Rogério Margis

List of Publications by Year in descending order

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

#	Article	IF	CITATIONS
1	Population structure and signals of local adaptation in <i>Eugenia uniflora</i> (Myrtaceae), a widely distributed species in the Atlantic Forest. Botanical Journal of the Linnean Society, 2023, 201, 100-113.	1.6	3
2	Transcriptional acclimation and spatial differentiation characterize drought response by the ectomycorrhizal fungus <i>Suillus pungens</i> . New Phytologist, 2022, 234, 1910-1913.	7.3	7
3	Perspectives in Myrtaceae evolution from plastomes and nuclear phylogenies. Genetics and Molecular Biology, 2022, 45, e20210191.	1.3	4
4	Trends in Synthetic Biology in the Bioeconomy of Non-Food-Competing Biofuels. SynBio, 2022, 1, 33-53.	3.0	1
5	Review: Unraveling the origin of the structural and functional diversity of plant cystatins. Plant Science, 2022, 321, 111342.	3.6	1
6	Methods for Predicting CircRNA–miRNA–mRNA : and as Study Cases. Methods in Molecular Biology, 2021, 2362, 181-193.	0.9	1
7	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	O
8	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
9	HDAC inhibitor affects soybean miRNA482bd expression under salt and osmotic stress. Journal of Plant Physiology, 2020, 253, 153261.	3.5	8
10	Transcriptional analyses of two soybean cultivars under salt stress. Molecular Biology Reports, 2020, 47, 2871-2888.	2.3	15
11	Gene stacking as a strategy to confer characteristics of agronomic importance in plants by genetic engineering. Ciencia Rural, 2020, 50, .	0.5	6
12	Identification of soybean trans-factors associated with plastid RNA editing sites. Genetics and Molecular Biology, 2020, 43, e20190067.	1.3	2
13	Transcriptomics analysis of Psidium cattleyanum Sabine (Myrtaceae) unveil potential genes involved in fruit pigmentation. Genetics and Molecular Biology, 2020, 43, e20190255.	1.3	8
14	Comparative analysis of the complete chloroplast genomes from six Neotropical species of Myrteae (Myrtaceae). Genetics and Molecular Biology, 2020, 43, e20190302.	1.3	10
15	SU1ANDROGEN RECEPTOR SIGNALING PATHWAYS INFLUENCE IN ATTENTION-DEFICIT/HYPERACTIVITY DISORDER. European Neuropsychopharmacology, 2019, 29, S1268.	0.7	0
16	Circular and Micro RNAs from Arabidopsis thaliana Flowers Are Simultaneously Isolated from AGO-IP Libraries. Plants, 2019, 8, 302.	3.5	19
17	Identification of root transcriptional responses to shoot illumination in Arabidopsis thaliana. Plant Molecular Biology, 2019, 101, 487-498.	3.9	14
18	Araucaria angustifolia chloroplast genome sequence and its relation to other Araucariaceae. Genetics and Molecular Biology, 2019, 42, 671-676.	1.3	6

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19	Exploring the Hospital Microbiome by High-Resolution 16S rRNA Profiling. International Journal of Molecular Sciences, 2019, 20, 3099.	4.1	37
20	Novel and Conserved miRNAs Among Brazilian Pine and Other Gymnosperms. Frontiers in Genetics, 2019, 10, 222.	2.3	14
21	microRNAs in Macrobrachium olfersii embryos: Identification, their biogenesis components and potential targets. Computational Biology and Chemistry, 2019, 78, 205-216.	2.3	5
22	De novo assembly of Vriesea carinata leaf transcriptome to identify candidate cysteine-proteases. Gene, 2019, 691, 96-105.	2.2	1
23	Transcriptome analysis of strawberry (<i>Fragaria × ananassa</i>) fruits under osmotic stresses and identification of genes related to ascorbic acid pathway. Physiologia Plantarum, 2019, 166, 979-995.	5.2	13
24	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
25	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
26	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
27	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
28	Sex Differences and Estrous Cycle Changes in Synaptic Plasticity-related microRNA in the Rat Medial Amygdala. Neuroscience, 2018, 379, 405-414.	2.3	13
29	Standardized genetic diversityâ€ife history correlates for improved genetic resource management of Neotropical trees. Diversity and Distributions, 2018, 24, 730-741.	4.1	21
30	Development, characterization, and transferability of <scp>SSR</scp> markers for <i>Vriesea carinata</i> (Bromeliaceae) based on <scp>RNA</scp> sequencing. Applications in Plant Sciences, 2018, 6, e01184.	2.1	2
31	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
32	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
33	The chloroplast genome sequence from Eugenia uniflora, a Myrtaceae from Neotropics. Plant Systematics and Evolution, 2017, 303, 1199-1212.	0.9	37
34	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
35	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
36	Unveiling Chloroplast RNA Editing Events Using Next Generation Small RNA Sequencing Data. Frontiers in Plant Science, 2017, 8, 1686.	3.6	17

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37	Complete sequence and comparative analysis of the chloroplast genome of Plinia trunciflora. Genetics and Molecular Biology, 2017, 40, 871-876.	1.3	8
38	Salt stress affects mRNA editing in soybean chloroplasts. Genetics and Molecular Biology, 2017, 40, 200-208.	1.3	28
39	Pequenos RNAs e aplicaçÃμes de RNAi em plantas. , 2017, , 675-708.		0
40	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
41	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
42	Phylogeography and ecological niche modelling in <i>Eugenia uniflora</i> (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
43	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
44	Rice bifunctional phytocystatin is a dual modulator of legumain and papain-like proteases. Plant Molecular Biology, 2016, 92, 193-207.	3.9	14
45	Rice <i>ASR1</i> and <i>ASR5</i> are complementary transcription factors regulating aluminium responsive genes. Plant, Cell and Environment, 2016, 39, 645-651.	5.7	75
46	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
47	Molecular evolution of the lysophosphatidic acid acyltransferase (LPAAT) gene family. Molecular Phylogenetics and Evolution, 2016, 96, 55-69.	2.7	51
48	Novel and conserved microRNAs in soybean floral whorls. Gene, 2016, 575, 213-223.	2.2	12
49	AtGRP3 Is Implicated in Root Size and Aluminum Response Pathways in Arabidopsis. PLoS ONE, 2016, 11, e0150583.	2.5	45
50	Expression of the histone chaperone SET/TAF-I <i>\hat{l}^2</i> during the strobilation process of <i>Mesocestoides corti</i> (Platyhelminthes, Cestoda). Parasitology, 2015, 142, 1171-1182.	1.5	6
51	Resveratrol Regulates the Quiescenceâ€Like Induction of Activated Stellate Cells by Modulating the PPARγ/SIRT1 Ratio. Journal of Cellular Biochemistry, 2015, 116, 2304-2312.	2.6	18
52	The Source of the River as a Nursery for Microbial Diversity. PLoS ONE, 2015, 10, e0120608.	2.5	44
53	Cold tolerance in rice germinating seeds revealed by deep RNAseq analysis of contrasting indica genotypes. Plant Science, 2015, 238, 1-12.	3.6	54
54	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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55	ASR5 is involved in the regulation of miRNA expression in rice. Plant Cell Reports, 2015, 34, 1899-1907.	5.6	8
56	NPK macronutrients and microRNA homeostasis. Frontiers in Plant Science, 2015, 6, 451.	3.6	55
57	Rice Arsenal Against Aluminum Toxicity. Signaling and Communication in Plants, 2015, , 155-168.	0.7	1
58	Identifying MicroRNAs and Transcript Targets in Jatropha Seeds. PLoS ONE, 2014, 9, e83727.	2.5	35
59	Identification of novel and conserved microRNAs in Coffea canephora and Coffea arabica. Genetics and Molecular Biology, 2014, 37, 671-682.	1.3	15
60	Functional characterization of castor bean (Ricinus communis) DGAT3 and DAcT enzymes in Arabidopsis thaliana. BMC Proceedings, 2014, 8, .	1.6	2
61	Expression of an osmotin-like protein from Solanum nigrumconfers drought tolerance in transgenic soybean. BMC Plant Biology, 2014, 14, 343.	3.6	45
62	Uncovering legumain genes in rice. Plant Science, 2014, 215-216, 100-109.	3.6	18
63	New insights on the evolution of Leafy cotyledon1 (LEC1) type genes in vascular plants. Genomics, 2014, 103, 380-387.	2.9	30
64	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
65	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
66	The Wall-associated Kinase gene family in rice genomes. Plant Science, 2014, 229, 181-192.	3.6	59
67	ISOLATION OF HIGH-QUALITY RNA FROM GRAINS OF DIFFERENT MAIZE VARIETIES. Preparative Biochemistry and Biotechnology, 2014, 44, 697-707.	1.9	6
68	The diversity of rice phytocystatins. Molecular Genetics and Genomics, 2014, 289, 1321-1330.	2.1	12
69	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
70	Transcriptome of tung tree mature seeds with an emphasis on lipid metabolism genes. Tree Genetics and Genomes, 2014, 10, 1353-1367.	1.6	15
71	A recombinant subtilisin with keratinolytic and fibrin(ogen)olytic activity. Process Biochemistry, 2014, 49, 948-954.	3.7	3
72	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

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73	Involvement of $\langle i \rangle$ ASR $\langle i \rangle$ genes in aluminium tolerance mechanisms in rice. Plant, Cell and Environment, 2013, 36, 52-67.	5.7	86
74	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
75	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
76	MAEWEST Expression in Flower Development of Two Petunia Species. International Journal of Molecular Sciences, 2013, 14, 13796-13807.	4.1	3
77	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
78	Identification of potential miRNAs and their targets in Vriesea carinata (Poales, Bromeliaceae). Plant Science, 2013, 210, 214-223.	3.6	33
79	Rapid detection of Echinococcus species by a high-resolution melting (HRM) approach. Parasites and Vectors, 2013, 6, 327.	2.5	28
80	isomiRID: a framework to identify microRNA isoforms. Bioinformatics, 2013, 29, 2521-2523.	4.1	45
81	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
82	RFMirTarget: Predicting Human MicroRNA Target Genes with a Random Forest Classifier. PLoS ONE, 2013, 8, e70153.	2.5	34
83	The rice ASR5 protein. Plant Signaling and Behavior, 2012, 7, 1263-1266.	2.4	13
84	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
85	Parallel Down-Regulation of FOXO1, PPARγ and Adiponectin mRNA Expression in Visceral Adipose Tissue of Class III Obese Individuals. Obesity Facts, 2012, 5, 452-459.	3.4	19
86	MicroRNAs play critical roles during plant development and in response to abiotic stresses. Genetics and Molecular Biology, 2012, 35, 1069-1077.	1.3	108
87	Large-scale phylogeography of the disjunct Neotropical tree species Schizolobium parahyba (Fabaceae-Caesalpinioideae). Molecular Phylogenetics and Evolution, 2012, 65, 174-182.	2.7	40
88	Reference Genes for the Normalization of Gene Expression in Eucalyptus Species. Plant and Cell Physiology, 2012, 53, 405-422.	3.1	69
89	Metatranscriptomic analysis of small RNAs present in soybean deep sequencing libraries. Genetics and Molecular Biology, 2012, 35, 292-303.	1.3	31
90	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

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91	Identification of MicroRNAs from Eugenia uniflora by High-Throughput Sequencing and Bioinformatics Analysis. PLoS ONE, 2012, 7, e49811.	2.5	38
92	Identifying Conserved and Novel MicroRNAs in Developing Seeds of Brassica napus Using Deep Sequencing. PLoS ONE, 2012, 7, e50663.	2.5	61
93	RFMirTarget: A Random Forest Classifier for Human miRNA Target Gene Prediction. Lecture Notes in Computer Science, 2012, , 97-108.	1.3	2
94	Two-Level Adsorption of Ibuprofen on C ₆₀ Fullerene for Transdermal Delivery: Classical Molecular Dynamics and Density Functional Theory Computations. Journal of Physical Chemistry C, 2011, 115, 24501-24511.	3.1	24
95	Biosynthesis of Triacylglycerols (TAGs) in Plants and algae. International Journal of Plant Biology, 2011, 2, e10.	2.6	81
96	Aluminum triggers broad changes in microRNA expression in rice roots. Genetics and Molecular Research, 2011, 10, 2817-2832.	0.2	85
97	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
98	Ecto-5′-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
99	Resveratrol Upregulated SIRT1, FOXO1, and Adiponectin and Downregulated PPARγ1–3 mRNA Expression in Human Visceral Adipocytes. Obesity Surgery, 2011, 21, 356-361.	2.1	84
100	Differential expression of cysteine desulfurases in soybean. BMC Plant Biology, 2011, 11, 166.	3.6	11
101	Environmental and health risk assessments of genetically modified eucalypts in Brazil. BMC Proceedings, 2011, 5, .	1.6	0
102	Phylogeography of the disjunct Schizolobium parahyba (Fabaceae-Caesalpinioideae). BMC Proceedings, 2011, 5, .	1.6	1
103	Chloroplast DNA variation and phylogeography of Eugenia uniflora L. (Myrtaceae)in the Brazilian Atlantic forest. BMC Proceedings, 2011, 5, .	1.6	0
104	Molecular Phylogenetics of the genus Hexachlamys (Myrtaceae)using chloroplast and nuclear markers. BMC Proceedings, 2011, 5, .	1.6	0
105	Evolutionary view of acyl-CoA diacylglycerol acyltransferase (DGAT), a key enzyme in neutral lipid biosynthesis. BMC Evolutionary Biology, 2011, 11, 263.	3.2	174
106	Identification of novel soybean microRNAs involved in abiotic and biotic stresses. BMC Genomics, 2011, 12, 307.	2.8	313
107	Identification of blood microRNAs associated to Parkinsońs disease. Journal of Biotechnology, 2011, 152, 96-101.	3.8	244
108	Ascorbate peroxidase-related (APx-R) is not a duplicable gene. Plant Signaling and Behavior, 2011, 6, 1908-1913.	2.4	13

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109	Theobroma cacao cystatins impair Moniliophthora perniciosa mycelial growth and are involved in postponing cell death symptoms. Planta, 2010, 232, 1485-1497.	3.2	21
110	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
111	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
112	Cytosolic APx knockdown indicates an ambiguous redox responses in rice. Phytochemistry, 2010, 71, 548-558.	2.9	115
113	The use of microRNAs as reference genes for quantitative polymerase chain reaction in soybean. Analytical Biochemistry, 2010, 406, 185-192.	2.4	138
114	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
115	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
116	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
117	AtGRP5, a vacuole-located glycine-rich protein involved in cell elongation. Planta, 2009, 230, 253-265.	3.2	56
118	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
119	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
120	The hobo transposon and hobo-related elements are expressed as developmental genes in Drosophila. Gene, 2009, 448, 57-63.	2.2	17
121	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
122	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
123	Glutathione peroxidase family – an evolutionary overview. FEBS Journal, 2008, 275, 3959-3970.	4.7	400
124	Activity and expression of ecto-5′-nucleotidase/CD73 are increased during phenotype conversion of a hepatic stellate cell line. Life Sciences, 2008, 82, 21-29.	4.3	22
125	Hepatic stellate cell line modulates lipogenic transcription factors. Liver International, 2007, 27, 1255-1264.	3.9	27
126	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

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127	Adipose Tissue Distribution and Quantification of PPARβ/δ and PPARγ1-3 mRNAs: Discordant Gene Expression in Subcutaneous, Retroperitoneal and Visceral Adipose Tissue of Morbidly Obese Patients. Obesity Surgery, 2007, 17, 934-940.	2.1	24
128	The evolution and diversification of Dicers in plants. FEBS Letters, 2006, 580, 2442-2450.	2.8	283
129	Relationship between oxidative stress levels and activation state on a hepatic stellate cell line. Liver International, 2006, 26, 477-485.	3.9	35
130	Rice ascorbate peroxidase gene family encodes functionally diverse isoforms localized in different subcellular compartments. Planta, 2006, 224, 300-314.	3.2	199
131	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
132	Characterization of nuclear microsatellite loci in South American Araucariaceae species. Molecular Ecology Notes, 2005, 5, 256-258.	1.7	24
133	Optimal sampling strategy for estimation of spatial genetic structure in tree populations. Heredity, 2005, 95, 281-289.	2.6	100
134	Monitoring genetic diversity in tropical trees with multilocus dominant markers. Heredity, 2005, 95, 274-280.	2.6	43
135	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
136	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
137	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
138	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
139	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
140	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
141	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
142	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
143	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
144	Phytocalpains: orthologous calcium-dependent cysteine proteinases. Trends in Plant Science, 2003, 8, 58-62.	8.8	34

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145	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
146	Title is missing!. Biodiversity and Conservation, 2002, 11, 149-163.	2.6	34
147	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
148	Identification, classification and expression pattern analysis of sugarcane cysteine proteinases. Genetics and Molecular Biology, 2001, 24, 275-283.	1.3	9
149	Sugarcane phytocystatins: Identification, classification and expression pattern analysis. Genetics and Molecular Biology, 2001, 24, 291-296.	1.3	16
150	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
151	Structural and Phylogenetic Relationships among Plant and Animal Cystatins. Archives of Biochemistry and Biophysics, 1998, 359, 24-30.	3.0	176
152	Differential Proteolytic Activities of Precursor and Mature Forms of the 24K Proteinase of Grapevine Fanleaf Nepovirus. Virology, 1994, 200, 79-86.	2.4	37
153	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
154	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
155	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
156	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
157	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
158	Complete nucleotide sequence and genetic organization of grapevine fanleaf nepovirus RNA1. Journal of General Virology, 1991, 72, 2357-2365.	2.9	108
159	Cloning and in vitro characterization of the grapevine fanleaf virus proteinase cistron. Virology, 1991, 185, 779-787.	2.4	41
160	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
161	Quantification of attached cells in tissue culture plates and on microcarriers. Analytical Biochemistry, 1989, 181, 209-211.	2.4	30
162	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

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163	The Evolutionary History of CBF Transcription Factors: Gene Duplication of CCAAT – Binding Factors NF-Y in Plants. , 0, , .		2