

Alberto Cenci

List of Publications by Year in descending order

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Version: 2024-02-01

44
papers

2,936
citations

218677

26
h-index

254184

43
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49
all docs

49
docs citations

49
times ranked

3875
citing authors

#	ARTICLE	IF	CITATIONS
1	First Report of <i>Fusarium oxysporum</i> f. sp. <i>cubense</i> Tropical Race 4 Causing Fusarium Wilt in Cavendish Bananas in Peru. <i>Plant Disease</i> , 2022, 106, 2268.	1.4	22
2	A Protocol for Detection of Large Chromosome Variations in Banana Using Next Generation Sequencing. , 2022, , 129-148.		1
3	Unravelling the complex story of intergenomic recombination in ABB allotriploid bananas. <i>Annals of Botany</i> , 2021, 127, 7-20.	2.9	27
4	Genome-wide and comparative phylogenetic analysis of senescence-associated NAC transcription factors in sunflower (<i>Helianthus annuus</i>). <i>BMC Genomics</i> , 2021, 22, 893.	2.8	6
5	Transcriptomic analysis of resistant and susceptible banana corms in response to infection by <i>Fusarium oxysporum</i> f. sp. <i>cubense</i> tropical race 4. <i>Scientific Reports</i> , 2019, 9, 8199.	3.3	40
6	Effect of paleopolyploidy and allopolyploidy on gene expression in banana. <i>BMC Genomics</i> , 2019, 20, 244.	2.8	22
7	Glycosyltransferase Family 61 in Liliopsida (Monocot): The Story of a Gene Family Expansion. <i>Frontiers in Plant Science</i> , 2018, 9, 1843.	3.6	10
8	Three new genome assemblies support a rapid radiation in <i>Musa acuminata</i> (wild banana). <i>Genome Biology and Evolution</i> , 2018, 10, 3129-3140.	2.5	29
9	Evolutionary Analyses of GRAS Transcription Factors in Angiosperms. <i>Frontiers in Plant Science</i> , 2017, 8, 273.	3.6	89
10	A Genome-Wide Association Study on the Seedless Phenotype in Banana (<i>Musa</i> spp.) Reveals the Potential of a Selected Panel to Detect Candidate Genes in a Vegetatively Propagated Crop. <i>PLoS ONE</i> , 2016, 11, e0154448.	2.5	61
11	Differential root transcriptomics in a polyploid non-model crop: the importance of respiration during osmotic stress. <i>Scientific Reports</i> , 2016, 6, 22583.	3.3	34
12	Improvement of the banana <i>Musa acuminata</i> reference sequence using NGS data and semi-automated bioinformatics methods. <i>BMC Genomics</i> , 2016, 17, 243.	2.8	129
13	Assessment of genetic and epigenetic changes during cell culture ageing and relations with somaclonal variation in <i>Coffea arabica</i> . <i>Plant Cell, Tissue and Organ Culture</i> , 2015, 122, 517-531.	2.3	63
14	Data for the characterization of the HSP70 family during osmotic stress in banana, a non-model crop. <i>Data in Brief</i> , 2015, 3, 78-84.	1.0	10
15	Genomic analysis of NAC transcription factors in banana (<i>Musa acuminata</i>) and definition of NAC orthologous groups for monocots and dicots. <i>Plant Molecular Biology</i> , 2014, 85, 63-80.	3.9	91
16	The coffee genome provides insight into the convergent evolution of caffeine biosynthesis. <i>Science</i> , 2014, 345, 1181-1184.	12.6	520
17	The pgip family in soybean and three other legume species: evidence for a birth-and-death model of evolution. <i>BMC Plant Biology</i> , 2014, 14, 189.	3.6	15
18	SNiPloid: A Utility to Exploit High-Throughput SNP Data Derived from RNA-Seq in Allopolyploid Species. <i>International Journal of Plant Genomics</i> , 2013, 2013, 1-6.	2.2	26

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19	The Banana Genome Hub. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat035.	3.0	151
20	Differences in Evolution Rates among Eudicotyledon Species Observed by Analysis of Protein Divergence. Journal of Heredity, 2013, 104, 459-464.	2.4	12
21	High Genetic and Epigenetic Stability in Coffea arabica Plants Derived from Embryogenic Suspensions and Secondary Embryogenesis as Revealed by AFLP, MSAP and the Phenotypic Variation Rate. PLoS ONE, 2013, 8, e56372.	2.5	59
22	Homeologous Gene Expression in Response to Growing Temperature in a Recent Allopolyploid (Coffea) Tj ETQq0 0 0 rgBT /Overlock 10	2.45	50
23	Fast computation of minimum hybridization networks. Bioinformatics, 2012, 28, 191-197.	4.1	56
24	Genome evolution in diploid and tetraploid Coffea species as revealed by comparative analysis of orthologous genome segments. Plant Molecular Biology, 2012, 78, 135-145.	3.9	64
25	Diversity and evolution of coffee trees in light of genomics. Cahiers Agricultures, 2012, 21, 134-142.	0.9	0
26	Multigenic phylogeny and analysis of tree incongruences in Triticeae (Poaceae). BMC Evolutionary Biology, 2011, 11, 181.	3.2	72
27	Organization and molecular evolution of a disease-resistance gene cluster in coffee trees. BMC Genomics, 2011, 12, 240.	2.8	31
28	Comparative sequence analyses indicate that Coffea (Asterids) and Vitis (Rosids) derive from the same paleo-hexaploid ancestral genome. Molecular Genetics and Genomics, 2010, 283, 493-501.	2.1	40
29	Genetic and physical mapping of the SH3 region that confers resistance to leaf rust in coffee tree (Coffea arabica L.). Tree Genetics and Genomes, 2010, 6, 973-980.	1.6	21
30	AN INTEGRATIVE TEST OF THE DEAD-END HYPOTHESIS OF SELFING EVOLUTION IN TRITICEAE (POACEAE). Evolution; International Journal of Organic Evolution, 2010, 64, no-no.	2.3	69
31	High-throughput single nucleotide polymorphism genotyping in wheat (<i>Triticum</i> spp.). Plant Biotechnology Journal, 2009, 7, 364-374.	8.3	60
32	A LTR copia retrotransposon and Mutator transposons interrupt Pgi genes in cultivated and wild wheats. Theoretical and Applied Genetics, 2008, 116, 859-867.	3.6	12
33	Molecular mapping of the novel powdery mildew resistance gene Pm36 introgressed from Triticum turgidum var. dicoccoides in durum wheat. Theoretical and Applied Genetics, 2008, 117, 135-142.	3.6	82
34	Mating system and recombination affect molecular evolution in four <i>Triticeae</i> species. Genetical Research, 2008, 90, 97-109.	0.9	66
35	Grinding up Wheat: A Massive Loss of Nucleotide Diversity Since Domestication. Molecular Biology and Evolution, 2007, 24, 1506-1517.	8.9	331
36	Sequencing of the Triticum monococcum Hardness locus reveals good microcolinearity with rice. Molecular Genetics and Genomics, 2004, 271, 377-386.	2.1	85

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37	PCR identification of durum wheat BAC clones containing genes coding for carotenoid biosynthesis enzymes and their chromosome localization. <i>Genome</i> , 2004, 47, 911-917.	2.0	38
38	Extension of the Messapia x dicoccoides linkage map of <i>Triticum turgidum</i> (L.) Thell. <i>Cellular and Molecular Biology Letters</i> , 2004, 9, 529-41.	7.0	18
39	Genetic analysis of the <i>Aegilops longissima</i> 3S chromosome carrying the Pm13 resistance gene. <i>Euphytica</i> , 2003, 130, 177-183.	1.2	12
40	Construction and characterization of a half million clone BAC library of durum wheat (<i>Triticum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 62	3.6	124
41	The cytogenetics and molecular characteristics of a translocated chromosome 1AS.1AL-1DL with a Glu-D1 locus in durum wheat. <i>Cellular and Molecular Biology Letters</i> , 2002, 7, 559-67.	7.0	12
42	Introgression of <i>Dasypyrum villosum</i> chromatin into common wheat improves grain protein quality. <i>Euphytica</i> , 2001, 117, 67-75.	1.2	60
43	Identification of molecular markers linked to Pm13, an <i>Aegilops longissima</i> gene conferring resistance to powdery mildew in wheat. <i>Theoretical and Applied Genetics</i> , 1999, 98, 448-454.	3.6	78
44	A genetic linkage map of durum wheat. <i>Theoretical and Applied Genetics</i> , 1998, 97, 721-728.	3.6	134