Anete Pereira Souza

List of Publications by Year in descending order

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		71102	82547
295	7,796	41	72
papers	citations	h-index	g-index
331	331	331	7476
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	Genomic prediction with allele dosage information in highly polyploid species. Theoretical and Applied Genetics, 2022, 135, 723-739.	3.6	13

2 Selective signatures and high genome-wide diversity in traditional Brazilian manioc (Manihot) Tj ETQq0 0 0 rgBT /Oyerlock 10 Tf 50 702

3	Network Analysis Reveals Different Cellulose Degradation Strategies Across Trichoderma harzianum Strains Associated With XYR1 and CRE1. Frontiers in Genetics, 2022, 13, 807243.	2.3	8
4	Differential Adaptive Potential and Vulnerability to Climate-Driven Habitat Loss in Brazilian Mangroves. Frontiers in Conservation Science, 2022, 3, .	1.9	0
5	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.	1.6	3
6	Nitrogen pulses increase fungal pathogens in Amazonian lowland tropical rain forests. Journal of Ecology, 2022, 110, 1775-1789.	4.0	1
7	Testing species hypotheses in the mangrove genus Rhizophora from the Western hemisphere and South Pacific islands. Estuarine, Coastal and Shelf Science, 2021, 248, 106948.	2.1	7
8	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.	1.7	10
9	Microsatellites for the Neotropical ant, Camponotus leydigi (Hymenoptera: Formicidae). Entomological Science, 2021, 24, 79-84.	0.6	0
10	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.	1.6	2
11	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.	1.2	2
12	A novel fungal metal-dependent α-l-arabinofuranosidase of family 54 glycoside hydrolase shows expanded substrate specificity. Scientific Reports, 2021, 11, 10961.	3.3	8
13	Genetic Variability, Correlation among Agronomic Traits, and Genetic Progress in a Sugarcane Diversity Panel. Agriculture (Switzerland), 2021, 11, 533.	3.1	9
14	The synergistic actions of hydrolytic genes reveal the mechanism of Trichoderma harzianum for cellulose degradation. Journal of Biotechnology, 2021, 334, 1-10.	3.8	14
15	The Wild Sugarcane and Sorghum Kinomes: Insights Into Expansion, Diversification, and Expression Patterns. Frontiers in Plant Science, 2021, 12, 668623.	3.6	18
16	North-south and climate-landscape-associated pattern of population structure for the Atlantic Forest White Morpho butterflies. Molecular Phylogenetics and Evolution, 2021, 161, 107157.	2.7	4
17	Genome-wide approaches for the identification of markers and genes associated with sugarcane yellow leaf virus resistance. Scientific Reports, 2021, 11, 15730.	3.3	21
18	Geographical and environmental contributions to genomic divergence in mangrove forests. Biological Journal of the Linnean Society, 2021, 132, 573-589.	1.6	10

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19	A Semi-Automated SNP-Based Approach for Contaminant Identification in Biparental Polyploid Populations of Tropical Forage Grasses. Frontiers in Plant Science, 2021, 12, 737919.	3.6	7
20	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.	2.2	3
21	Unravelling Rubber Tree Growth by Integrating GWAS and Biological Network-Based Approaches. Frontiers in Plant Science, 2021, 12, 768589.	3.6	14
22	An Overview of the Genetics and Genomics of the Urochloa Species Most Commonly Used in Pastures. Frontiers in Plant Science, 2021, 12, 770461.	3.6	12
23	Temporal Gene Expression in Apical Culms Shows Early Changes in Cell Wall Biosynthesis Genes in Sugarcane. Frontiers in Plant Science, 2021, 12, 736797.	3.6	1
24	Molecular responses to freshwater limitation in the mangrove tree <i>Avicennia germinans</i> (Acanthaceae). Molecular Ecology, 2020, 29, 344-362.	3.9	12
25	Genetic structure and molecular diversity of Brazilian grapevine germplasm: Management and use in breeding programs. PLoS ONE, 2020, 15, e0240665.	2.5	14
26	Microsatellites for the Neotropical Ant, Odontomachus chelifer (Hymenoptera: Formicidae). Journal of Insect Science, 2020, 20, .	1.5	3
27	Machine learning approaches reveal genomic regions associated with sugarcane brown rust resistance. Scientific Reports, 2020, 10, 20057.	3.3	19
28	"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.	2.8	5
29	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.	2.3	5
30	Secondary origin, hybridization and sexual reproduction in a diploid–tetraploid contact zone of the facultatively apomictic orchidZygopetalum mackayi. Plant Biology, 2020, 22, 939-948.	3.8	4
31	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.	1.3	1
32	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.	3.6	22
33	A population genomics appraisal suggests independent dispersals for bitter and sweet manioc in Brazilian Amazonia. Evolutionary Applications, 2020, 13, 342-361.	3.1	9
34	Coexpression and Transcriptome analyses identify active Apomixis-related genes in Paspalum notatum leaves. BMC Genomics, 2020, 21, 78.	2.8	12
35	A genome-wide association study identified loci for yield component traits in sugarcane (Saccharum) Tj ETQq1 1	0.784314	rgBT /Overlo
36	Deep expression analysis reveals distinct cold-response strategies in rubber tree (Hevea brasiliensis).	2.8	19

BMC Genomics, 2019, 20, 455.

2.8 19

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37	Genomic Diversity of Three Brazilian Native Food Crops Based on Double-Digest Restriction Site-Associated DNA Sequencing. Tropical Plant Biology, 2019, 12, 268-281.	1.9	7
38	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.	3.6	23
39	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.	1.6	5
40	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.	3.6	32
41	An engineered CH1 l²-glucosidase displays enhanced glucose tolerance and increased sugar release from lignocellulosic materials. Scientific Reports, 2019, 9, 4903.	3.3	36
42	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.	5.8	17
43	Local adaptation of a dominant coastal tree to freshwater availability and solar radiation suggested by genomic and ecophysiological approaches. Scientific Reports, 2019, 9, 19936.	3.3	19
44	Genomic Selection in Rubber Tree Breeding: A Comparison of Models and Methods for Managing G×E Interactions. Frontiers in Plant Science, 2019, 10, 1353.	3.6	28
45	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
46	Population genetic structure, introgression, and hybridization in the genus <i>Rhizophora</i> along the Brazilian coast. Ecology and Evolution, 2018, 8, 3491-3504.	1.9	53
47	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.	3.2	7
48	Network of proteins, enzymes and genes linked to biomass degradation shared by Trichoderma species. Scientific Reports, 2018, 8, 1341.	3.3	48
49	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.	0.8	1
50	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.	3.6	15
51	Genetic diversity of reintroduced tree populations in restoration plantations of the Brazilian Atlantic Forest. Restoration Ecology, 2018, 26, 694-701.	2.9	29
52	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
53	Molecular genotyping, diversity studies and high-resolution molecular markers unveiled by microsatellites in Giardia duodenalis. PLoS Neglected Tropical Diseases, 2018, 12, e0006928.	3.0	7
54	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.	1.2	22

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55	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.	3.6	10
56	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.	3.6	18
57	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.	1.9	10
58	"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.	3.6	18
59	Linkage Disequilibrium and Population Structure in Wild and Cultivated Populations of Rubber Tree (Hevea brasiliensis). Frontiers in Plant Science, 2018, 9, 815.	3.6	20
60	Passion Fruit (Passiflora spp.) Breeding. , 2018, , 929-951.		3
61	Development and cross-validation of microsatellite markers for Rauvolfia weddeliana Müll.Arg. (Apocynaceae) species complex. Revista Brasileira De Botanica, 2018, 41, 681-686.	1.3	1
62	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.	3.6	27
63	A high level of outcrossing in the vulnerable species Prosopis rubriflora in a Chaco remnant. Australian Journal of Botany, 2018, 66, 360.	0.6	2
64	Genomic diversity is similar between Atlantic Forest restorations and natural remnants for the native tree Casearia sylvestris Sw PLoS ONE, 2018, 13, e0192165.	2.5	10
65	Population genetic analysis of <i>Giardia duodenalis</i> : genetic diversity and haplotype sharing between clinical and environmental sources. MicrobiologyOpen, 2017, 6, e00424.	3.0	12
66	Functional metagenomics of oil-impacted mangrove sediments reveals high abundance of hydrolases of biotechnological interest. World Journal of Microbiology and Biotechnology, 2017, 33, 141.	3.6	20
67	GBS-based single dosage markers for linkage and QTL mapping allow gene mining for yield-related traits in sugarcane. BMC Genomics, 2017, 18, 72.	2.8	91
68	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.	0.8	7
69	New Developments in Sugarcane Genetics and Genomics. , 2017, , 159-174.		5
70	InP Nanowire Biosensor with Tailored Biofunctionalization: Ultrasensitive and Highly Selective Disease Biomarker Detection. Nano Letters, 2017, 17, 5938-5949.	9.1	111
71	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.	2.6	0
72	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.	4.0	29

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73	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.	4.8	5
74	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.	2.5	42
75	Carbohydrate-active enzymes in Trichoderma harzianum: a bioinformatic analysis bioprospecting for key enzymes for the biofuels industry. BMC Genomics, 2017, 18, 779.	2.8	48
76	Isolation and characterization of microsatellite loci in Sisyrinchium (Iridaceae) and cross amplification in other genera. Genetics and Molecular Research, 2016, 15, .	0.2	3
77	Genetic diversity of mango accessions (Mangifera indica) using new microsatellite markers and morphological descriptors. Australian Journal of Crop Science, 2016, 10, 1281-1287.	0.3	5
78	The Antitoxin Protein of a Toxin-Antitoxin System from Xylella fastidiosa Is Secreted via Outer Membrane Vesicles. Frontiers in Microbiology, 2016, 7, 2030.	3.5	20
79	In vitro Determination of Extracellular Proteins from Xylella fastidiosa. Frontiers in Microbiology, 2016, 7, 2090.	3.5	15
80	Pollen contamination and nonrandom mating in a Eucalyptus camaldulensis Dehnh seedling seed orchard. Silvae Genetica, 2016, 65, 1-11.	0.8	13
81	Mixed Modeling of Yield Components and Brown Rust Resistance in Sugarcane Families. Agronomy Journal, 2016, 108, 1824-1837.	1.8	34
82	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.	1.6	14
83	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.	2.3	25
84	Development of single nucleotide polymorphism markers in the large and complex rubber tree genome using next-generation sequence data. Molecular Breeding, 2016, 36, 1.	2.1	22
85	QTL mapping including codominant SNP markers with ploidy level information in a sugarcane progeny. Euphytica, 2016, 211, 1-16.	1.2	39
86	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.	2.8	15
87	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.	1.4	4
88	Microsatellite loci for Urochloa decumbens (Stapf) R.D. Webster and cross-amplification in other Urochloa species. BMC Research Notes, 2016, 9, 152.	1.4	21
89	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
90	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.	1.5	9

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91	The Genetic Diversity, Conservation, and Use of Passion Fruit (Passiflora spp.). Sustainable Development and Biodiversity, 2016, , 215-231.	1.7	22
92	Evidence of Allopolyploidy in Urochloa humidicola Based on Cytological Analysis and Genetic Linkage Mapping. PLoS ONE, 2016, 11, e0153764.	2.5	39
93	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.	1.9	26
94	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.	2.5	71
95	Analysis of Genomic Regions of Trichoderma harzianum IOC-3844 Related to Biomass Degradation. PLoS ONE, 2015, 10, e0122122.	2.5	17
96	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.	2.5	32
97	VapD in Xylella fastidiosa Is a Thermostable Protein with Ribonuclease Activity. PLoS ONE, 2015, 10, e0145765.	2.5	8
98	Identification of oxidoreductases from the petroleum Bacillus safensis strain. Biotechnology Reports (Amsterdam, Netherlands), 2015, 8, 152-159.	4.4	17
99	Microsatellites for two Neotropical dominant ant species, Camponotus renggeri and C. rufipes (Hymenoptera: Formicidae). Conservation Genetics Resources, 2015, 7, 459-462.	0.8	6
100	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.	1.2	20
101	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.	2.3	12
102	Detection of genetic resistance to cocoa black pod disease caused by three Phytophthora species. Euphytica, 2015, 206, 677-687.	1.2	35
103	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
104	Microsatellite markers for Urochloa humidicola (Poaceae) and their transferability to other Urochloa species. BMC Research Notes, 2015, 8, 83.	1.4	12
105	Characterization of the LysR-type transcriptional regulator YcjZ-like from Xylella fastidiosa overexpressed in Escherichia coli. Protein Expression and Purification, 2015, 113, 72-78.	1.3	8
106	Development and Characterization of Microsatellite Markers forPiptadenia gonoacantha(Fabaceae). Applications in Plant Sciences, 2015, 3, 1400107.	2.1	1
107	Microsatellite Markers for Studies with the Carnivorous PlantPhilcoxia minensis(Plantaginaceae). Applications in Plant Sciences, 2015, 3, 1500035.	2.1	2
108	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.	2.1	19

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109	Marker-trait association and epistasis for brown rust resistance in sugarcane. Euphytica, 2015, 203, 533-547.	1.2	13
110	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.	2.5	15
111	De Novo Assembly and Transcriptome Analysis of Contrasting Sugarcane Varieties. PLoS ONE, 2014, 9, e88462.	2.5	129
112	New Hydrocarbon Degradation Pathways in the Microbial Metagenome from Brazilian Petroleum Reservoirs. PLoS ONE, 2014, 9, e90087.	2.5	83
113	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.	0.2	1
114	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.	0.2	7
115	Microsatellite in Aeschynomene falcata (Leguminosae): diversity, cross-amplification, and chromosome localization. Genetics and Molecular Research, 2014, 13, 10390-10397.	0.2	0
116	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.	4.1	15
117	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.	4.1	75
118	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.	3.8	16
119	New microsatellite markers for wild and commercial species of <i>Passiflora</i> (Passifloraceae) and crossâ€amplification. Applications in Plant Sciences, 2014, 2, 1300061.	2.1	22
120	Recent Introduction and Recombination in Colletotrichum acutatum Populations Associated with Citrus Postbloom Fruit Drop Epidemics in São Paulo, Brazil. Phytopathology, 2014, 104, 769-778.	2.2	17
121	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.	1.7	34
122	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.	1.5	14
123	Development and Characterization of 32 Microsatellite Loci in Genipa americana (Rubiaceae). Applications in Plant Sciences, 2014, 2, 1300084.	2.1	7
124	Building the sugarcane genome for biotechnology and identifying evolutionary trends. BMC Genomics, 2014, 15, 540.	2.8	136
125	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.	1.4	17
126	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.	3.6	5

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127	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.	2.1	32
128	Temporal genetic structure of major dengue vector Aedes aegypti from Manaus, Amazonas, Brazil. Acta Tropica, 2014, 134, 80-88.	2.0	14
129	Genome Sequence of Bacillus safensis CFA06, Isolated from Biodegraded Petroleum in Brazil. Genome Announcements, 2014, 2, .	0.8	5
130	Transcriptome Profile of Trichoderma harzianum IOC-3844 Induced by Sugarcane Bagasse. PLoS ONE, 2014, 9, e88689.	2.5	41
131	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.	2.5	113
132	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.	2.5	44
133	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.	0.2	1
134	Isolation and characterization of microsatellite markers in Rhaphiodon vulpinus (Cynodontidae,) Tj ETQq0 0 0 rg Resources, 2013, 5, 1175-1177.	gBT /Overlo 0.8	ock 10 Tf 50 4 0
135	Genetic variation in polyploid forage grass: Assessing the molecular genetic variability in the Paspalumgenus. BMC Genetics, 2013, 14, 50.	2.7	54
136	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.	2.3	6
137	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.	2.9	8
138	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.	3.2	11
139	A novel and enantioselective epoxide hydrolase from Aspergillus brasiliensis CCT 1435: Purification and characterization. Protein Expression and Purification, 2013, 91, 175-183.	1.3	17
140	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.	0.9	13
141	Microsatellite markers for the endangered orchids Cattleya labiata Lindl. and C. warneri T. Moore (Orchidaceae). Conservation Genetics Resources, 2013, 5, 791-794.	0.8	2
142	Development of microsatellite loci for the fish Poecilia vivipara (Cyprinodontiformes: Poeciliidae). Conservation Genetics Resources, 2013, 6, 383.	0.8	0
143	Phylogeny and biogeography of the genus <i>Zornia</i> (Leguminosae: Papilionoideae: Dalbergieae). Taxon, 2013, 62, 723-732.	0.7	21
144	Characterization of 10 Microsatellite Loci forBathysa australis(Rubiaceae). Applications in Plant Sciences, 2013, 1, 1300055.	2.1	1

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145	SNP genotyping allows an in-depth characterisation of the genome of sugarcane and other complex autopolyploids. Scientific Reports, 2013, 3, 3399.	3.3	129
146	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.	2.5	72
147	De Novo Transcriptome Assembly for the Tropical Grass Panicum maximum Jacq. PLoS ONE, 2013, 8, e70781.	2.5	32
148	Molecular genetic variability, population structure and mating system in tropical forages. Tropical Grasslands - Forrajes Tropicales, 2013, 1, 25.	0.5	11
149	Identification of Stylosanthes guianensis varieties using molecular genetic analysis. AoB PLANTS, 2012, 2012, pls001.	2.3	13
150	Development and characterization of nine microsatellite loci for <i>Sisyrinchium micranthum</i> (Iridaceae). American Journal of Botany, 2012, 99, e402-4.	1.7	2
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