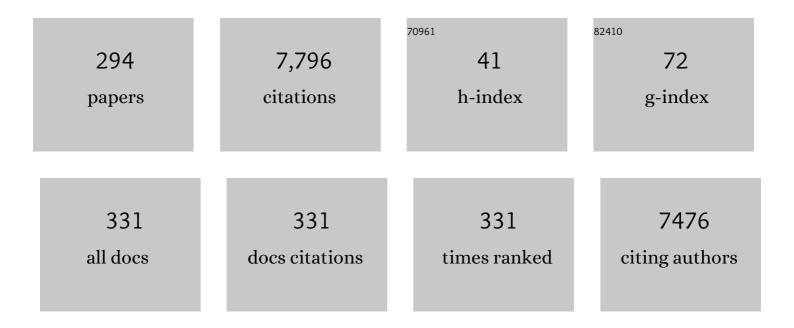
Anete Pereira Souza

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	The genome sequence of the plant pathogen Xylella fastidiosa. Nature, 2000, 406, 151-157.	13.7	827
2	OneMap: software for genetic mapping in outcrossing species. Hereditas, 2007, 144, 78-79.	0.5	326
3	Comparison of RAPD, RFLP, AFLP and SSR markers for diversity studies in tropical maize inbred lines. Genetics and Molecular Biology, 2004, 27, 579-588.	0.6	162
4	Analysis of genetic similarity detected by AFLP and coefficient of parentage among genotypes of sugar cane (Saccharum spp.). Theoretical and Applied Genetics, 2002, 104, 30-38.	1.8	141
5	Building the sugarcane genome for biotechnology and identifying evolutionary trends. BMC Genomics, 2014, 15, 540.	1.2	136
6	SNP genotyping allows an in-depth characterisation of the genome of sugarcane and other complex autopolyploids. Scientific Reports, 2013, 3, 3399.	1.6	129
7	De Novo Assembly and Transcriptome Analysis of Contrasting Sugarcane Varieties. PLoS ONE, 2014, 9, e88462.	1.1	129
8	Genetic distance of inbred lines and prediction of maize single-cross performance using RAPD markers. Theoretical and Applied Genetics, 1997, 94, 1023-1030.	1.8	115
9	Survey in the sugarcane expressed sequence tag database (SUCEST) for simple sequence repeats. Genome, 2004, 47, 795-804.	0.9	113
10	De Novo Assembly and Transcriptome Analysis of the Rubber Tree (Hevea brasiliensis) and SNP Markers Development for Rubber Biosynthesis Pathways. PLoS ONE, 2014, 9, e102665.	1.1	113
11	InP Nanowire Biosensor with Tailored Biofunctionalization: Ultrasensitive and Highly Selective Disease Biomarker Detection. Nano Letters, 2017, 17, 5938-5949.	4.5	111
12	Comparison of similarity coefficients used for cluster analysis with dominant markers in maize (Zea) Tj ETQq0 0) rgBT /Ov	erlock 10 Tf 5 104
13	Development of an integrated genetic map of a sugarcane (Saccharum spp.) commercial cross, based on a maximum-likelihood approach for estimation of linkage and linkage phases. Theoretical and Applied Genetics, 2006, 112, 298-314.	1.8	101
14	A trans-splicing model for the expression of the tripartite nad5 gene in wheat and maize mitochondria Plant Cell, 1991, 3, 1363-1378.	3.1	92
15	GBS-based single dosage markers for linkage and QTL mapping allow gene mining for yield-related traits in sugarcane. BMC Genomics, 2017, 18, 72.	1.2	91
16	Characterization of new polymorphic functional markers for sugarcane. Genome, 2009, 52, 191-209.	0.9	87

17	Mapping QTL for Grain Yield and Plant Traits in a Tropical Maize Population. Molecular Breeding, 2006, 17, 227-239.	1.0	85

Development, characterization, and comparative analysis of polymorphism at common bean SSR loci isolated from genic and genomic sources. Genome, 2007, 50, 266-277. 0.9 18 85

#	Article	IF	CITATIONS
19	Characterization of novel sugarcane expressed sequence tag microsatellites and their comparison with genomic SSRs. Plant Breeding, 2006, 125, 378-384.	1.0	84
20	New Hydrocarbon Degradation Pathways in the Microbial Metagenome from Brazilian Petroleum Reservoirs. PLoS ONE, 2014, 9, e90087.	1.1	83
21	Functional integrated genetic linkage map based on EST-markers for a sugarcane (Saccharum spp.) commercial cross. Molecular Breeding, 2007, 20, 189-208.	1.0	79
22	Molecular mapping in tropical maize (Zea mays L.) using microsatellite markers. 2. Quantitative trait loci (QTL) for grain yield, plant heigth, ear height and grain moisture. Hereditas, 2004, 139, 107-115.	0.5	77
23	Genetic Breeding and Diversity of the Genus Passiflora: Progress and Perspectives in Molecular and Genetic Studies. International Journal of Molecular Sciences, 2014, 15, 14122-14152.	1.8	75
24	A mixed model QTL analysis for sugarcane multiple-harvest-location trial data. Theoretical and Applied Genetics, 2012, 124, 835-849.	1.8	73
25	QTL Mapping of Growth-Related Traits in a Full-Sib Family of Rubber Tree (Hevea brasiliensis) Evaluated in a Sub-Tropical Climate. PLoS ONE, 2013, 8, e61238.	1.1	72
26	Multiple-Geographic-Scale Genetic Structure of Two Mangrove Tree Species: The Roles of Mating System, Hybridization, Limited Dispersal and Extrinsic Factors. PLoS ONE, 2015, 10, e0118710.	1.1	71
27	Genetic diversity in tropical maize inbred lines: heterotic group assignment and hybrid performance determined by RFLP markers. Plant Breeding, 2000, 119, 491-496.	1.0	70
28	Tropical maize germplasm: what can we say about its genetic diversity in the light of molecular markers?. Theoretical and Applied Genetics, 2005, 111, 1288-1299.	1.8	69
29	Structure of genetic diversity among common bean (Phaseolus vulgaris L.) varieties of Mesoamerican and Andean origins using new developed microsatellite markers. Genetic Resources and Crop Evolution, 2007, 54, 1747-1762.	0.8	65
30	The Biotechnology Roadmap for Sugarcane Improvement. Tropical Plant Biology, 2010, 3, 75-87.	1.0	62
31	Expression of <i>Xylella fastidiosa</i> Fimbrial and Afimbrial Proteins during Biofilm Formation. Applied and Environmental Microbiology, 2010, 76, 4250-4259.	1.4	62
32	Mapping of a chromosome 15 region involved in limb girdle muscular dystrophy. Human Molecular Genetics, 1994, 3, 285-293.	1.4	59
33	Two genes control aluminum tolerance in maize: Genetic and molecular mapping analyses. Genome, 1999, 42, 475-482.	0.9	58
34	Title is missing!. Euphytica, 2003, 130, 87-99.	0.6	57
35	Permanent Genetic Resources added to Molecular Ecology Resources Database 1 December 2009–31 January 2010. Molecular Ecology Resources, 2010, 10, 576-579.	2.2	56
36	Genetic variation in polyploid forage grass: Assessing the molecular genetic variability in the Paspalumgenus. BMC Genetics, 2013, 14, 50.	2.7	54

#	Article	IF	CITATIONS
37	A genome-wide association study identified loci for yield component traits in sugarcane (Saccharum) Tj ETQq1 1	0.784314 1.1	l rgBT /Over
38	Population genetic structure, introgression, and hybridization in the genus <i>Rhizophora</i> along the Brazilian coast. Ecology and Evolution, 2018, 8, 3491-3504.	0.8	53
39	Functional markers for gene mapping and genetic diversity studies in sugarcane. BMC Research Notes, 2011, 4, 264.	0.6	51
40	QTL mapping for yield components in a tropical maize population using microsatellite markers. Hereditas, 2008, 145, 194-203.	0.5	49
41	Microsatellite-assisted backcross selection in maize. Genetics and Molecular Biology, 2005, 28, 789-797.	0.6	48
42	Carbohydrate-active enzymes in Trichoderma harzianum: a bioinformatic analysis bioprospecting for key enzymes for the biofuels industry. BMC Genomics, 2017, 18, 779.	1.2	48
43	Network of proteins, enzymes and genes linked to biomass degradation shared by Trichoderma species. Scientific Reports, 2018, 8, 1341.	1.6	48
44	Analysis of genomic and functional RFLP derived markers associated with sucrose content, fiber and yield QTLs in a sugarcane (Saccharum spp.) commercial cross. Euphytica, 2010, 172, 313-327.	0.6	46
45	Genetic diversity and population structure analysis of the tropical pasture grass <i>Brachiaria humidicola</i> based on microsatellites, cytogenetics, morphological traits, and geographical origin. Genome, 2010, 53, 698-709.	0.9	46
46	Crystal structure and biochemical characterization of the recombinant ThBgl, a GH1 β-glucosidase overexpressed in Trichoderma harzianum under biomass degradation conditions. Biotechnology for Biofuels, 2016, 9, 71.	6.2	45
47	Genetic Diversity of Giardia duodenalis: Multilocus Genotyping Reveals Zoonotic Potential between Clinical and Environmental Sources in a Metropolitan Region of Brazil. PLoS ONE, 2014, 9, e115489.	1.1	44
48	Mapping QTLs for kernel oil content in a tropical maize population. Euphytica, 2004, 137, 251-259.	0.6	43
49	Analysis of three sugarcane homo/homeologous regions suggests independent polyploidization events of <i>Saccharum officinarum</i> and <i>Saccharum spontaneum</i> . Genome Biology and Evolution, 2017, 9, evw293.	1.1	42
50	Transcriptome Profile of Trichoderma harzianum IOC-3844 Induced by Sugarcane Bagasse. PLoS ONE, 2014, 9, e88689.	1.1	41
51	QTL mapping including codominant SNP markers with ploidy level information in a sugarcane progeny. Euphytica, 2016, 211, 1-16.	0.6	39
52	Evidence of Allopolyploidy in Urochloa humidicola Based on Cytological Analysis and Genetic Linkage Mapping. PLoS ONE, 2016, 11, e0153764.	1.1	39
53	Molecular mapping in tropical maize (Zea mays L.) using microsatellite markers. 1. Map construction and localization of loci showing distorted segregation. Hereditas, 2004, 139, 96-106.	0.5	37
54	Microsatellites from rubber tree (Hevea brasiliensis) for genetic diversity analysis and cross-amplification in six Hevea wild species. Conservation Genetics Resources, 2009, 1, 75-79.	0.4	37

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55	An engineered GH1 β-glucosidase displays enhanced glucose tolerance and increased sugar release from lignocellulosic materials. Scientific Reports, 2019, 9, 4903.	1.6	36
56	Detection of genetic resistance to cocoa black pod disease caused by three Phytophthora species. Euphytica, 2015, 206, 677-687.	0.6	35
57	Somaclonal-variation-induced aluminum-sensitive mutant from an aluminum-inbred maize tolerant line. Plant Cell Reports, 1997, 16, 686-691.	2.8	34
58	A novel linkage map of sugarcane with evidence for clustering of retrotransposon-based markers. BMC Genetics, 2012, 13, 51.	2.7	34
59	A history of passion fruit woodiness disease with emphasis on the current situation in Brazil and prospects for Brazilian passion fruit cultivation. European Journal of Plant Pathology, 2014, 139, 261-270.	0.8	34
60	Mixed Modeling of Yield Components and Brown Rust Resistance in Sugarcane Families. Agronomy Journal, 2016, 108, 1824-1837.	0.9	34
61	Inheritance of growth habit detected by genetic linkage analysis using microsatellites in the common bean (Phaseolus vulgaris L.). Molecular Breeding, 2011, 27, 549-560.	1.0	33
62	Genetic diversity in cultivated carioca common beans based on molecular marker analysis. Genetics and Molecular Biology, 2011, 34, 88-102.	0.6	32
63	De Novo Transcriptome Assembly for the Tropical Grass Panicum maximum Jacq. PLoS ONE, 2013, 8, e70781.	1.1	32
64	Leaf-, panel- and latex-expressed sequenced tags from the rubber tree (Hevea brasiliensis) under cold-stressed and suboptimal growing conditions: the development of gene-targeted functional markers for stress response. Molecular Breeding, 2014, 34, 1035-1053.	1.0	32
65	Genetic Diversity Strategy for the Management and Use of Rubber Genetic Resources: More than 1,000 Wild and Cultivated Accessions in a 100-Genotype Core Collection. PLoS ONE, 2015, 10, e0134607.	1.1	32
66	Genetic Mapping With Allele Dosage Information in Tetraploid Urochloa decumbens (Stapf) R. D. Webster Reveals Insights Into Spittlebug (Notozulia entreriana Berg) Resistance. Frontiers in Plant Science, 2019, 10, 92.	1.7	32
67	Genetic-diversity assessed by microsatellites in tropical maize populations submitted to a high-intensity reciprocal recurrent selection. Euphytica, 2003, 134, 277-286.	0.6	31
68	Microsatellite marker development for the rubber tree (Hevea brasiliensis): characterization and cross-amplification in wild Hevea species. BMC Research Notes, 2012, 5, 329.	0.6	31
69	Isolation and characterization of microsatellite loci in <i>Pitcairnia albiflos</i> (Bromeliaceae), an endemic bromeliad from the Atlantic Rainforest, and crossâ€amplification in other species. Molecular Ecology Resources, 2008, 8, 980-982.	2.2	30
70	Production of a recombinant swollenin from Trichoderma harzianum in Escherichia coli and its potential synergistic role in biomass degradation. Microbial Cell Factories, 2017, 16, 83.	1.9	29
71	Genetic diversity of reintroduced tree populations in restoration plantations of the Brazilian Atlantic Forest. Restoration Ecology, 2018, 26, 694-701.	1.4	29
72	Genomic Selection in Rubber Tree Breeding: A Comparison of Models and Methods for Managing G×E Interactions. Frontiers in Plant Science, 2019, 10, 1353.	1.7	28

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73	Genetic Diversity and Population Structure of the Brachiaria brizantha Germplasm. Tropical Plant Biology, 2011, 4, 157-169.	1.0	27
74	High-Resolution Genetic Map and QTL Analysis of Growth-Related Traits of Hevea brasiliensis Cultivated Under Suboptimal Temperature and Humidity Conditions. Frontiers in Plant Science, 2018, 9, 1255.	1.7	27
75	Evaluating genetic relationships between tropical maize inbred lines by means of AFLP profiling. Hereditas, 2004, 140, 24-33.	0.5	26
76	Molecular Phylogeny of the Neotropical Genus Christensonella (Orchidaceae, Maxillariinae): Species Delimitation and Insights into Chromosome Evolution. Annals of Botany, 2008, 102, 491-507.	1.4	26
77	Elevation as a barrier: genetic structure for an <scp>A</scp> tlantic rain forest tree (<i><scp>B</scp>athysa australis</i>) in the <scp>S</scp> erra do <scp>M</scp> ar mountain range, <scp>SE</scp> Brazil. Ecology and Evolution, 2015, 5, 1919-1931.	0.8	26
78	The wheat mitochondrial genome contains an ORF showing sequence homology to the gene encoding the subunit 6 of the NADH-ubiquinone oxidoreductase. Plant Molecular Biology, 1992, 20, 395-404.	2.0	25
79	Three ways to distinguish species: using behavioural, ecological, and molecular data to tell apart two closely related ants, <i>Camponotus renggeri</i> and <i>Camponotus rufipes</i> (Hymenoptera: Formicidae). Zoological Journal of the Linnean Society, 2016, 176, 170-181.	1.0	25
80	Permanent Genetic Resources added to Molecular Ecology Resources Database 1 February 2011–31 March 2011. Molecular Ecology Resources, 2011, 11, 757-758.	2.2	24
81	Development and characterization of microsatellite markers for the wild South American <i>Passiflora cincinnata</i> (Passifloraceae). American Journal of Botany, 2012, 99, e170-2.	0.8	23
82	Development of a recombinant fusion protein based on the dynein light chain LC8 for non-viral gene delivery. Journal of Controlled Release, 2012, 159, 222-231.	4.8	23
83	Species distribution and introgressive hybridization of two Avicennia species from the Western Hemisphere unveiled by phylogeographic patterns. BMC Evolutionary Biology, 2015, 15, 61.	3.2	23
84	Gene Duplication in the Sugarcane Genome: A Case Study of Allele Interactions and Evolutionary Patterns in Two Genic Regions. Frontiers in Plant Science, 2019, 10, 553.	1.7	23
85	RAPD Genomic Fingerprinting Differentiates Thiobacillus ferrooxidans Strains. Systematic and Applied Microbiology, 1996, 19, 91-95.	1.2	22
86	New microsatellite markers for wild and commercial species of <i>Passiflora</i> (Passifloraceae) and crossâ€amplification. Applications in Plant Sciences, 2014, 2, 1300061.	0.8	22
87	Development of single nucleotide polymorphism markers in the large and complex rubber tree genome using next-generation sequence data. Molecular Breeding, 2016, 36, 1.	1.0	22
88	The Genetic Diversity, Conservation, and Use of Passion Fruit (Passiflora spp.). Sustainable Development and Biodiversity, 2016, , 215-231.	1.4	22
89	QTL mapping and identification of corresponding genomic regions for black pod disease resistance to three Phytophthora species in Theobroma cacao L Euphytica, 2018, 214, 1.	0.6	22
90	High-Resolution Linkage Map With Allele Dosage Allows the Identification of Regions Governing Complex Traits and Apospory in Guinea Grass (Megathyrsus maximus). Frontiers in Plant Science, 2020, 11, 15.	1.7	22

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91	Composition of theLecointeaclade (Leguminosae, Papilionoideae, Swartzieae), a reÂevaluation based on combined evidence from morphology and molecular data. Taxon, 2004, 53, 1007-1018.	0.4	21
92	Highly-sensitive and label-free indium phosphide biosensor for early phytopathogen diagnosis. Biosensors and Bioelectronics, 2012, 36, 62-68.	5.3	21
93	Phylogeny and biogeography of the genus <i>Zornia</i> (Leguminosae: Papilionoideae: Dalbergieae). Taxon, 2013, 62, 723-732.	0.4	21
94	Microsatellite loci for Urochloa decumbens (Stapf) R.D. Webster and cross-amplification in other Urochloa species. BMC Research Notes, 2016, 9, 152.	0.6	21
95	Genome-wide approaches for the identification of markers and genes associated with sugarcane yellow leaf virus resistance. Scientific Reports, 2021, 11, 15730.	1.6	21
96	QTL mapping for reaction to Phaeosphaeria leaf spot in a tropical maize population. Theoretical and Applied Genetics, 2009, 119, 1361-1369.	1.8	20
97	Characterization and selection of passion fruit (yellow and purple) accessions based on molecular markers and disease reactions for use in breeding programs. Euphytica, 2015, 202, 345-359.	0.6	20
98	The Antitoxin Protein of a Toxin-Antitoxin System from Xylella fastidiosa Is Secreted via Outer Membrane Vesicles. Frontiers in Microbiology, 2016, 7, 2030.	1.5	20
99	Functional metagenomics of oil-impacted mangrove sediments reveals high abundance of hydrolases of biotechnological interest. World Journal of Microbiology and Biotechnology, 2017, 33, 141.	1.7	20
100	Linkage Disequilibrium and Population Structure in Wild and Cultivated Populations of Rubber Tree (Hevea brasiliensis). Frontiers in Plant Science, 2018, 9, 815.	1.7	20
101	Multi-trait multi-environment quantitative trait loci mapping for a sugarcane commercial cross provides insights on the inheritance of important traits. Molecular Breeding, 2015, 35, 175.	1.0	19
102	Deep expression analysis reveals distinct cold-response strategies in rubber tree (Hevea brasiliensis). BMC Genomics, 2019, 20, 455.	1.2	19
103	Local adaptation of a dominant coastal tree to freshwater availability and solar radiation suggested by genomic and ecophysiological approaches. Scientific Reports, 2019, 9, 19936.	1.6	19
104	Machine learning approaches reveal genomic regions associated with sugarcane brown rust resistance. Scientific Reports, 2020, 10, 20057.	1.6	19
105	Mapping analysis of the Xylella fastidiosa genome. Nucleic Acids Research, 2000, 28, 3100-3104.	6.5	18
106	Reciprocal recurrent selection effects on the genetic structure of tropical maize populations assessed at microsatellite loci. Genetics and Molecular Biology, 2003, 26, 355-364.	0.6	18
107	Genetic analysis of forest species Eugenia uniflora L. through of newly developed SSR markers. Conservation Genetics, 2008, 9, 1281-1285.	0.8	18
108	Isolation and characterization of microsatellite loci in the Brazilian orchid Epidendrum fulgens. Conservation Genetics, 2008, 9, 1661-1663.	0.8	18

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109	Isolation and characterization of microsatellite loci in Paspalum notatum Flüggé (Poaceae). Conservation Genetics, 2009, 10, 1977-1980.	0.8	18
110	Isolation and characterization of microsatellite loci in the black pepper, Piper nigrum L. (piperaceae). Conservation Genetics Resources, 2009, 1, 209-212.	0.4	18
111	Development of microsatellite markers for Brachiaria humidicola (Rendle) Schweick. Conservation Genetics Resources, 2009, 1, 475-479.	0.4	18
112	Microsatellites for the mangrove tree <i>Avicennia germinans</i> (Acanthaceae): Tools for hybridization and mating system studies. American Journal of Botany, 2010, 97, e79-81.	0.8	18
113	A novel protein refolding protocol for the solubilization and purification of recombinant peptidoglycan-associated lipoprotein from Xylella fastidiosa overexpressed in Escherichia coli. Protein Expression and Purification, 2012, 82, 284-289.	0.6	18
114	QTL detection for growth and latex production in a full-sib rubber tree population cultivated under suboptimal climate conditions. BMC Plant Biology, 2018, 18, 223.	1.6	18
115	"Targeted Sequencing by Gene Synteny,―a New Strategy for Polyploid Species: Sequencing and Physical Structure of a Complex Sugarcane Region. Frontiers in Plant Science, 2018, 9, 397.	1.7	18
116	The Wild Sugarcane and Sorghum Kinomes: Insights Into Expansion, Diversification, and Expression Patterns. Frontiers in Plant Science, 2021, 12, 668623.	1.7	18
117	Microsatellites for genetic studies and breeding programs in common bean. Pesquisa Agropecuaria Brasileira, 2007, 42, 589-592.	0.9	17
118	Correlação da heterose de hÃbridos de milho com divergência genética entre linhagens. Pesquisa Agropecuaria Brasileira, 2007, 42, 811-816.	0.9	17
119	Structural and kinetic characterization of a maize aldose reductase. Plant Physiology and Biochemistry, 2009, 47, 98-104.	2.8	17
120	A novel and enantioselective epoxide hydrolase from Aspergillus brasiliensis CCT 1435: Purification and characterization. Protein Expression and Purification, 2013, 91, 175-183.	0.6	17
121	Recent Introduction and Recombination in Colletotrichum acutatum Populations Associated with Citrus Postbloom Fruit Drop Epidemics in São Paulo, Brazil. Phytopathology, 2014, 104, 769-778.	1.1	17
122	Characterization of microsatellite markers developed from Prosopis rubriflora and Prosopis ruscifolia (Leguminosae - Mimosoideae), legume species that are used as models for genetic diversity studies in Chaquenian areas under anthropization in South America. BMC Research Notes, 2014, 7, 375.	0.6	17
123	Analysis of Genomic Regions of Trichoderma harzianum IOC-3844 Related to Biomass Degradation. PLoS ONE, 2015, 10, e0122122.	1.1	17
124	Identification of oxidoreductases from the petroleum Bacillus safensis strain. Biotechnology Reports (Amsterdam, Netherlands), 2015, 8, 152-159.	2.1	17
125	Impacts of landscape composition, marginality of distribution, soil fertility and climatic stability on the patterns of woody plant endemism in the Cerrado. Global Ecology and Biogeography, 2019, 28, 904-916.	2.7	17
126	Development and characterization of microsatellite markers for turmeric (<i>Curcuma longa</i>). Plant Breeding, 2009, 129, 570.	1.0	16

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127	Mating systems in tropical forages: Stylosanthes capitata Vog. and Stylosanthes guianensis (Aubl.) Sw Euphytica, 2011, 178, 185-193.	0.6	16
128	Development of a non-viral gene delivery vector based on the dynein light chain Rp3 and the TAT peptide. Journal of Biotechnology, 2014, 173, 10-18.	1.9	16
129	Isolation and characterization of microsatellite markers for Brachiaria brizantha (Hochst. ex A. Rich.) Stap. Conservation Genetics, 2009, 10, 1873-1876.	0.8	15
130	Overexpression and purification of PWL2D, a mutant of the effector protein PWL2 from Magnaporthe grisea. Protein Expression and Purification, 2010, 74, 24-31.	0.6	15
131	Molecular Genetic Variability of Commercial and Wild Accessions of Passion Fruit (Passiflora spp.) Targeting ex Situ Conservation and Breeding. International Journal of Molecular Sciences, 2014, 15, 22933-22959.	1.8	15
132	In vitro Determination of Extracellular Proteins from Xylella fastidiosa. Frontiers in Microbiology, 2016, 7, 2090.	1.5	15
133	Leaf transcriptome of two highly divergent genotypes of Urochloa humidicola (Poaceae), a tropical polyploid forage grass adapted to acidic soils and temporary flooding areas. BMC Genomics, 2016, 17, 910.	1.2	15
134	Of mammals and bacteria in a rainforest: Temporal dynamics of soil bacteria in response to simulated N pulse from mammalian urine. Functional Ecology, 2018, 32, 773-784.	1.7	15
135	Genetic Structure and Molecular Diversity of Cacao Plants Established as Local Varieties for More than Two Centuries: The Genetic History of Cacao Plantations in Bahia, Brazil. PLoS ONE, 2015, 10, e0145276.	1.1	15
136	PCR-RFLP analysis of non-coding regions of cpDNA in Araucaria angustifolia (Bert.) O. Kuntze. Genetics and Molecular Biology, 2007, 30, 423-427.	0.6	14
137	Characterization of an oxidative stress response regulator, homologous to Escherichia coli OxyR, from the phytopathogen Xylella fastidiosa. Protein Expression and Purification, 2011, 75, 204-210.	0.6	14
138	New microsatellite markers developed from Urochloa humidicola (Poaceae) and cross amplification in different Urochloa species. BMC Research Notes, 2011, 4, 523.	0.6	14
139	Genetic diversity, spatial genetic structure and realised seed and pollen dispersal of Himatanthus drasticus (Apocynaceae) in the Brazilian savanna. Conservation Genetics, 2014, 15, 1073-1083.	0.8	14
140	Temporal genetic structure of major dengue vector Aedes aegypti from Manaus, Amazonas, Brazil. Acta Tropica, 2014, 134, 80-88.	0.9	14
141	Genetic structure and diversity of populations of polyploid Tibouchina pulchra Cogn. (Melastomataceae) under different environmental conditions in extremes of an elevational gradient. Tree Genetics and Genomes, 2016, 12, 1.	0.6	14
142	Genetic structure and molecular diversity of Brazilian grapevine germplasm: Management and use in breeding programs. PLoS ONE, 2020, 15, e0240665.	1.1	14
143	The synergistic actions of hydrolytic genes reveal the mechanism of Trichoderma harzianum for cellulose degradation. Journal of Biotechnology, 2021, 334, 1-10.	1.9	14
144	Unravelling Rubber Tree Growth by Integrating GWAS and Biological Network-Based Approaches. Frontiers in Plant Science, 2021, 12, 768589.	1.7	14

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145	Targeted Development of Microsatellite Markers from Inter-Alu Amplification of YAC Clones. Genomics, 1994, 19, 391-393.	1.3	13
146	Isolation and characterization of microsatellite loci in <i>Epidendrum puniceoluteum</i> , an endemic orchid from the Atlantic Rainforest. Molecular Ecology Resources, 2008, 8, 1114-1116.	2.2	13
147	Microsatellite loci for Paspalum atratum (Poaceae) and cross-amplification in other species. American Journal of Botany, 2010, 97, e107-e110.	0.8	13
148	Identification of Stylosanthes guianensis varieties using molecular genetic analysis. AoB PLANTS, 2012, 2012, pls001.	1.2	13
149	Species boundaries inferred from microsatellite markers in the Kielmeyera coriacea complex (Calophyllaceae) and evidence of asymmetric hybridization. Plant Systematics and Evolution, 2013, 299, 731-741.	0.3	13
150	Marker-trait association and epistasis for brown rust resistance in sugarcane. Euphytica, 2015, 203, 533-547.	0.6	13
151	Pollen contamination and nonrandom mating in a Eucalyptus camaldulensis Dehnh seedling seed orchard. Silvae Genetica, 2016, 65, 1-11.	0.4	13
152	Genomic prediction with allele dosage information in highly polyploid species. Theoretical and Applied Genetics, 2022, 135, 723-739.	1.8	13
153	Expression and purification of a small heat shock protein from the plant pathogen Xylella fastidiosa. Protein Expression and Purification, 2004, 33, 297-303.	0.6	12
154	Capacidade combinatória, divergência genética entre linhagens de milho e correlação com heterose. Bragantia, 2008, 67, 639-648.	1.3	12
155	Isolation and characterization of microsatellite loci in the tropical forage legume Stylosanthes guianensis (Aubl.) Sw Conservation Genetics Resources, 2009, 1, 43-46.	0.4	12
156	Isolation and characterization of microsatellite loci in tropical forageStylosanthes capitataVogel. Molecular Ecology Resources, 2009, 9, 192-194.	2.2	12
157	Molecular Diversity and Genetic Structure of Guineagrass (Panicum maximum Jacq.), a Tropical Pasture Grass. Tropical Plant Biology, 2011, 4, 185-202.	1.0	12
158	Using genetic diversity information to establish core collections of Stylosanthes capitata and Stylosanthes macrocephala. Genetics and Molecular Biology, 2012, 35, 847-861.	0.6	12
159	Characterization of the TolB–Pal trans-envelope complex from Xylella fastidiosa reveals a dynamic and coordinated protein expression profile during the biofilm development process. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2015, 1854, 1372-1381.	1.1	12
160	Microsatellite markers for Urochloa humidicola (Poaceae) and their transferability to other Urochloa species. BMC Research Notes, 2015, 8, 83.	0.6	12
161	Population genetic analysis of <i>Giardia duodenalis</i> : genetic diversity and haplotype sharing between clinical and environmental sources. MicrobiologyOpen, 2017, 6, e00424.	1.2	12
162	Molecular responses to freshwater limitation in the mangrove tree <i>Avicennia germinans</i> (Acanthaceae). Molecular Ecology, 2020, 29, 344-362.	2.0	12

#	Article	IF	CITATIONS
163	Coexpression and Transcriptome analyses identify active Apomixis-related genes in Paspalum notatum leaves. BMC Genomics, 2020, 21, 78.	1.2	12
164	An Overview of the Genetics and Genomics of the Urochloa Species Most Commonly Used in Pastures. Frontiers in Plant Science, 2021, 12, 770461.	1.7	12
165	Isolation and characterization of microsatellite markers inAcca sellowiana(Berg) Burret. Molecular Ecology Resources, 2008, 8, 998-1000.	2.2	11
166	Isolation and characterization of microsatellite loci in Colletotrichum acutatum, the causal agent of postbloom fruit drop on citrus. Conservation Genetics Resources, 2011, 3, 651-654.	0.4	11
167	Tapping latex and alleles? The impacts of latex and bark harvesting on the genetic diversity of Himatanthus drasticus (Apocynaceae). Forest Ecology and Management, 2013, 310, 434-441.	1.4	11
168	Molecular genetic variability, population structure and mating system in tropical forages. Tropical Grasslands - Forrajes Tropicales, 2013, 1, 25.	0.1	11
169	Molecular and cytogenetic characterization of an AT-rich satellite DNA family in Urvillea chacoensis Hunz. (Paullinieae, Sapindaceae). Genetica, 2009, 136, 171-177.	0.5	10
170	Microsatellite loci for an endemic stingless bee MeliponaÂseminigraÂmerrillae (Apidae, Meliponini) from Amazon. Conservation Genetics Resources, 2009, 1, 487-490.	0.4	10
171	Development of a genetic linkage map of rubber tree (Hevea braziliensis) based on microsatellite markers. BMC Proceedings, 2011, 5, .	1.8	10
172	Extremophiles as a Model of a Natural Ecosystem: Transcriptional Coordination of Genes Reveals Distinct Selective Responses of Plants Under Climate Change Scenarios. Frontiers in Plant Science, 2018, 9, 1376.	1.7	10
173	Genetic structure of two <i>Prosopis</i> species in Chaco areas: A lack of allelic diversity diagnosis and insights into the allelic conservation of the affected species. Ecology and Evolution, 2018, 8, 6558-6574.	0.8	10
174	Population Genetics of Polyploid Complex Psidium cattleyanum Sabine (Myrtaceae): Preliminary Analyses Based on New Species-Specific Microsatellite Loci and Extension to Other Species of the Genus. Biochemical Genetics, 2021, 59, 219-234.	0.8	10
175	Geographical and environmental contributions to genomic divergence in mangrove forests. Biological Journal of the Linnean Society, 2021, 132, 573-589.	0.7	10
176	Genomic diversity is similar between Atlantic Forest restorations and natural remnants for the native tree Casearia sylvestris Sw PLoS ONE, 2018, 13, e0192165.	1.1	10
177	Cloning, expression, and purification of the virulence-associated protein D from Xylella fastidiosa. Protein Expression and Purification, 2004, 37, 320-326.	0.6	9
178	Cytological behaviour of the somatic hybridsPassiflora edulisf.flavicarpa +P.Âcincinnata. Plant Breeding, 2007, 126, 323-328.	1.0	9
179	New microsatellite markers developed from an enriched microsatellite common bean library. Pesquisa Agropecuaria Brasileira, 2008, 43, 929-936.	0.9	9
180	Polymorphic microsatellite loci for Stylosanthes macrocephala Ferr. et Costa, a tropical forage legume. Conservation Genetics Resources, 2009, 1, 481-485.	0.4	9

#	Article	IF	CITATIONS
181	Genetic diversity of Parides ascanius (Lepidoptera: Papilionidae: Troidini): implications for the conservation of Brazil's most iconic endangered invertebrate species. Conservation Genetics, 2016, 17, 533-546.	0.8	9
182	Genetic Variability, Correlation among Agronomic Traits, and Genetic Progress in a Sugarcane Diversity Panel. Agriculture (Switzerland), 2021, 11, 533.	1.4	9
183	A population genomics appraisal suggests independent dispersals for bitter and sweet manioc in Brazilian Amazonia. Evolutionary Applications, 2020, 13, 342-361.	1.5	9
184	Selective signatures and high genome-wide diversity in traditional Brazilian manioc (Manihot) Tj ETQq0 0 0 rgBT	/Oyerlock	10 ₉ Tf 50 622
185	A new member of the aldo–keto reductase family from the plant pathogen Xylella fastidiosa. Archives of Biochemistry and Biophysics, 2006, 453, 143-150.	1.4	8
186	Development and characterization of 14 microsatellite loci from an enriched genomic library of Eucalyptus camaldulensis Dehnh. Conservation Genetics Resources, 2009, 1, 465-469.	0.4	8
187	Phylogeographic studies of Brazilian "campo-rupestre―species: Wunderlichia mirabilis Riedel ex Baker (Asteraceae). Biotemas, 2011, 22, 17.	0.2	8
188	Development of microsatellite markers in Guineagrass (<i>Panicum maximum</i> Jacq.) and their transferability to other tropical forage grass species. Plant Breeding, 2011, 130, 104-108.	1.0	8
189	Initial biochemical and functional characterization of a 5′-nucleotidase from Xylella fastidiosa related to the human cytosolic 5′-nucleotidase I. Microbial Pathogenesis, 2013, 59-60, 1-6.	1.3	8
190	VapD in Xylella fastidiosa Is a Thermostable Protein with Ribonuclease Activity. PLoS ONE, 2015, 10, e0145765.	1.1	8
191	Characterization of the LysR-type transcriptional regulator YcjZ-like from Xylella fastidiosa overexpressed in Escherichia coli. Protein Expression and Purification, 2015, 113, 72-78.	0.6	8
192	A novel fungal metal-dependent α-l-arabinofuranosidase of family 54 glycoside hydrolase shows expanded substrate specificity. Scientific Reports, 2021, 11, 10961.	1.6	8
193	Adaptation of fluorescent technique for genotyping with new microsatellite markers in common bean. Pesquisa Agropecuaria Brasileira, 2009, 44, 638-644.	0.9	8
194	Network Analysis Reveals Different Cellulose Degradation Strategies Across Trichoderma harzianum Strains Associated With XYR1 and CRE1. Frontiers in Genetics, 2022, 13, 807243.	1.1	8
195	Transcription of succinate dehydrogenase subunit 4 (sdh4) gene in potato: detection of extensive RNA editing and co-transcription with cytochrome oxidase subunit III (cox3) gene. Current Genetics, 2002, 41, 282-290.	0.8	7
196	Isolation and characterization of microsatellite loci in the stingless bee Melipona interrupta manaosensis (Apidae: Meliponini). Conservation Genetics Resources, 2010, 2, 27-30.	0.4	7
197	Molecular diversity, genetic structure and mating system of Calopogonium mucunoides Desv Genetic Resources and Crop Evolution, 2012, 59, 1449-1464.	0.8	7
198	Microsatellite markers for the Cabreúva tree, Myroxylon peruiferum (Fabaceae), an endangered medicinal species from the Brazilian Atlantic Forest. Genetics and Molecular Research, 2014, 13, 6920-6925.	0.3	7

#	Article	IF	CITATIONS
199	Development and Characterization of 32 Microsatellite Loci in Genipa americana (Rubiaceae). Applications in Plant Sciences, 2014, 2, 1300084.	0.8	7
200	Crystal structure of a small heat-shock protein from <i>Xylella fastidiosa</i> reveals a distinct high-order structure. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 222-227.	0.4	7
201	Shelter from the storm: Restored populations of the neotropical tree Myroxylon peruiferum are as genetically diverse as those from conserved remnants. Forest Ecology and Management, 2018, 410, 95-103.	1.4	7
202	Molecular genotyping, diversity studies and high-resolution molecular markers unveiled by microsatellites in Giardia duodenalis. PLoS Neglected Tropical Diseases, 2018, 12, e0006928.	1.3	7
203	Genomic Diversity of Three Brazilian Native Food Crops Based on Double-Digest Restriction Site-Associated DNA Sequencing. Tropical Plant Biology, 2019, 12, 268-281.	1.0	7
204	Testing species hypotheses in the mangrove genus Rhizophora from the Western hemisphere and South Pacific islands. Estuarine, Coastal and Shelf Science, 2021, 248, 106948.	0.9	7
205	A Semi-Automated SNP-Based Approach for Contaminant Identification in Biparental Polyploid Populations of Tropical Forage Grasses. Frontiers in Plant Science, 2021, 12, 737919.	1.7	7
206	Isolation and characterization of microsatellite markers from the stingless bee Nannotrigona testaceicornis. Conservation Genetics Resources, 2009, 1, 97-99.	0.4	6
207	Drosophila mediopunctata microsatellites I: more than a hundred polymorphic loci available for genetic studies. Conservation Genetics Resources, 2009, 1, 297-307.	0.4	6
208	Functional and smallâ€angle Xâ€ray scattering studies of a new stationary phase survival protein E (SurE) from <i>Xylella fastidiosa</i> – evidence of allosteric behaviour. FEBS Journal, 2009, 276, 6751-6762.	2.2	6
209	Potato cultivar identification using molecular markers. Pesquisa Agropecuaria Brasileira, 2010, 45, 110-113.	0.9	6
210	Genetic diversity analysis among pigeonpea genotypes adapted to South American regions based on microsatellite markers. Scientia Agricola, 2011, 68, 431-439.	0.6	6
211	Genetic studies in Centrosema pubescens benth, a tropical forage legume: the mating system, genetic variability and genetic relationships between Centrosema species. Euphytica, 2011, 181, 223-235.	0.6	6
212	New polymorphic microsatellite loci for Theobroma cacao: isolation and characterization of microsatellites from enriched genomic libraries. Biologia Plantarum, 2012, 56, 789-792.	1.9	6
213	Small-angle X-ray scattering and in silico modeling approaches for the accurate functional annotation of an LysR-type transcriptional regulator. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 697-707.	1.1	6
214	Microsatellites for two Neotropical dominant ant species, Camponotus renggeri and C. rufipes (Hymenoptera: Formicidae). Conservation Genetics Resources, 2015, 7, 459-462.	0.4	6
215	A trans-Splicing Model for the Expression of the Tripartite nad5 Gene in Wheat and Maize Mitochondria. Plant Cell, 1991, 3, 1363.	3.1	5
216	The higher plant nad5 mitochondrial gene: a conserved discontinuous transcription pattern. Current Genetics, 1992, 22, 75-82.	0.8	5

#	Article	IF	CITATIONS
217	Identification and characterization of the trnS/pseudo-tRNA/nad3/rps12 gene cluster from Coix lacryma-jobi L: organization, transcription and RNA editing. Plant Science, 2000, 158, 97-105.	1.7	5
218	Microsatellite markers isolated from polyploid Kielmeyera coriacea Mart. & Zucc. (Clusiaceae) from an enriched genomic library. Conservation Genetics, 2009, 10, 1533-1535.	0.8	5
219	Isolation and characterization of microsatellite markers for Cichla monoculus (Agassiz, 1831), an important freshwater fish in the Amazon. Conservation Genetics Resources, 2010, 2, 215-218.	0.4	5
220	Study of closely related species within the Physalaemus cuvieri group (Anura): contribution of microsatellite markers. Genetics and Molecular Research, 2011, 10, 1434-1444.	0.3	5
221	Characterization of the human dynein light chain Rp3 and its use as a non-viral gene delivery vector. Applied Microbiology and Biotechnology, 2014, 98, 3591-3602.	1.7	5
222	Genome Sequence of Bacillus safensis CFA06, Isolated from Biodegraded Petroleum in Brazil. Genome Announcements, 2014, 2, .	0.8	5
223	Genetic diversity of mango accessions (Mangifera indica) using new microsatellite markers and morphological descriptors. Australian Journal of Crop Science, 2016, 10, 1281-1287.	0.1	5
224	New Developments in Sugarcane Genetics and Genomics. , 2017, , 159-174.		5
225	Restriction site associated <scp>DNA</scp> (<scp>RAD</scp>) for de novo sequencing and marker discovery in sugarcane borer, <i>Diatraea saccharalis</i> Fab. (Lepidoptera: Crambidae). Molecular Ecology Resources, 2017, 17, 454-465.	2.2	5
226	Solubilization, Folding, and Purification of a Recombinant Peptidoglycanâ€Associated Lipoprotein (PAL) Expressed in <i>Escherichia coli</i> . Current Protocols in Protein Science, 2018, 92, e53.	2.8	5
227	GENETIC DIVERSITY AND MATING SYSTEM OF Rhizophora mangle L. (RHIZOPHORACEAE) IN NORTHERN BRAZIL REVEALED BY MICROSATELLITE ANALYSIS. Cerne, 2018, 24, 295-302.	0.9	5
228	Elucidating the Clusia criuva species â€~complex': cryptic taxa can exhibit great genetic and geographical variation. Botanical Journal of the Linnean Society, 2019, 190, 67-82.	0.8	5
229	"Integrative genomic analysis of the bioprospection of regulators and accessory enzymes associated with cellulose degradation in a filamentous fungus (Trichoderma harzianum)― BMC Genomics, 2020, 21, 757.	1.2	5
230	Breeding systems and genetic diversity in tropical carpenter ant colonies: different strategies for similar outcomes in Brazilian Cerrado savanna. Zoological Journal of the Linnean Society, 2020, 190, 1020-1035.	1.0	5
231	Development and characterization of microsatellite markers in Astronotus crassipinis (Heckel, 1840). Conservation Genetics Resources, 2009, 1, 277-280.	0.4	4
232	Drosophila mediopunctata microsatellites II: cross-species amplification in the tripunctata group and other Drosophila species. Conservation Genetics Resources, 2009, 1, 281-296.	0.4	4
233	Characterization of microsatellite loci in <i>Himatanthus drasticus</i> (Apocynaceae), a medicinal plant from the Brazilian savanna. American Journal of Botany, 2011, 98, e244-6.	0.8	4
234	Structural characterization of the H-NS protein from Xylella fastidiosa and its interaction with DNA. Archives of Biochemistry and Biophysics, 2012, 526, 22-28.	1.4	4

#	Article	IF	CITATIONS
235	A molecular linkage map for <i>Drosophila mediopunctata</i> confirms synteny with <i>Drosophila melanogaster</i> and suggests a region that controls the variation in the number of abdominal spots. Insect Molecular Biology, 2012, 21, 89-95.	1.0	4
236	First microsatellite markers for Paspalum plicatulum (Poaceae) characterization and cross-amplification in different Paspalum species of the Plicatula group. BMC Research Notes, 2016, 9, 511.	0.6	4
237	Secondary origin, hybridization and sexual reproduction in a diploid–tetraploid contact zone of the facultatively apomictic orchidZygopetalum mackayi. Plant Biology, 2020, 22, 939-948.	1.8	4
238	North-south and climate-landscape-associated pattern of population structure for the Atlantic Forest White Morpho butterflies. Molecular Phylogenetics and Evolution, 2021, 161, 107157.	1.2	4
239	Avaliação de métodos de preservação de amostras de plantas de savanas neotropicais para a obtenção de DNA de alta qualidade para estudos moleculares. Revista Brasileira De Botanica, 2005, 28, 277-283.	0.5	4
240	A first draft genome of the Sugarcane borer, Diatraea saccharalis F1000Research, 0, 9, 1269.	0.8	4
241	Marchantia polymorpha mitochondrial orf identifies transcribed sequence in angiosperm mitochondrial genome. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 2001, 1520, 203-211.	2.4	3
242	Expression and purification of a putative H-NS nucleoid-associated protein from the phytopathogen Xylella fastidiosa. Protein Expression and Purification, 2003, 32, 61-67.	0.6	3
243	Microsatellite markers in tropical legume (Centrosema pubescens Benth): development, characterization, and cross-species amplification in Centrosema sp. Conservation Genetics Resources, 2009, 1, 347-352.	0.4	3
244	Functional and structural studies of the disulfide isomerase <scp>D</scp> sb <scp>C</scp> from the plant pathogen <i><scp>X</scp>ylellaÂfastidiosa</i> reveals a redoxâ€dependent oligomeric modulation <i>inÂvitro</i> . FEBS Journal, 2012, 279, 3828-3843.	2.2	3
245	Isolation and characterization of microsatellites from Scaptotrigona xanthotricha (Apidae,) Tj ETQq1 1 0.784314 r	gBT /Over	lgck 10 Tf 5
246	Isolation and characterization of microsatellite loci in Sisyrinchium (Iridaceae) and cross amplification in other genera. Genetics and Molecular Research, 2016, 15, .	0.3	3
247	Passion Fruit (Passiflora spp.) Breeding. , 2018, , 929-951.		3
248	Microsatellites for the Neotropical Ant, Odontomachus chelifer (Hymenoptera: Formicidae). Journal of Insect Science, 2020, 20, .	0.6	3
249	Sugarcane. , 2012, , 523-561.		3
250	A recombination point is conserved in the mitochondrial genome of higher plant species and located downstream from the cox2 pseudogene in Solanum tuberosum L Genetics and Molecular Biology, 2006, 29, 83-89.	0.6	3
251	Trends in biological data integration for the selection of enzymes and transcription factors related to cellulose and hemicellulose degradation in fungi. 3 Biotech, 2021, 11, 475.	1.1	3
252	Population structure and intraspecific ecological niche differentiation point to lineage divergence promoted by polyploidization in Psidium cattleyanum (Myrtaceae). Tree Genetics and Genomes, 2022, 18, 1.	0.6	3

#	Article	IF	CITATIONS
253	Taxonomically Restricted Genes Are Associated With Responses to Biotic and Abiotic Stresses in Sugarcane (Saccharum spp.). Frontiers in Plant Science, 0, 13, .	1.7	3
254	Isolation and characterization of microsatellite markers in <i>Acca sellowiana</i> (Berg) Burret. Molecular Ecology Resources, 2008, 8, 1417-1419.	2.2	2
255	Isolation and characterization of polymorphic microsatellites for the natural populations of barker frog Physalaemus cuvieri. Conservation Genetics, 2009, 10, 1849-1852.	0.8	2
256	Characterization of 12 microsatellite loci from an enriched genomic library in polyploid Tibouchina pulchra Cogn. (Melastomataceae). Conservation Genetics Resources, 2010, 2, 193-196.	0.4	2
257	Development and characterization of nine microsatellite loci for <i>Sisyrinchium micranthum</i> (Iridaceae). American Journal of Botany, 2012, 99, e402-4.	0.8	2
258	Initial crystallographic studies of a small heat-shock protein from <i>Xylella fastidiosa</i> . Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 535-539.	0.7	2
259	Microsatellite markers for the endangered orchids Cattleya labiata Lindl. and C. warneri T. Moore (Orchidaceae). Conservation Genetics Resources, 2013, 5, 791-794.	0.4	2
260	Microsatellite Markers for Studies with the Carnivorous PlantPhilcoxia minensis(Plantaginaceae). Applications in Plant Sciences, 2015, 3, 1500035.	0.8	2
261	A high level of outcrossing in the vulnerable species Prosopis rubriflora in a Chaco remnant. Australian Journal of Botany, 2018, 66, 360.	0.3	2
262	Development of microsatellite markers for the predatory mite Phytoseiulus macropilis and cross-amplification in three otherÂspecies of phytoseiid mites. Experimental and Applied Acarology, 2021, 83, 1-12.	0.7	2
263	Characterization of microsatellite loci for three species of Tomoplagia (Diptera: Tephritidae) and absence of cross-species amplification. Applied Entomology and Zoology, 2021, 56, 125-132.	0.6	2
264	SUGARCANE: BREEDING METHODS AND GENETIC MAPPING. , 0, , 333-344.		2
265	Three dinucleotide markers on chromosome 21. Human Molecular Genetics, 1994, 3, 381-381.	1.4	1
266	Dinucleotide repeat polymorphism at D15S221. Human Molecular Genetics, 1994, 3, 382-382.	1.4	1
267	Identification of microsatellite loci in Pinus tecunumanii. BMC Proceedings, 2011, 5, P1.	1.8	1
268	Development of microsatellite molecular markers and genetic diversity in Hevea Braziliensis. BMC Proceedings, 2011, 5, .	1.8	1
269	Crystallization and preliminary X-ray analysis of stationary phase survival protein E (SurE) fromXylella fastidiosain two crystal forms. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 464-467.	0.7	1
270	Characterization of 10 Microsatellite Loci forBathysa australis(Rubiaceae). Applications in Plant Sciences, 2013, 1, 1300055.	0.8	1

#	Article	IF	CITATIONS
271	Short Communication New loci of Lychnophora ericoides and transferability to Lychnophora pinaster, endangered medicinal species from Brazil. Genetics and Molecular Research, 2014, 13, 10878-10882.	0.3	1
272	Development and Characterization of Microsatellite Markers forPiptadenia gonoacantha(Fabaceae). Applications in Plant Sciences, 2015, 3, 1400107.	0.8	1
273	A new set of microsatellite loci for <i>Cattleya walkeriana</i> Gardner, an endangered tropical orchid species and its transferability to <i>Cattleya loddigesii</i> Lindl. and <i>Cattleya nobilior</i> Reichenbach. Plant Genetic Resources: Characterisation and Utilisation, 2018, 16, 284-287.	0.4	1
274	Development and cross-validation of microsatellite markers for Rauvolfia weddeliana Müll.Arg. (Apocynaceae) species complex. Revista Brasileira De Botanica, 2018, 41, 681-686.	0.5	1
275	Development and transferability of microsatellite markers for a complex of Aspidosperma Mart. & Zucc. (Apocynaceae) species from South American Seasonally Dry Tropical Forests. Revista Brasileira De Botanica, 2020, 43, 139-145.	0.5	1
276	Development of Microsatellite Markers for Brachiaria brizantha and Germplasm Diversity Characterization of this Tropical Forage Grass. , 2009, , 103-110.		1
277	Microsatellite-dense genetic map: towards genome coverage in a tropical maize (Zea mays L.) population. Revista Brasileira De Botanica, 2009, 32, .	0.5	1
278	Unraveling the variability and genetic structure of barker frog Physalaemus cuvieri (Leiuperinae) populations from different regions of Brazil. Genetics and Molecular Research, 2014, 13, 8055-8065.	0.3	1
279	Temporal Gene Expression in Apical Culms Shows Early Changes in Cell Wall Biosynthesis Genes in Sugarcane. Frontiers in Plant Science, 2021, 12, 736797.	1.7	1
280	Nitrogen pulses increase fungal pathogens in Amazonian lowland tropical rain forests. Journal of Ecology, 2022, 110, 1775-1789.	1.9	1
281	Two dinucleotide repeats tightly linked to D12S91. Human Molecular Genetics, 1994, 3, 382-382.	1.4	0
282	Biophysical Studies Of The Hn-s Protein From Xyllela fastidiosa And Dna. Biophysical Journal, 2009, 96, 410a.	0.2	0
283	Development of microsatellite markers for Pinus maximinoiderived from microsatellite-enriched libraries. BMC Proceedings, 2011, 5, .	1.8	0
284	Isolation and characterization of microsatellite markers in Rhaphiodon vulpinus (Cynodontidae,) Tj ETQq0 0 0 rgB Resources, 2013, 5, 1175-1177.	Г /Overloc 0.4	k 10 Tf 50 2 0
285	Development of microsatellite loci for the fish Poecilia vivipara (Cyprinodontiformes: Poeciliidae). Conservation Genetics Resources, 2013, 6, 383.	0.4	0
286	Microsatellite in Aeschynomene falcata (Leguminosae): diversity, cross-amplification, and chromosome localization. Genetics and Molecular Research, 2014, 13, 10390-10397.	0.3	0
287	Conformational variability of the stationary phase survival protein E from <i>Xylella fastidiosa</i> revealed by X-ray crystallography, small-angle X-ray scattering studies, and normal mode analysis. Proteins: Structure, Function and Bioinformatics, 2017, 85, 1931-1943.	1.5	0
288	Microsatellites for the Neotropical ant, Camponotus leydigi (Hymenoptera: Formicidae). Entomological Science, 2021, 24, 79-84.	0.3	0

#	Article	IF	CITATIONS
289	Host specialization, genetic variability, and differentiation in three species of Tomoplagia from Brazilian rupestrian grasslands. Entomologia Experimentalis Et Applicata, 0, , .	0.7	0
290	Development of Microsatellite Markers for Brachiaria brizantha and Germplasm Diversity Characterization of this Tropical Forage Grass. , 2008, , 1-7.		0
291	In vitro studies of the PilT protein from Xylella fastidiosa twitching motility system. , 0, , .		Ο
292	Development and characterization of microsatellite markers for genetic studies of a Cerrado ant, Odontomachus chelifer (Formicidae: Ponerinae). , 0, , .		0
293	Development and characterization of microsatellite molecular markers for the investigation of polydomy in a Cerrado savanna ant, Camponotus leydigi (Formicidae: Formicinae). , 0, , .		Ο
294	Differential Adaptive Potential and Vulnerability to Climate-Driven Habitat Loss in Brazilian Mangroves. Frontiers in Conservation Science, 2022, 3, .	0.9	0