

Albero Acquadro

List of Publications by Year in descending order

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Version: 2024-02-01

82
papers

2,672
citations

126907

33
h-index

197818

49
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89
all docs

89
docs citations

89
times ranked

2770
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-Wide Survey and Development of the First Microsatellite Markers Database (AnCorDB) in <i>Anemone coronaria</i> L.. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3126.	4.1	13
2	Whole-genome assembly of <i>Corylus avellana</i> cv "Tonda Gentile delle Langhe" using linked-reads (10X Genomics). <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	15
3	Oleosin Cor a 15 is a novel allergen for Italian hazelnut allergic children. <i>Pediatric Allergy and Immunology</i> , 2021, 32, 1743-1755.	2.6	11
4	Global range expansion history of pepper (<i>Capsicum</i> spp.) revealed by over 10,000 genebank accessions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	48
5	Transcriptome-Based Identification and Functional Characterization of NAC Transcription Factors Responsive to Drought Stress in <i>Capsicum annuum</i> L.. <i>Frontiers in Genetics</i> , 2021, 12, 743902.	2.3	4
6	Mapping the Genetic Regions Responsible for Key Phenology-Related Traits in the European Hazelnut. <i>Frontiers in Plant Science</i> , 2021, 12, 749394.	3.6	6
7	Transcriptome characterization and expression profiling in chestnut cultivars resistant or susceptible to the gall wasp <i>Dryocosmus kuriphilus</i> . <i>Molecular Genetics and Genomics</i> , 2020, 295, 107-120.	2.1	11
8	Different Phenotypes, Similar Genomes: Three Newly Sequenced <i>Fusarium fujikuroi</i> Strains Induce Different Symptoms in Rice Depending on Temperature. <i>Phytopathology</i> , 2020, 110, 656-665.	2.2	11
9	Transcriptome Analyses and Antioxidant Activity Profiling Reveal the Role of a Lignin-Derived Biostimulant Seed Treatment in Enhancing Heat Stress Tolerance in Soybean. <i>Plants</i> , 2020, 9, 1308.	3.5	39
10	Whole genome resequencing of four Italian sweet pepper landraces provides insights on sequence variation in genes of agronomic value. <i>Scientific Reports</i> , 2020, 10, 9189.	3.3	18
11	"Mind the Gap" Hi-C Technology Boosts Contiguity of the Globe Artichoke Genome in Low-Recombination Regions. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3557-3564.	1.8	12
12	Development of High-Density Genetic Linkage Maps and Identification of Loci for Chestnut Gall Wasp Resistance in <i>Castanea</i> spp.. <i>Plants</i> , 2020, 9, 1048.	3.5	12
13	Simultaneous CRISPR/Cas9 Editing of Three PPO Genes Reduces Fruit Flesh Browning in <i>Solanum melongena</i> L.. <i>Frontiers in Plant Science</i> , 2020, 11, 607161.	3.6	64
14	Identification of a caleosin associated with hazelnut (<i>Corylus avellana</i> L.) oil bodies. <i>Plant Biology</i> , 2020, 22, 404-409.	3.8	6
15	MCSed (Methylation Context Sensitive Enzyme ddRAD): A New Method to Analyze DNA Methylation. <i>Methods in Molecular Biology</i> , 2020, 2093, 47-64.	0.9	4
16	Single Primer Enrichment Technology (SPET) for High-Throughput Genotyping in Tomato and Eggplant Germplasm. <i>Frontiers in Plant Science</i> , 2019, 10, 1005.	3.6	71
17	A chromosome-anchored eggplant genome sequence reveals key events in Solanaceae evolution. <i>Scientific Reports</i> , 2019, 9, 11769.	3.3	179
18	Methylation content sensitive enzyme ddRAD (MCSed): a reference-free, whole genome profiling system to address cytosine/adenine methylation changes. <i>Scientific Reports</i> , 2019, 9, 14864.	3.3	14

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19	Identification of DNA methyltransferases and demethylases in <i>Solanum melongena</i> L., and their transcription dynamics during fruit development and after salt and drought stresses. <i>PLoS ONE</i> , 2019, 14, e0223581.	2.5	20
20	miRNome. <i>Compendium of Plant Genomes</i> , 2019, , 195-203.	0.5	0
21	Genetics and Breeding. <i>Compendium of Plant Genomes</i> , 2019, , 115-128.	0.5	0
22	Insights into the Population Structure and Association Mapping in Globe Artichoke. <i>Compendium of Plant Genomes</i> , 2019, , 129-143.	0.5	0
23	Genome Resequencing. <i>Compendium of Plant Genomes</i> , 2019, , 205-218.	0.5	0
24	Analysis of DNA Methylation Patterns Associated with In Vitro Propagated Globe Artichoke Plants Using an EpiRADseq-Based Approach. <i>Genes</i> , 2019, 10, 263.	2.4	7
25	Genome Database (www.artichokegenome.unito.it). <i>Compendium of Plant Genomes</i> , 2019, , 219-229.	0.5	0
26	Construction of a high-density genetic linkage map and QTL analysis for hazelnut breeding. <i>Acta Horticulturae</i> , 2018, , 25-30.	0.2	0
27	An integrated model to accelerate the development of seed-propagated varieties of globe artichoke. <i>Crop Breeding and Applied Biotechnology</i> , 2018, 18, 72-80.	0.4	7
28	Resequencing of <i>Cynara cardunculus</i> L. genotypes and detection of chromosome-scale single nucleotide polymorphisms (SNPs)/indels. <i>Acta Horticulturae</i> , 2018, , 17-26.	0.2	0
29	Comprehensive Characterization of Simple Sequence Repeats in Eggplant (<i>Solanum melongena</i> L.) Genome and Construction of a Web Resource. <i>Frontiers in Plant Science</i> , 2018, 9, 401.	3.6	40
30	Mapping the genomic regions encoding biomass-related traits in <i>Cynara cardunculus</i> L. <i>Molecular Breeding</i> , 2018, 38, 1.	2.1	6
31	High density SNP mapping and QTL analysis for time of leaf budburst in <i>Corylus avellana</i> L.. <i>PLoS ONE</i> , 2018, 13, e0195408.	2.5	52
32	Genome reconstruction in <i>Cynara cardunculus</i> taxa gains access to chromosome-scale DNA variation. <i>Scientific Reports</i> , 2017, 7, 5617.	3.3	30
33	Genomic assessment in <i>Lactobacillus plantarum</i> links the butyrogenic pathway with glutamine metabolism. <i>Scientific Reports</i> , 2017, 7, 15975.	3.3	25
34	Coding SNPs analysis highlights genetic relationships and evolution pattern in eggplant complexes. <i>PLoS ONE</i> , 2017, 12, e0180774.	2.5	61
35	The genome-wide identification and transcriptional levels of DNA methyltransferases and demethylases in globe artichoke. <i>PLoS ONE</i> , 2017, 12, e0181669.	2.5	13
36	A Genome-Wide Survey of the Microsatellite Content of the Globe Artichoke Genome and the Development of a Web-Based Database. <i>PLoS ONE</i> , 2016, 11, e0162841.	2.5	31

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37	Genome-Wide Identification of BAHD Acyltransferases and In vivo Characterization of HQT-like Enzymes Involved in Caffeoylquinic Acid Synthesis in Globe Artichoke. <i>Frontiers in Plant Science</i> , 2016, 7, 1424.	3.6	39
38	Genomics of <i>Cynara cardunculus</i> through the exploitation of NGS technologies. <i>Acta Horticulturae</i> , 2016, , 1-8.	0.2	0
39	The globe artichoke microsatellite database. <i>Acta Horticulturae</i> , 2016, , 297-300.	0.2	0
40	RAD2seq: an efficient protocol for plant genotyping by sequencing. <i>Acta Horticulturae</i> , 2016, , 1-8.	0.2	4
41	Development of genetic maps and QTL analyses in <i>Cynara cardunculus</i> L.: state of the art. <i>Acta Horticulturae</i> , 2016, , 197-208.	0.2	0
42	Towards a genome-wide association (GWA) mapping approach in globe artichoke. <i>Acta Horticulturae</i> , 2016, , 51-56.	0.2	3
43	The genome sequence of the outbreeding globe artichoke constructed de novo incorporating a phase-aware low-pass sequencing strategy of F1 progeny. <i>Scientific Reports</i> , 2016, 6, 19427.	3.3	106
44	The inheritance of bract pigmentation and fleshy thorns on the globe artichoke capitulum. <i>Euphytica</i> , 2015, 206, 523-531.	1.2	11
45	Mapping yield-associated QTL in globe artichoke. <i>Molecular Breeding</i> , 2014, 34, 615-630.	2.1	21
46	CYNERGIA PROJECT: EXPLOITABILITY OF <i>CYNARA CARDUNCULUS</i> L. AS ENERGY CROP. <i>Acta Horticulturae</i> , 2013, , 109-115.	0.2	10
47	Large-scale transcriptome characterization and mass discovery of SNPs in globe artichoke and its related taxa. <i>Plant Biotechnology Journal</i> , 2012, 10, 956-969.	8.3	33
48	RAD tag sequencing as a source of SNP markers in <i>Cynara cardunculus</i> L. <i>BMC Genomics</i> , 2012, 13, 3.	2.8	82
49	Genetic mapping and identification of QTL for earliness in the globe artichoke/cultivated cardoon complex. <i>BMC Research Notes</i> , 2012, 5, 252.	1.4	39
50	2D DIGE analysis of UV-C radiation-responsive proteins in globe artichoke leaves. <i>Proteomics</i> , 2012, 12, 448-460.	2.2	11
51	Morphology and SSR fingerprinting of newly developed <i>Cynara cardunculus</i> genotypes exploitable as ornamentals. <i>Euphytica</i> , 2012, 184, 311-321.	1.2	33
52	Strain dependent expression of stress response and virulence genes of <i>Listeria monocytogenes</i> in meat juices as determined by microarray. <i>International Journal of Food Microbiology</i> , 2012, 152, 116-122.	4.7	61
53	Proteomic Analysis of PEG-Fractionated UV-C Stress-Response Proteins in Globe Artichoke. <i>Plant Molecular Biology Reporter</i> , 2012, 30, 111-122.	1.8	7
54	Identification of SNP and SSR markers in eggplant using RAD tag sequencing. <i>BMC Genomics</i> , 2011, 12, 304.	2.8	193

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55	Production and fingerprinting of virus-free clones in a reflowering globe artichoke. <i>Plant Cell, Tissue and Organ Culture</i> , 2010, 100, 329-337.	2.3	36
56	Potentiality of <i>Cynara cardunculus</i> L. as energy crop. <i>Journal of Biotechnology</i> , 2010, 150, 165-166.	3.8	12
57	Ontology and diversity of transcript-associated microsatellites mined from a globe artichoke EST database. <i>BMC Genomics</i> , 2009, 10, 454.	2.8	50
58	Proteomics in globe artichoke: Protein extraction and sample complexity reduction by PEG fractionation. <i>Electrophoresis</i> , 2009, 30, 1594-1602.	2.4	21
59	Genetic diversity of globe artichoke landraces from Sicilian small-holdings: implications for evolution and domestication of the species. <i>Conservation Genetics</i> , 2009, 10, 431-440.	1.5	63
60	Isolation and characterization of microsatellite markers from <i>Hibiscus rosa-sinensis</i> (Malvaceae) and cross-species amplifications. <i>Conservation Genetics</i> , 2009, 10, 771-774.	1.5	10
61	Genetic mapping and annotation of genomic microsatellites isolated from globe artichoke. <i>Theoretical and Applied Genetics</i> , 2009, 118, 1573-1587.	3.6	38
62	Construction of a reference molecular linkage map of globe artichoke (<i>Cynara cardunculus</i> var.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 46	3.6	46
63	Isolation and mapping of a C3â€²H gene (CYP98A49) from globe artichoke, and its expression upon UV-C stress. <i>Plant Cell Reports</i> , 2009, 28, 963-974.	5.6	46
64	Potentiality of Methylation-sensitive Amplification Polymorphism (MSAP) in Identifying Genes Involved in Tomato Response to Tomato Yellow Leaf Curl Sardinia Virus. <i>Plant Molecular Biology Reporter</i> , 2008, 26, 156-173.	1.8	46
65	Use of AFLP for differentiation of <i>Metschnikowia pulcherrima</i> strains for postharvest disease biological control. <i>Microbiological Research</i> , 2008, 163, 523-530.	5.3	40
66	Stress-Induced Biosynthesis of Dicafeoylquinic Acids in Globe Artichoke. <i>Journal of Agricultural and Food Chemistry</i> , 2008, 56, 8641-8649.	5.2	108
67	Isolation and functional characterization of a cDNA coding a hydroxycinnamoyltransferase involved in phenylpropanoid biosynthesis in <i>Cynara cardunculus</i> L. <i>BMC Plant Biology</i> , 2007, 7, 14.	3.6	78
68	Retrotransposon-based S-SAP as a platform for the analysis of genetic variation and linkage in globe artichoke. <i>Genome</i> , 2006, 49, 1149-1159.	2.0	14
69	dbEST-derived microsatellite markers in celery (<i>Apium graveolens</i> L. var. dulce). <i>Molecular Ecology Notes</i> , 2006, 6, 1080-1082.	1.7	18
70	A first linkage map of globe artichoke (<i>Cynara cardunculus</i> var. scolymus L.) based on AFLP, S-SAP, M-AFLP and microsatellite markers. <i>Theoretical and Applied Genetics</i> , 2006, 112, 1532-1542.	3.6	82
71	M-AFLP-based protocol for microsatellite loci isolation in <i>Cynara cardunculus</i> L. (Asteraceae). <i>Molecular Ecology Notes</i> , 2005, 5, 272-274.	1.7	36
72	Genetic diversity assessment in cultivated cardoon by AFLP (amplified fragment length polymorphism) and microsatellite markers. <i>Plant Breeding</i> , 2005, 124, 299-304.	1.9	63

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73	Development and characterization of microsatellite markers in <i>Cynara cardunculus</i> L. Genome, 2005, 48, 217-225.	2.0	56
74	Genetic structure of island populations of wild cardoon [<i>Cynara cardunculus</i> L. var. <i>sylvestris</i> (Lamk) Fiori] detected by AFLPs and SSRs. Plant Science, 2005, 169, 199-210.	3.6	45
75	Molecular fingerprinting and evaluation of genetic distances among selected clones of globe artichoke (<i>Cynara cardunculus</i> L. var. <i>scolymus</i> L.). Journal of Horticultural Science and Biotechnology, 2004, 79, 863-870.	1.9	28
76	Development of PCR Primers for a New <i>Fusarium oxysporum</i> Pathogenic on Paris Daisy (<i>Argyranthemum frutescens</i> L.). European Journal of Plant Pathology, 2004, 110, 7-11.	1.7	12
77	Effect of farmers' seed selection on genetic variation of a landrace population of pepper (<i>Capsicum</i>) Tj ETQq1 1 0.784314 rgBT / Overl 1.6 23	1.6	23
78	Analysis of DNA methylation during germination of pepper (<i>Capsicum annuum</i> L.) seeds using methylation-sensitive amplification polymorphism (MSAP). Plant Science, 2004, 166, 169-178.	3.6	109
79	Title is missing!. Genetic Resources and Crop Evolution, 2003, 50, 723-735.	1.6	44
80	RAPD Characterization of <i>Fusarium oxysporum</i> Isolates Pathogenic on <i>Argyranthemum frutescens</i> L.. Journal of Phytopathology, 2003, 151, 30-35.	1.0	19
81	Isolation of microsatellite loci in artichoke (<i>Cynara cardunculus</i> L. var. <i>scolymus</i>). Molecular Ecology Notes, 2003, 3, 37-39.	1.7	35
82	The Population Structure of a Globe Artichoke Worldwide Collection, as Revealed by Molecular and Phenotypic Analyzes. Frontiers in Plant Science, 0, 13, .	3.6	2