxidaseâ€related (APxâ€R) is a new hemeâ€containing protein functionally associated with ascorbate peroxidase but evolutionarily divergent. New Phytologist, 2011, 191, 234-250.	7.3	57
32	AtGRP5, a vacuole-located glycine-rich protein involved in cell elongation. Planta, 2009, 230, 253-265.	3.2	56
33	NPK macronutrients and microRNA homeostasis. Frontiers in Plant Science, 2015, 6, 451.	3.6	55
34	Cold tolerance in rice germinating seeds revealed by deep RNAseq analysis of contrasting indica genotypes. Plant Science, 2015, 238, 1-12.	3.6	54
35	Genome organization of grapevine fanleaf nepovirus RNA2 deduced from the 122K polyprotein P2 in vitro cleavage products. Journal of General Virology, 1993, 74, 1919-1926.	2.9	53
36	Molecular evolution of the lysophosphatidic acid acyltransferase (LPAAT) gene family. Molecular Phylogenetics and Evolution, 2016, 96, 55-69.	2.7	51

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37	Effects of site-directed mutagenesis on the presumed catalytic triad and substrate-binding pocket of grapevine fanleaf nepovirus 24-kDa proteinase. Virology, 1992, 190, 884-888.	2.4	49
38	Genome-wide analysis of the Glycerol-3-Phosphate Acyltransferase (GPAT) gene family reveals the evolution and diversification of plant GPATs. Genetics and Molecular Biology, 2018, 41, 355-370.	1.3	48
39	Identification and expression analysis of castor bean (Ricinus communis) genes encoding enzymes from the triacylglycerol biosynthesis pathway. Plant Science, 2010, 179, 499-509.	3.6	47
40	Even population differentiation for maternal and biparental gene markers in Eugenia uniflora, a widely distributed species from the Brazilian coastal Atlantic rain forest. Diversity and Distributions, 2004, 10, 201-210.	4.1	46
41	isomiRID: a framework to identify microRNA isoforms. Bioinformatics, 2013, 29, 2521-2523.	4.1	45
42	Expression of an osmotin-like protein from Solanum nigrumconfers drought tolerance in transgenic soybean. BMC Plant Biology, 2014, 14, 343.	3.6	45
43	AtGRP3 Is Implicated in Root Size and Aluminum Response Pathways in Arabidopsis. PLoS ONE, 2016, 11, e0150583.	2.5	45
44	The Source of the River as a Nursery for Microbial Diversity. PLoS ONE, 2015, 10, e0120608.	2.5	44
45	Monitoring genetic diversity in tropical trees with multilocus dominant markers. Heredity, 2005, 95, 274-280.	2.6	43
46	Cloning and in vitro characterization of the grapevine fanleaf virus proteinase cistron. Virology, 1991, 185, 779-787.	2.4	41
47	Phylogeography and ecological niche modelling inEugenia uniflora(Myrtaceae) suggest distinct vegetational responses to climate change between the southern and the northern Atlantic Forest. Botanical Journal of the Linnean Society, 2016, 182, 670-688.	1.6	41
48	In vitro induction of the fat-storing phenotype in a liver connective tissue cell line-GRX. In Vitro Cellular & Developmental Biology, 1990, 26, 361-368.	1.0	40
49	Large-scale phylogeography of the disjunct Neotropical tree species Schizolobium parahyba (Fabaceae-Caesalpinioideae). Molecular Phylogenetics and Evolution, 2012, 65, 174-182.	2.7	40
50	Behavioral alterations in autism model induced by valproic acid and translational analysis of circulating microRNA. Food and Chemical Toxicology, 2018, 115, 336-343.	3.6	39
51	Retinoid-mediated induction of the fat-storing phenotype in a liver connective tissue cell line (GRX). Biochimica Et Biophysica Acta - Molecular Cell Research, 1989, 1011, 1-5.	4.1	38
52	Identification of MicroRNAs from Eugenia uniflora by High-Throughput Sequencing and Bioinformatics Analysis. PLoS ONE, 2012, 7, e49811.	2.5	38
53	Differential Proteolytic Activities of Precursor and Mature Forms of the 24K Proteinase of Grapevine Fanleaf Nepovirus. Virology, 1994, 200, 79-86.	2.4	37
54	The chloroplast genome sequence from Eugenia uniflora, a Myrtaceae from Neotropics. Plant Systematics and Evolution, 2017, 303, 1199-1212.	0.9	37

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55	Exploring the Hospital Microbiome by High-Resolution 16S rRNA Profiling. International Journal of Molecular Sciences, 2019, 20, 3099.	4.1	37
56	Relationship between oxidative stress levels and activation state on a hepatic stellate cell line. Liver International, 2006, 26, 477-485.	3.9	35
57	Identifying MicroRNAs and Transcript Targets in Jatropha Seeds. PLoS ONE, 2014, 9, e83727.	2.5	35
58	Classification, expression pattern and comparative analysis of sugarcane expressed sequences tags (ESTs) encoding glycine-rich proteins (GRPs). Genetics and Molecular Biology, 2001, 24, 263-273.	1.3	34
59	Title is missing!. Biodiversity and Conservation, 2002, 11, 149-163.	2.6	34
60	Phytocalpains: orthologous calcium-dependent cysteine proteinases. Trends in Plant Science, 2003, 8, 58-62.	8.8	34
61	Diversity and evolution of plant diacylglycerol acyltransferase (DGATs) unveiled by phylogenetic, gene structure and expression analyses. Genetics and Molecular Biology, 2016, 39, 524-538.	1.3	34
62	RFMirTarget: Predicting Human MicroRNA Target Genes with a Random Forest Classifier. PLoS ONE, 2013, 8, e70153.	2.5	34
63	Identification of potential miRNAs and their targets in Vriesea carinata (Poales, Bromeliaceae). Plant Science, 2013, 210, 214-223.	3.6	33
64	De novo assembly of Eugenia uniflora L. transcriptome and identification of genes from the terpenoid biosynthesis pathway. Plant Science, 2014, 229, 238-246.	3.6	33
65	Streptomyces drozdowiczii sp. nov., a novel cellulolytic streptomycete from soil in Brazil. International Journal of Systematic and Evolutionary Microbiology, 2004, 54, 1323-1328.	1.7	32
66	A Plant Orthologue of RNase L Inhibitor (RLI) Is Induced in Plants Showing RNA Interference. Journal of Molecular Evolution, 2004, 59, 20-30.	1.8	32
67	Retinol uptake and metabolism, and cellular retinol binding protein expression in an in vitro model of hepatic stellate cells. Molecular and Cellular Biochemistry, 1998, 187, 11-21.	3.1	31
68	Metatranscriptomic analysis of small RNAs present in soybean deep sequencing libraries. Genetics and Molecular Biology, 2012, 35, 292-303.	1.3	31
69	Quantification of attached cells in tissue culture plates and on microcarriers. Analytical Biochemistry, 1989, 181, 209-211.	2.4	30
70	Patterns of genetic diversity in southern and southeastern Araucaria angustifolia (Bert.) O. Kuntze relict populations. Genetics and Molecular Biology, 2009, 32, 546-556.	1.3	30
71	New insights on the evolution of Leafy cotyledon1 (LEC1) type genes in vascular plants. Genomics, 2014, 103, 380-387.	2.9	30
72	Comprehensive selection of reference genes for quantitative gene expression analysis during seed development in Brassica napus. Plant Cell Reports, 2015, 34, 1139-1149.	5.6	30

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73	Authentication of Medicinal Plant Botanical Identity by Amplified Fragmented Length Polymorphism Dominant DNA Marker: Inferences from thePlectranthusGenus. Planta Medica, 2006, 72, 929-931.	1.3	29
74	Rapid detection of Echinococcus species by a high-resolution melting (HRM) approach. Parasites and Vectors, 2013, 6, 327.	2.5	28
75	Salt stress affects mRNA editing in soybean chloroplasts. Genetics and Molecular Biology, 2017, 40, 200-208.	1.3	28
76	Enzymes of glycerol-3-phosphate pathway in triacylglycerol synthesis in plants: Function, biotechnological application and evolution. Progress in Lipid Research, 2019, 73, 46-64.	11.6	28
77	Hepatic stellate cell line modulates lipogenic transcription factors. Liver International, 2007, 27, 1255-1264.	3.9	27
78	Molecular Analysis of the Differentiation Potential of Murine Mesenchymal Stem Cells from Tissues of Endodermal or Mesodermal Origin. Stem Cells and Development, 2012, 21, 1761-1768.	2.1	27
79	Fumarate reductase superfamily: A diverse group of enzymes whose evolution is correlated to the establishment of different metabolic pathways. Mitochondrion, 2017, 34, 56-66.	3.4	25
80	Characterization of nuclear microsatellite loci in South American Araucariaceae species. Molecular Ecology Notes, 2005, 5, 256-258.	1.7	24
81	Adipose Tissue Distribution and Quantification of PPARÎ²/Î´ and PPARÎ³1-3 mRNAs: Discordant Gene Expression in Subcutaneous, Retroperitoneal and Visceral Adipose Tissue of Morbidly Obese Patients. Obesity Surgery, 2007, 17, 934-940.	2.1	24
82	Two-Level Adsorption of Ibuprofen on C₆₀ Fullerene for Transdermal Delivery: Classical Molecular Dynamics and Density Functional Theory Computations. Journal of Physical Chemistry C, 2011, 115, 24501-24511.	3.1	24
83	Activity and expression of ecto-5â€²-nucleotidase/CD73 are increased during phenotype conversion of a hepatic stellate cell line. Life Sciences, 2008, 82, 21-29.	4.3	22
84	Identification and evaluation of reference genes for expression studies by RT-qPCR during embryonic development of the emerging model organism, Macrobrachium olfersii. Gene, 2017, 598, 97-106.	2.2	22
85	Theobroma cacao cystatins impair Moniliophthora perniciosa mycelial growth and are involved in postponing cell death symptoms. Planta, 2010, 232, 1485-1497.	3.2	21
86	Unusual RNA plant virus integration in the soybean genome leads to the production of small RNAs. Plant Science, 2016, 246, 62-69.	3.6	21
87	Standardized genetic diversityâ€life history correlates for improved genetic resource management of Neotropical trees. Diversity and Distributions, 2018, 24, 730-741.	4.1	21
88	Effects of retinol on proliferation, cell adherence and extracellular matrix synthesis in a liver myofibroblast or lipocyte cell line (GRX). International Journal of Experimental Pathology, 1992, 73, 125-35.	1.3	21
89	Ecto-5â€²-nucleotidase/CD73 knockdown increases cell migration and mRNA level of collagen I in a hepatic stellate cell line. Cell and Tissue Research, 2011, 344, 279-286.	2.9	20
90	Thylakoidal APX modulates hydrogen peroxide content and stomatal closure in rice (Oryza sativa L.). Environmental and Experimental Botany, 2018, 150, 46-56.	4.2	20

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91	Parallel Down-Regulation of FOXO1, PPARÎ³ and Adiponectin mRNA Expression in Visceral Adipose Tissue of Class III Obese Individuals. Obesity Facts, 2012, 5, 452-459.	3.4	19
92	Circular and Micro RNAs from Arabidopsis thaliana Flowers Are Simultaneously Isolated from AGO-IP Libraries. Plants, 2019, 8, 302.	3.5	19
93	Molecular evolution and diversification of plant cysteine proteinase inhibitors: New insights after the poplar genome. Molecular Phylogenetics and Evolution, 2008, 49, 349-355.	2.7	18
94	Analysis of castor bean ribosome-inactivating proteins and their gene expression during seed development. Genetics and Molecular Biology, 2013, 36, 74-86.	1.3	18
95	Uncovering legumain genes in rice. Plant Science, 2014, 215-216, 100-109.	3.6	18
96	Resveratrol Regulates the Quiescenceâ€Like Induction of Activated Stellate Cells by Modulating the PPARÎ³/SIRT1 Ratio. Journal of Cellular Biochemistry, 2015, 116, 2304-2312.	2.6	18
97	AtchitIV gene expression is stimulated under abiotic stresses and is spatially and temporally regulated during embryo development. Genetics and Molecular Biology, 2004, 27, 118-123.	1.3	17
98	The hobo transposon and hobo-related elements are expressed as developmental genes in Drosophila. Gene, 2009, 448, 57-63.	2.2	17
99	Modulation of genes related to specific metabolic pathways in response to cytosolic ascorbate peroxidase knockdown in rice plants. Plant Biology, 2012, 14, 944-955.	3.8	17
100	Unveiling Chloroplast RNA Editing Events Using Next Generation Small RNA Sequencing Data. Frontiers in Plant Science, 2017, 8, 1686.	3.6	17
101	Sugarcane phytocystatins: Identification, classification and expression pattern analysis. Genetics and Molecular Biology, 2001, 24, 291-296.	1.3	16
102	Lipoteichoic acid from Staphylococcus aureus increases matrix metalloproteinase 9 expression in RAW 264.7 macrophages: Modulation by A2A and A2B adenosine receptors. Molecular Immunology, 2009, 46, 937-942.	2.2	16
103	Identification and expression analysis of genes associated with the early berry development in the seedless grapevine (Vitis vinifera L.) cultivar Sultanine. Plant Science, 2010, 179, 510-519.	3.6	15
104	Identification of novel and conserved microRNAs in Coffea canephora and Coffea arabica. Genetics and Molecular Biology, 2014, 37, 671-682.	1.3	15
105	Transcriptome of tung tree mature seeds with an emphasis on lipid metabolism genes. Tree Genetics and Genomes, 2014, 10, 1353-1367.	1.6	15
106	Transcriptional analyses of two soybean cultivars under salt stress. Molecular Biology Reports, 2020, 47, 2871-2888.	2.3	15
107	Collagen synthesis in an established liver connective tissue cell line (GRX) during induction of the fat-storing phenotype. Experimental and Molecular Pathology, 1992, 56, 108-118.	2.1	14
108	Exploring developmental gene toolkit and associated pathways in a potential new model crustacean using transcriptomic analysis. Development Genes and Evolution, 2016, 226, 325-337.	0.9	14

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109	Rice bifunctional phytocystatin is a dual modulator of legumain and papain-like proteases. Plant Molecular Biology, 2016, 92, 193-207.	3.9	14
110	Identification of root transcriptional responses to shoot illumination in Arabidopsis thaliana. Plant Molecular Biology, 2019, 101, 487-498.	3.9	14
111	Novel and Conserved miRNAs Among Brazilian Pine and Other Gymnosperms. Frontiers in Genetics, 2019, 10, 222.	2.3	14
112	Ascorbate peroxidase-related (APx-R) is not a duplicable gene. Plant Signaling and Behavior, 2011, 6, 1908-1913.	2.4	13
113	The rice ASR5 protein. Plant Signaling and Behavior, 2012, 7, 1263-1266.	2.4	13
114	Sex Differences and Estrous Cycle Changes in Synaptic Plasticity-related microRNA in the Rat Medial Amygdala. Neuroscience, 2018, 379, 405-414.	2.3	13
115	Transcriptome analysis of strawberry (Fragariaâ€‰Ã—â€‰ananassa) fruits under osmotic stresses and identification of genes related to ascorbic acid pathway. Physiologia Plantarum, 2019, 166, 979-995.	5.2	13
116	Phylogenetic analysis of the genusHexachlamys(Myrtaceae) based on plastid and nuclear DNA sequences and their taxonomic implications. Botanical Journal of the Linnean Society, 2013, 172, 532-543.	1.6	12
117	The diversity of rice phytocystatins. Molecular Genetics and Genomics, 2014, 289, 1321-1330.	2.1	12
118	Novel and conserved microRNAs in soybean floral whorls. Gene, 2016, 575, 213-223.	2.2	12
119	Differential expression of cysteine desulfurases in soybean. BMC Plant Biology, 2011, 11, 166.	3.6	11
120	VPg Northern-immunoblots as a means for detection of viral RNAs in protoplasts or plants infected with grapevine fanleaf nepovirus. Archives of Virology, 1993, 131, 225-232.	2.1	10
121	Comparative transcriptomic analysis of Listeria monocytogenes reveals upregulation of stress genes and downregulation of virulence genes in response to essential oil extracted from Baccharis psiadioides. Annals of Microbiology, 2017, 67, 479-490.	2.6	10
122	Comparative analysis of the complete chloroplast genomes from six Neotropical species of Myrteae (Myrtaceae). Genetics and Molecular Biology, 2020, 43, e20190302.	1.3	10
123	Identification, classification and expression pattern analysis of sugarcane cysteine proteinases. Genetics and Molecular Biology, 2001, 24, 275-283.	1.3	9
124	Unravelling MADS-box gene family in Eucalyptus spp.: a starting point to an understanding of their developmental role in trees. Genetics and Molecular Biology, 2005, 28, 501-510.	1.3	9
125	Suppression of post-transcriptional gene silencing by callus induction and virus infection reveals the existence of aberrant RNAs. Plant Science, 2004, 167, 159-164.	3.6	8
126	ASR5 is involved in the regulation of miRNA expression in rice. Plant Cell Reports, 2015, 34, 1899-1907.	5.6	8

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127	Complete sequence and comparative analysis of the chloroplast genome of Plinia trunciflora. Genetics and Molecular Biology, 2017, 40, 871-876.	1.3	8
128	HDAC inhibitor affects soybean miRNA482bd expression under salt and osmotic stress. Journal of Plant Physiology, 2020, 253, 153261.	3.5	8
129	Transcriptomics analysis of Psidium cattleyanum Sabine (Myrtaceae) unveil potential genes involved in fruit pigmentation. Genetics and Molecular Biology, 2020, 43, e20190255.	1.3	8
130	Characterization and expression analysis of P5CS (Î"1-pyrroline-5-carboxylate synthase) gene in two distinct populations of the Atlantic Forest native species Eugenia uniflora L.. Molecular Biology Reports, 2020, 47, 1033-1043.	2.3	7
131	Transcriptional acclimation and spatial differentiation characterize drought response by the ectomycorrhizal fungus Suillus pungens. New Phytologist, 2022, 234, 1910-1913.	7.3	7
132	ISOLATION OF HIGH-QUALITY RNA FROM GRAINS OF DIFFERENT MAIZE VARIETIES. Preparative Biochemistry and Biotechnology, 2014, 44, 697-707.	1.9	6
133	Obesity Associated with Type 2 Diabetes Mellitus Is Linked to Decreased PC1/3 mRNA Expression in the Jejunum. Obesity Surgery, 2014, 24, 2075-2081.	2.1	6
134	Expression of the histone chaperone SET/TAF-IÎ² during the strobilation process of Mesocestoides corti (Platyhelminthes, Cestoda). Parasitology, 2015, 142, 1171-1182.	1.5	6
135	Araucaria angustifolia chloroplast genome sequence and its relation to other Araucariaceae. Genetics and Molecular Biology, 2019, 42, 671-676.	1.3	6
136	Gene stacking as a strategy to confer characteristics of agronomic importance in plants by genetic engineering. Ciencia Rural, 2020, 50, .	0.5	6
137	Activity and expression of ecto-nucleotide pyrophosphate/phosphodiesterases in a hepatic stellate cell line. Molecular and Cellular Biochemistry, 2009, 325, 179-185.	3.1	5
138	microRNAs in Macrobrachium olfersii embryos: Identification, their biogenesis components and potential targets. Computational Biology and Chemistry, 2019, 78, 205-216.	2.3	5
139	Changes in E-NTPDase 3 expression and extracellular nucleotide hydrolysis during the myofibroblast/lipocyte differentiation. Molecular and Cellular Biochemistry, 2010, 339, 79-87.	3.1	4
140	Data on social transmission of food preference in a model of autism induced by valproic acid and translational analysis of circulating microRNA. Data in Brief, 2018, 18, 1433-1440.	1.0	4
141	Perspectives in Myrtaceae evolution from plastomes and nuclear phylogenies. Genetics and Molecular Biology, 2022, 45, e20210191.	1.3	4
142	MAEWEST Expression in Flower Development of Two Petunia Species. International Journal of Molecular Sciences, 2013, 14, 13796-13807.	4.1	3
143	A recombinant subtilisin with keratinolytic and fibrin(ogen)olytic activity. Process Biochemistry, 2014, 49, 948-954.	3.7	3
144	Population structure and signals of local adaptation in Eugenia uniflora (Myrtaceae), a widely distributed species in the Atlantic Forest. Botanical Journal of the Linnean Society, 2023, 201, 100-113.	1.6	3

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145	Variations of ganglioside biosynthetic pathways in the phenotype conversion from myofibroblasts to lipocytes in murine hepatic stellate cell line. Molecular and Cellular Biochemistry, 2007, 303, 121-130.	3.1	2
146	Functional characterization of castor bean (Ricinus communis) DGAT3 and DAcT enzymes in Arabidopsis thaliana. BMC Proceedings, 2014, 8, .	1.6	2
147	Development, characterization, and transferability of <scp>SSR</scp> markers for Vriesea carinata (Bromeliaceae) based on <scp>RNA</scp> sequencing. Applications in Plant Sciences, 2018, 6, e01184.	2.1	2
148	Identification of soybean trans-factors associated with plastid RNA editing sites. Genetics and Molecular Biology, 2020, 43, e20190067.	1.3	2
149	The Evolutionary History of CBF Transcription Factors: Gene Duplication of CCAAT â€“ Binding Factors NF-Y in Plants. , 0, , .		2
150	RFMirTarget: A Random Forest Classifier for Human miRNA Target Gene Prediction. Lecture Notes in Computer Science, 2012, , 97-108.	1.3	2
151	The 42-kDa coat protein of Andean potato mottle virus acts as a transcriptional activator in yeast. Brazilian Journal of Medical and Biological Research, 2002, 35, 411-420.	1.5	1
152	Phylogeography of the disjunct Schizolobium parahyba (Fabaceae-Caesalpinioideae). BMC Proceedings, 2011, 5, .	1.6	1
153	De novo assembly of Vriesea carinata leaf transcriptome to identify candidate cysteine-proteases. Gene, 2019, 691, 96-105.	2.2	1
154	Methods for Predicting CircRNAâ€“miRNAâ€“mRNA : and as Study Cases. Methods in Molecular Biology, 2021, 2362, 181-193.	0.9	1
155	Rice Arsenal Against Aluminum Toxicity. Signaling and Communication in Plants, 2015, , 155-168.	0.7	1
156	Trends in Synthetic Biology in the Bioeconomy of Non-Food-Competing Biofuels. SynBio, 2022, 1, 33-53.	3.0	1
157	Review: Unraveling the origin of the structural and functional diversity of plant cystatins. Plant Science, 2022, 321, 111342.	3.6	1
158	Environmental and health risk assessments of genetically modified eucalypts in Brazil. BMC Proceedings, 2011, 5, .	1.6	0
159	Chloroplast DNA variation and phylogeography of Eugenia uniflora L. (Myrtaceae)in the Brazilian Atlantic forest. BMC Proceedings, 2011, 5, .	1.6	0
160	Molecular Phylogenetics of the genus Hexachlamys (Myrtaceae)using chloroplast and nuclear markers. BMC Proceedings, 2011, 5, .	1.6	0
161	SU1ANDROGEN RECEPTOR SIGNALING PATHWAYS INFLUENCE IN ATTENTION-DEFICIT/HYPERACTIVITY DISORDER. European Neuropsychopharmacology, 2019, 29, S1268.	0.7	0
162	Transcriptional profiling and physiological responses reveal new insights into drought tolerance in a semiarid adapted species, Anacardium occidentale. Plant Biology, 2021, 23, 1074-1085.	3.8	0

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163	Pequenos RNAs e aplicaÃ§Ãµes de RNAi em plantas. , 2017, , 675-708.		0