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List of Publications by Year
in descending order

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Version: 2024-02-01

115 papers	2,889 citations	172207 29 h-index	223531 46 g-index
117 all docs	117 docs citations	117 times ranked	2881 citing authors

#	Article	IF	Citations
1	Genetically Modified Organism-Free RNA Interference: Exogenous Application of RNA Molecules in Plants. Plant Physiology, 2020, 182, 38-50.	2.3	163
2	Microsatellite high resolution melting (SSR-HRM) analysis for authenticity testing of protected designation of origin (PDO) sweet cherry products. Food Control, 2011, 22, 532-541.	2.8	104
3	Genetic diversity, structure and fruit trait associations in Greek sweet cherry cultivars using microsatellite based (SSR/ISSR) and morpho-physiological markers. Euphytica, 2011, 181, 237-251.	0.6	102
4	Advances of DNA-based methods for tracing the botanical origin of food products. Food Research International, 2014, 60, 163-172.	2.9	91
5	Exploring priming responses involved in peach fruit acclimation to cold stress. Scientific Reports, 2017, 7, 11358.	1.6	83
6	Barcode <scp>DNA</scp> highâ€resolution melting (Barâ€<scp>HRM</scp>) analysis as a novel closeâ€tubed and accurate tool for olive oil forensic use. Journal of the Science of Food and Agriculture, 2013, 93, 2281-2286.	1.7	82
7	The application of Bar-HRM (Barcode DNA-High Resolution Melting) analysis for authenticity testing and quantitative detection of bean crops (Leguminosae) without prior DNA purification. Food Control, 2012, 25, 576-582.	2.8	78
8	Microsatellite and DNA-barcode regions typing combined with High Resolution Melting (HRM) analysis for food forensic uses: A case study on lentils (Lens culinaris). Food Research International, 2012, 46, 141-147.	2.9	77
9	Barcode High Resolution Melting (Bar-HRM) analysis for detection and quantification of PDO â€œFava Santorinisâ€•(Lathyrus clymenum) adulterants. Food Chemistry, 2012, 133, 505-512.	4.2	76
10	Adulterations in Basmati rice detected quantitatively by combined use of microsatellite and fragrance typing with High Resolution Melting (HRM) analysis. Food Chemistry, 2011, 129, 652-659.	4.2	74
11	The Use of Lupin as a Source of Protein in Animal Feeding: Genomic Tools and Breeding Approaches. International Journal of Molecular Sciences, 2019, 20, 851.	1.8	72
12	Ethylene â€“dependent and â€“independent superficial scald resistance mechanisms in â€˜Granny Smithâ€™ apple fruit. Scientific Reports, 2018, 8, 11436.	1.6	65
13	DNA barcode ITS2 coupled with high resolution melting (HRM) analysis for taxonomic identification of Sideritis species growing in Greece. Molecular Biology Reports, 2014, 41, 5147-5155.	1.0	60
14	A fast and accurate method for controlling the correct labeling of products containing buffalo meat using High Resolution Melting (HRM) analysis. Meat Science, 2013, 94, 84-88.	2.7	59
15	Molecular studies of inheritable grafting induced changes in pepper (Capsicum annuum) fruit shape. Scientia Horticulturae, 2013, 149, 2-8.	1.7	55
16	Microsatellite high-resolution melting (SSR-HRM) analysis for genotyping and molecular characterization of an Olea europaea germplasm collection. Plant Genetic Resources: Characterisation and Utilisation, 2014, 12, 273-277.	0.4	49
17	A novel arrangement of zinc finger nuclease system for in vivo targeted genome engineering: the tomato LEC1-LIKE4 gene case. Plant Cell Reports, 2016, 35, 2241-2255.	2.8	44
18	A novel closed-tube method based on high resolution melting (HRM) analysis for authenticity testing and quantitative detection in Greek PDO Feta cheese. Food Chemistry, 2013, 141, 835-840.	4.2	42

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19	Universal ITS2 Barcoding DNA Region Coupled with High-Resolution Melting (HRM) Analysis for Seed Authentication and Adulteration Testing in Leguminous Forage and Pasture Species. Plant Molecular Biology Reporter, 2012, 30, 1322-1328.	1.0	41
20	Barcode High Resolution Melting analysis for forensic uses in nuts: A case study on allergenic hazelnuts (Corylus avellana). Food Research International, 2013, 50, 351-360.	2.9	41
21	Multiplex HRM analysis as a tool for rapid molecular authentication of nine herbal teas. Food Control, 2016, 60, 113-116.	2.8	34
22	Poisonous or non-poisonous plants? DNA-based tools and applications for accurate identification. International Journal of Legal Medicine, 2017, 131, 1-19.	1.2	34
23	Whole-genome resequencing of Cucurbita pepo morphotypes to discover genomic variants associated with morphology and horticulturally valuable traits. Horticulture Research, 2019, 6, 94.	2.9	34
24	Global DNA methylation changes in Cucurbitaceae inter-species grafting. Crop Breeding and Applied Biotechnology, 2015, 15, 112-116.	0.1	33
25	High-resolution melting analysis allowed fast and accurate closed-tube genotyping of Fusarium oxysporum formae speciales complex. FEMS Microbiology Letters, 2012, 334, 16-21.	0.7	32
26	An integrated metabolomic and gene expression analysis identifies heat and calcium metabolic networks underlying postharvest sweet cherry fruit senescence. Planta, 2019, 250, 2009-2022.	1.6	32
27	The study of a SPATULA-like bHLH transcription factor expressed during peach (Prunus persica) fruit development. Plant Physiology and Biochemistry, 2011, 49, 654-663.	2.8	31
28	Sweet Cherry Cultivar Identification by High-Resolution-Melting (HRM) Analysis Using Gene-Based SNP Markers. Plant Molecular Biology Reporter, 2013, 31, 763-768.	1.0	30
29	High resolution melting analysis for quantitative detection of bovine milk in pure water buffalo mozzarella and other buffalo dairy products. International Dairy Journal, 2013, 28, 32-35.	1.5	30
30	Taxonomic Identification of Mediterranean Pines and Their Hybrids Based on the High Resolution Melting (HRM) and trnL Approaches: From Cytoplasmic Inheritance to Timber Tracing. PLoS ONE, 2013, 8, e60945.	1.1	30
31	De novo comparative transcriptome analysis of genes involved in fruit morphology of pumpkin cultivars with extreme size difference and development of EST-SSR markers. Gene, 2017, 622, 50-66.	1.0	29
32	Genetic diversity and metabolic profile of Salvia officinalis populations: implications for advanced breeding strategies. Planta, 2017, 246, 201-215.	1.6	29
33	Is the genetic diversity of small scattered forest tree populations at the southern limits of their range more prone to stochastic events? A wild cherry case study by microsatellite-based markers. Tree Genetics and Genomes, 2011, 7, 1299-1313.	0.6	27
34	Novel insights into the calcium action in cherry fruit development revealed by high-throughput mapping. Plant Molecular Biology, 2020, 104, 597-614.	2.0	27
35	Whole genome re-sequencing of sweet cherry (Prunus avium L.) yields insights into genomic diversity of a fruit species. Horticulture Research, 2020, 7, 60.	2.9	27
36	Fruit quality trait discovery and metabolic profiling in sweet cherry genebank collection in Greece. Food Chemistry, 2021, 342, 128315.	4.2	27

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37	Epigenetics, Epigenomics and Crop Improvement. Advances in Botanical Research, 2018, 86, 287-324.	0.5	26
38	Diversity of morpho-physiological traits in worldwide sweet cherry cultivars of GeneBank collection using multivariate analysis. Scientia Horticulturae, 2015, 197, 381-391.	1.7	25
39	The study of two barley Type I-like MADS-boxgenes as potential targets of epigenetic regulation during seed development. BMC Plant Biology, 2012, 12, 166.	1.6	24
40	Highâ€resolution melting analysis for rapid detection and characterization of <scp>B</scp>otrytis cinerea phenotypes resistant to fenhexamid and boscalid. Plant Pathology, 2014, 63, 1336-1343.	1.2	24
41	A draft genome of sweet cherry (Prunus avium L.) reveals genomeâ€wide and local effects of domestication. Plant Journal, 2020, 103, 1420-1432.	2.8	23
42	Barcoding the major Mediterranean leguminous crops by combining universal chloroplast and nuclear DNA sequence targets. Genetics and Molecular Research, 2012, 11, 2548-2558.	0.3	22
43	Exploring genetic diversity of tomato (Solanum lycopersicum L.)Âgermplasm of genebank collection employing SSR and SCAR markers. Genetic Resources and Crop Evolution, 2019, 66, 1295-1309.	0.8	22
44	Assessing molecular and morpho-agronomical diversity and identification of ISSR markers associated with fruit traits in quince (Cydonia oblonga). Genetics and Molecular Research, 2011, 10, 2729-2746.	0.3	21
45	Comprehensive approaches reveal key transcripts and metabolites highlighting metabolic diversity among three oriental tobacco varieties. Industrial Crops and Products, 2020, 143, 111933.	2.5	21
46	DNA fingerprinting of elite Greek wild cherry (Prunus avium L.) genotypes using microsatellite markers. Forestry, 2010, 83, 527-533.	1.2	20
47	Population genetic variability and distribution of the endangered Greek endemic Cicer graecum under climate change scenarios. AoB PLANTS, 2020, 12, plaa007.	1.2	20
48	Microsatellites: Evolution and Contribution. Methods in Molecular Biology, 2013, 1006, 1-13.	0.4	18
49	Genetic diversity and structure of natural Dactylis glomerata L. populations revealed by morphological and microsatellite-based (SSR/ISSR) markers. Genetics and Molecular Research, 2014, 13, 4226-4240.	0.3	18
50	Genetic diversity of Barbary fig (Opuntia ficus-indica) collection in Greece with ISSR molecular markers. Plant Gene, 2015, 2, 29-33.	1.4	18
51	RNA sequencing-based transcriptome analysis of kiwifruit infected by Botrytis cinerea. Physiological and Molecular Plant Pathology, 2020, 111, 101514.	1.3	18
52	Development of a two-step high-resolution melting (HRM) analysis for screening sequence variants associated with resistance to the QoIs, benzimidazoles and dicarboximides in airborne inoculum ofBotrytis cinerea. FEMS Microbiology Letters, 2014, 360, 126-131.	0.7	17
53	Summer Squash Identification by High-Resolution-Melting (HRM) Analysis Using Gene-Based ESTâ€“SSR Molecular Markers. Plant Molecular Biology Reporter, 2014, 32, 395-405.	1.0	17
54	Î™ntra-species grafting induces epigenetic and metabolic changes accompanied by alterations in fruit size and shape of Cucurbita pepo L.. Plant Growth Regulation, 2019, 87, 93-108.	1.8	17

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55	Pre- and Post-harvest Melatonin Application Boosted Phenolic Compounds Accumulation and Altered Respiratory Characters in Sweet Cherry Fruit. Frontiers in Nutrition, 2021, 8, 695061.	1.6	17
56	The perennial fruit tree proteogenomics atlas: a spatial map of the sweet cherry proteome and transcriptome. Plant Journal, 2022, 109, 1319-1336.	2.8	17
57	Microsatellite genotyping with HRM (High Resolution Melting) analysis for identification of the PGI common bean variety Plake Megalosperma Prespon. European Food Research and Technology, 2012, 234, 501-508.	1.6	16
58	Molecular characterization of Greek pepper (Capsicum annuum L) landraces with neutral (ISSR) and gene-based (SCoT and EST-SSR) molecular markers. Biochemical Systematics and Ecology, 2015, 59, 256-263.	0.6	16
59	Mediterranean basin Ficus carica L.: from genetic diversity and structure to authentication of a Protected Designation of Origin cultivar using microsatellite markers. Trees - Structure and Function, 2015, 29, 1959-1971.	0.9	16
60	High-Resolution Melting approaches towards plant fungal molecular diagnostics. Phytoparasitica, 2015, 43, 265-272.	0.6	15
61	High Resolution Melting (HRM) analysis in eggplant (Solanum melongena L.): A tool for microsatellite genotyping and molecular characterization of a Greek Genebank collection. Biochemical Systematics and Ecology, 2015, 58, 64-71.	0.6	15
62	Morpho-physiological diversity in the collection of sour cherry (Prunus cerasus) cultivars of the Fruit Genebank in Naoussa, Greece using multivariate analysis. Scientia Horticulturae, 2016, 207, 225-232.	1.7	15
63	Systems biology reveals key tissue-specific metabolic and transcriptional signatures involved in the response of Medicago truncatula plant genotypes to salt stress. Computational and Structural Biotechnology Journal, 2021, 19, 2133-2147.	1.9	15
64	Induction of Promoter DNA Methylation Upon High-Pressure Spraying of Double-Stranded RNA in Plants. Agronomy, 2021, 11, 789.	1.3	15
65	Evaluation of parsley (Petroselinum crispum) germplasm diversity from the Greek Gene Bank using morphological, molecular and metabolic markers. Industrial Crops and Products, 2021, 170, 113767.	2.5	15
66	De novo transcriptome assembly of two contrasting pumpkin cultivars. Genomics Data, 2016, 7, 200-201.	1.3	14
67	Cosmeceutical Properties of Two Cultivars of Red Raspberry Grown under Different Conditions. Cosmetics, 2018, 5, 20.	1.5	14
68	Rapid and accurate identification of black aspergilli from grapes using highâ€resolution melting (HRM) analysis. Journal of the Science of Food and Agriculture, 2019, 99, 309-314.	1.7	14
69	Genome and population dynamics under selection and neutrality: an example of S-allele diversity in wild cherry (Prunus avium L.). Tree Genetics and Genomes, 2012, 8, 1181-1190.	0.6	13
70	LEC1-LIKE paralog transcription factor: how to survive extinction and fit in NF-Y protein complex. Gene, 2014, 543, 220-233.	1.0	13
71	Genetic diversity of Lotus corniculatus in relation to habitat type, species composition and species diversity. Biochemical Systematics and Ecology, 2015, 63, 59-67.	0.6	13
72	Combination of high resolution melting (HRM) analysis and SSR molecular markers speeds up plum genotyping: case study genotyping the Greek plum GeneBank collection. Plant Genetic Resources: Characterisation and Utilisation, 2017, 15, 366-375.	0.4	13

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73	Genetic diversity of Thymus sibthorpii Bentham in mountainous natural grasslands of Northern Greece as related to local factors and plant community structure. Industrial Crops and Products, 2018, 111, 651-659.	2.5	13
74	Phenotypic and molecular characterization of apple (Malus Ã— domestica Borkh) genetic resources in Greece. Scientia Agricola, 2018, 75, 509-518.	0.6	13
75	High-Resolution Melting (HRM) Analysis Reveals Genotypic Differentiation of Venturia inaequalis Populations in Greece. Frontiers in Ecology and Evolution, 2019, 7, .	1.1	13
76	Metagenomics analysis of fungal communities associated with postharvest diseases in pear fruits under the effect of management practices. Archives of Microbiology, 2020, 202, 2391-2400.	1.0	13
77	Genetic Analysis by nuSSR Markers of Silver Birch (Betula pendula Roth) Populations in Their Southern European Distribution Range. Frontiers in Plant Science, 2020, 11, 310.	1.7	13
78	Olive Fruit Development and Ripening: Break on through to the â€œ-Omicsâ€•Side. International Journal of Molecular Sciences, 2021, 22, 5806.	1.8	13
79	A multi-farm assessment of Greek black pig genetic diversity using microsatellite molecular markers. Genetics and Molecular Research, 2014, 13, 2752-2765.	0.3	12
80	A comprehensive RNA-Seq-based gene expression atlas of the summer squash (Cucurbita pepo) provides insights into fruit morphology and ripening mechanisms. BMC Genomics, 2021, 22, 341.	1.2	12
81	Assessing inter- and intra-cultivar variation in Greek Prunus avium by SSR markers. Plant Genetic Resources: Characterisation and Utilisation, 2010, 8, 242-248.	0.4	11
82	The GenTree Leaf Collection: Interâ€•and intraspecific leaf variation in seven forest tree species in Europe. Global Ecology and Biogeography, 2021, 30, 590-597.	2.7	11
83	Characterization of the Genetic Diversity Present in a Diverse Sesame Landrace Collection Based on Phenotypic Traits and EST-SSR Markers Coupled With an HRM Analysis. Plants, 2021, 10, 656.	1.6	11
84	Genotype- and tissue-specific metabolic networks and hub genes involved in water-induced distinct sweet cherry fruit cracking phenotypes. Computational and Structural Biotechnology Journal, 2021, 19, 5406-5420.	1.9	11
85	Unraveling saltâ€responsive tissueâ€specific metabolic pathways in olive tree. Physiologia Plantarum, 2021, 173, 1643-1656.	2.6	11
86	Molecular Authentication, Phytochemical Evaluation and Asexual Propagation of Wild-Growing Rosa canina L. (Rosaceae) Genotypes of Northern Greece for Sustainable Exploitation. Plants, 2021, 10, 2634.	1.6	10
87	Population and Conservation Genomics in Forest and Fruit Trees. Advances in Botanical Research, 2015, , 125-155.	0.5	8
88	Microsatellite genotyping and molecular screening of pea (Pisum sativum L.) germplasm with high-resolution melting analysis for resistance to powdery mildew. Plant Gene, 2018, 15, 1-5.	1.4	8
89	Metabolomic Fingerprinting and Molecular Characterization of the Rock Samphire Germplasm Collection from the Balkan Botanic Garden of Kroussia, Northern Greece. Plants, 2022, 11, 573.	1.6	8
90	Genotyping ofListeria monocytogenesisolates from poultry carcasses using high resolution melting (HRM) analysis. Biotechnology and Biotechnological Equipment, 2014, 28, 107-111.	0.5	7

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91	Evidence of extensive positive selection acting on cherry (Prunus avium L.) resistance gene analogs (RGAs). Australian Journal of Crop Science, 2016, 10, 1324-1329.	0.1	7
92	Application of the ITS2 region for barcoding plants of the genus Triticum L. and Aegilops L.. Cereal Research Communications, 2017, 45, 381-389.	0.8	7
93	Proteo-metabolomic journey across olive drupe development and maturation. Food Chemistry, 2021, 363, 130339.	4.2	7
94	Molecular Authentication, Propagation Trials and Field Establishment of Greek Native Genotypes of Sambucus nigra L. (Caprifoliaceae): Setting the Basis for Domestication and Sustainable Utilization. Agronomy, 2022, 12, 114.	1.3	7
95	Identification of genes and metabolic pathways involved in wounding-induced kiwifruit ripening. Plant Physiology and Biochemistry, 2022, 179, 179-190.	2.8	7
96	Could Causal Discovery in Proteogenomics Assist in Understanding Geneâ€“Protein Relations? A Perennial Fruit Tree Case Study Using Sweet Cherry as a Model. Cells, 2022, 11, 92.	1.8	7
97	Identification of lactic acid bacteria isolated from poultry carcasses by high-resolution melting (HRM) analysis. European Food Research and Technology, 2014, 238, 691-697.	1.6	6
98	Phenotypic, Genetic, and Epigenetic Variation among Diverse Sweet Cherry Gene Pools. Agronomy, 2021, 11, 680.	1.3	6
99	Genetic Diversity and Structure of Tobacco in Greece on the Basis of Morphological and Microsatellite Markers. Crop Science, 2016, 56, 2652-2662.	0.8	5
100	Towards sweet cherry (Prunus avium L.) breeding: phenotyping evaluation of newly developed hybrids. Euphytica, 2018, 214, 1.	0.6	5
101	Evaluation of the Nutraceutical and Cosmeceutical Potential of Two Cultivars of Rubus fruticosus L. under Different Cultivation Conditions. Current Pharmaceutical Biotechnology, 2018, 18, 890-899.	0.9	5
102	Documenting Greek Indigenous Germplasm of Cornelian Cherry (Cornus mas L.) for Sustainable Utilization: Molecular Authentication, Asexual Propagation, and Phytochemical Evaluation. Plants, 2022, 11, 1345.	1.6	5
103	Comparative Genomics of Botrytis cinerea Strains with Differential Multi-Drug Resistance. Frontiers in Plant Science, 2016, 7, 554.	1.7	4
104	Comparative metagenomics reveals alterations in the soil bacterial community driven by N-fertilizer and Amino 16Â® application in lettuce. Genomics Data, 2017, 14, 14-17.	1.3	4
105	Exploring morpho-physiological profiles of a collection of tomato (Solanum lycopersicum) germplasm using multivariate statistics. Plant Genetic Resources: Characterisation and Utilisation, 2020, 18, 88-97.	0.4	4
106	In silico analysis of the LRR receptor-like serine threonine kinases subfamily in Morus notabilis. Plant OMICS, 2016, 9, 319-326.	0.4	4
107	Identification and evidence of positive selection upon resistance gene analogs in cotton (Gossypium) Tj ETQq1 1 0.784314 rgBT /Ove	1.4	3
108	The GenTree Platform: growth traits and tree-level environmental data in 12 European forest tree species. GigaScience, 2021, 10, .	3.3	3

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109	The pleiotropic effects of Prunus avium L. extract against oxidative stress on human fibroblasts. An in vitro approach. Molecular Biology Reports, 2021, 48, 4441-4448.	1.0	3
110	Fast and Accurate Screening ofSolanum melongenawith High-Resolution Melting Analysis for Resistance to Fusarium Wilt. International Journal of Vegetable Science, 2016, 22, 183-189.	0.6	2
111	Genomics Opportunities and Breeding Strategies Towards Improvement of Climate-Smart Traits and Disease Resistance Against Pathogens in Sweet Cherry. , 2020, , 385-404.		2
112	Probing the effects of sweet cherry (PrunusÂavium L.) extract on 2D and 3D human skin models. Molecular Biology Reports, 2022, 49, 2687-2693.	1.0	2
113	Epigenetic and Physiological Responses to Varying Root-Zone Temperatures in Greenhouse Rocket. Genes, 2022, 13, 364.	1.0	2
114	Expanding Phaseolus coccineus Genomic Resources: De Novo Transcriptome Assembly and Analysis of Landraces â€˜Gigantesâ€™ and â€˜Elephantesâ€™ Reveals Rich Functional Variation. Biochemical Genetics, 2019, 57, 747-766.	1.8	1
115	â€˜Tsolakeikoâ€™: A Greek Sweet Cherry Cultivar. Hortscience: A Publication of the American Society for Hortcultural Science, 2015, 50, 1591-1592.	0.5	1