

Andreia Carina Turchetto-Zolet

List of Publications by Year in descending order

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#	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. <i>Botanical Journal of the Linnean Society</i> , 2023, 201, 100-113.	1.6	3
2	Advances and perspectives on the evolutionary history and diversification of Neotropical Myrteae (Myrtaceae). <i>Botanical Journal of the Linnean Society</i> , 2022, 199, 173-195.	1.6	5
3	Drivers of exceptional Neotropical biodiversity: an updated view. <i>Botanical Journal of the Linnean Society</i> , 2022, 199, 1-7.	1.6	3
4	Perspectives in Myrtaceae evolution from plastomes and nuclear phylogenies. <i>Genetics and Molecular Biology</i> , 2022, 45, e20210191.	1.3	4
5	Glutamine synthetase evolutionary history revisited: Tracing back beyond the Last Universal Common Ancestor. <i>Evolution; International Journal of Organic Evolution</i> , 2022, 76, 605-622.	2.3	8
6	Going Forward and Back: The Complex Evolutionary History of the GPx. <i>Biology</i> , 2021, 10, 1165.	2.8	15
7	Characterization and expression analysis of P5CS (γ -1-pyrroline-5-carboxylate synthase) gene in two distinct populations of the Atlantic Forest native species <i>Eugenia uniflora</i> L. <i>Molecular Biology Reports</i> , 2020, 47, 1033-1043.	2.3	7
8	Haplotype analysis and origin of the most common pathogenic mutation causing Mucopolidosis II and III alpha/beta in Brazilian patients. <i>Gene Reports</i> , 2020, 19, 100645.	0.8	1
9	Comparative phylogeography of two free-living cosmopolitan cyanobacteria: Insights on biogeographic and latitudinal distribution. <i>Journal of Biogeography</i> , 2020, 47, 1106-1118.	3.0	8
10	The Mitochondrial Iron-Regulated (MIR) gene is <i>Oryza</i> genus specific and evolved before speciation within the <i>Oryza sativa</i> complex. <i>Planta</i> , 2020, 251, 94.	3.2	7
11	Transcriptomics analysis of <i>Psidium cattleianum</i> Sabine (Myrtaceae) unveil potential genes involved in fruit pigmentation. <i>Genetics and Molecular Biology</i> , 2020, 43, e20190255.	1.3	8
12	Molecular evolution and diversification of the GRF transcription factor family. <i>Genetics and Molecular Biology</i> , 2020, 43, 20200080.	1.3	15
13	The Role of Co-Deleted Genes in Neurofibromatosis Type 1 Microdeletions: An Evolutive Approach. <i>Genes</i> , 2019, 10, 839.	2.4	3
14	Genome-wide analysis and evolution of plant thaumatin-like proteins: a focus on the origin and diversification of osmotins. <i>Molecular Genetics and Genomics</i> , 2019, 294, 1137-1157.	2.1	19
15	Enzymes of glycerol-3-phosphate pathway in triacylglycerol synthesis in plants: Function, biotechnological application and evolution. <i>Progress in Lipid Research</i> , 2019, 73, 46-64.	11.6	28
16	Genome-wide analysis of the Glycerol-3-Phosphate Acyltransferase (GPAT) gene family reveals the evolution and diversification of plant GPATs. <i>Genetics and Molecular Biology</i> , 2018, 41, 355-370.	1.3	48
17	Fumarate reductase superfamily: A diverse group of enzymes whose evolution is correlated to the establishment of different metabolic pathways. <i>Mitochondrion</i> , 2017, 34, 56-66.	3.4	25
18	Diversity and evolution of plant diacylglycerol acyltransferase (DGATs) unveiled by phylogenetic, gene structure and expression analyses. <i>Genetics and Molecular Biology</i> , 2016, 39, 524-538.	1.3	34

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19	De novo assembly and characterization of leaf and floral transcriptomes of the hybridizing bromeliad species (<i>Pitcairnia</i> spp.) adapted to Neotropical Inselbergs. <i>Molecular Ecology Resources</i> , 2016, 16, 1012-1022.	4.8	37
20	The evolutionary history of the E2F and DEL genes in Viridiplantae. <i>Molecular Phylogenetics and Evolution</i> , 2016, 99, 225-234.	2.7	3
21	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. <i>Botanical Journal of the Linnean Society</i> , 2016, 182, 670-688.	1.6	41
22	Molecular evolution of the lysophosphatidic acid acyltransferase (LPAAT) gene family. <i>Molecular Phylogenetics and Evolution</i> , 2016, 96, 55-69.	2.7	51
23	Environmental drivers of diversity in Subtropical Highland Grasslands. <i>Perspectives in Plant Ecology, Evolution and Systematics</i> , 2015, 17, 360-368.	2.7	47
24	Revisiting the Non-Animal Peroxidase Superfamily. <i>Trends in Plant Science</i> , 2015, 20, 807-813.	8.8	27
25	Genome-wide annotation of the soybean WRKY family and functional characterization of genes involved in response to <i>Phakopsora pachyrhizi</i> infection. <i>BMC Plant Biology</i> , 2014, 14, 236.	3.6	79
26	Uncovering legumain genes in rice. <i>Plant Science</i> , 2014, 215-216, 100-109.	3.6	18
27	New insights on the evolution of Leafy cotyledon1 (LEC1) type genes in vascular plants. <i>Genomics</i> , 2014, 103, 380-387.	2.9	30
28	De novo assembly of <i>Eugenia uniflora</i> L. transcriptome and identification of genes from the terpenoid biosynthesis pathway. <i>Plant Science</i> , 2014, 229, 238-246.	3.6	33
29	MAEWEST Expression in Flower Development of Two <i>Petunia</i> Species. <i>International Journal of Molecular Sciences</i> , 2013, 14, 13796-13807.	4.1	3
30	Heavy metal-associated isoprenylated plant protein (HIPP): characterization of a family of proteins exclusive to plants. <i>FEBS Journal</i> , 2013, 280, 1604-1616.	4.7	187
31	Phylogeographical patterns shed light on evolutionary process in South America. <i>Molecular Ecology</i> , 2013, 22, 1193-1213.	3.9	362
32	Phylogenetic analysis of the genus <i>Hexachlamys</i> (Myrtaceae) based on plastid and nuclear DNA sequences and their taxonomic implications. <i>Botanical Journal of the Linnean Society</i> , 2013, 172, 532-543.	1.6	12
33	Analysis of castor bean ribosome-inactivating proteins and their gene expression during seed development. <i>Genetics and Molecular Biology</i> , 2013, 36, 74-86.	1.3	18
34	Large-scale phylogeography of the disjunct Neotropical tree species <i>Schizolobium parahyba</i> (Fabaceae-Caesalpinioideae). <i>Molecular Phylogenetics and Evolution</i> , 2012, 65, 174-182.	2.7	40
35	Identification and in silico characterization of soybean trihelix-GT and bHLH transcription factors involved in stress responses. <i>Genetics and Molecular Biology</i> , 2012, 35, 233-246.	1.3	42
36	Identifying Conserved and Novel MicroRNAs in Developing Seeds of <i>Brassica napus</i> Using Deep Sequencing. <i>PLoS ONE</i> , 2012, 7, e50663.	2.5	61

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37	Biosynthesis of Triacylglycerols (TAGs) in Plants and algae. International Journal of Plant Biology, 2011, 2, e10.	2.6	81
38	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
39	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