Panagiotis Madesis

List of Publications by Year
in descending order

156	3,365	159358	214527
papers	citations	30 h-index	47 g-index

161	161	161	3174
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Plant glutathione transferase-mediated stress tolerance: functions and biotechnological applications. Plant Cell Reports, 2017, 36, 791-805.	2.8	178
2	Plant growth promoting rhizobacteria isolated from halophytes and drought-tolerant plants: genomic characterisation and exploration of phyto-beneficial traits. Scientific Reports, 2020, 10, 14857.	1.6	99
3	Overexpression of a specific soybean GmGSTU4 isoenzyme improves diphenyl ether and chloroacetanilide herbicide tolerance of transgenic tobacco plants. Journal of Biotechnology, 2010, 150, 195-201.	1.9	92
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	Tobacco plants over-expressing the sweet orange tau glutathione transferases (CsGSTUs) acquire tolerance to the diphenyl ether herbicide fluorodifen and to salt and drought stresses. Phytochemistry, 2015, 116, 69-77.	1.4	76
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	Bar-HRM for Authentication of Plant-Based Medicines: Evaluation of Three Medicinal Products Derived from Acanthaceae Species. PLoS ONE, 2015, 10, e0128476.	1.1	71
13	Ethylene â€“dependent and â€“independent superficial scald resistance mechanisms in â€˜Granny Smithâ€™ apple fruit. Scientific Reports, 2018, 8, 11436.	1.6	65
14	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
15	Transfer of Plastid DNA to the Nucleus Is Elevated during Male Gametogenesis in Tobacco. Plant Physiology, 2008, 148, 328-336.	2.3	59
16	DNA replication, recombination, and repair in plastids. Topics in Current Genetics, 2007, , 65-119.	0.7	55
17	Binding and Glutathione Conjugation of Porphyrinogens by Plant Glutathione Transferases. Journal of Biological Chemistry, 2008, 283, 20268-20276.	1.6	52
18	Authenticity analyses of Phyllanthus amarus using barcoding coupled with HRM analysis to control its quality for medicinal plant product. Gene, 2015, 573, 84-90.	1.0	51

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19	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
20	Evaluation of DNA barcoding coupled high resolution melting for discrimination of closely related species in phytopharmaceuticals. Phytomedicine, 2016, 23, 156-165.	2.3	45
21	Catalytic and structural diversity of the fluazifop-inducible glutathione transferases from Phaseolus vulgaris. Planta, 2012, 235, 1253-1269.	1.6	42
22	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
23	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
24	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
25	A synthetic gene increases TGFÎ²3 accumulation by 75â€fold in tobacco chloroplasts enabling rapid purification and folding into a biologically active molecule. Plant Biotechnology Journal, 2011, 9, 618-628.	4.1	34
26	Multiplex HRM analysis as a tool for rapid molecular authentication of nine herbal teas. Food Control, 2016, 60, 113-116.	2.8	34
27	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
28	Global DNA methylation changes in Cucurbitaceae inter-species grafting. Crop Breeding and Applied Biotechnology, 2015, 15, 112-116.	0.1	33
29	Vegetable Grafting From a Molecular Point of View: The Involvement of Epigenetics in Rootstock-Scion Interactions. Frontiers in Plant Science, 2020, 11, 621999.	1.7	33
30	Refining DNA Barcoding Coupled High Resolution Melting for Discrimination of 12 Closely Related Croton Species. PLoS ONE, 2015, 10, e0138888.	1.1	33
31	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
32	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
33	Stress-inducible GmGSTU4 shapes transgenic tobacco plants metabolome towards increased salinity tolerance. Acta Physiologiae Plantarum, 2015, 37, 1.	1.0	31
34	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
35	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
36	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

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37	Genetic diversity and metabolic profile of Salvia officinalis populations: implications for advanced breeding strategies. Planta, 2017, 246, 201-215.	1.6	29
38	A hepatitis C virus core polypeptide expressed in chloroplasts detects anti-core antibodies in infected human sera. Journal of Biotechnology, 2010, 145, 377-386.	1.9	28
39	Cloning and Characterization of a Biotic-Stress-Inducible Glutathione Transferase from Phaseolus vulgaris. Applied Biochemistry and Biotechnology, 2014, 172, 595-609.	1.4	28
40	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
41	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
42	Identification and Differentiation of Monilinia Species Causing Brown Rot of Pome and Stone Fruit using High-Resolution Melting (HRM) Analysis. Phytopathology, 2016, 106, 1055-1064.	1.1	25
43	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
44	Greek PDO saffron authentication studies using species specific molecular markers. Food Research International, 2017, 100, 899-907.	2.9	24
45	Maintenance of metabolic homeostasis and induction of cytoprotectants and secondary metabolites in alachlor-treated GmGSTU4-overexpressing tobacco plants, as resolved by metabolomics. Plant Biotechnology Reports, 2015, 9, 287-296.	0.9	23
46	Plant Glutathione Transferases in Abiotic Stress Response and Herbicide Resistance. , 2017, , 215-233.		23
47	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
48	Detection of sdhB Gene Mutations in SDHI-Resistant Isolates of Botrytis cinerea Using High Resolution Melting (HRM) Analysis. Frontiers in Microbiology, 2016, 7, 1815.	1.5	22
49	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
50	Isolation of a CENTRORADIALIS/TERMINAL FLOWER1 homolog in saffron (Crocus sativus L.): characterization and expression analysis. Molecular Biology Reports, 2012, 39, 7899-7910.	1.0	21
51	Mechanisms of Lolium rigidum multiple resistance to ALS- and ACCase-inhibiting herbicides and their impact on plant fitness. Pesticide Biochemistry and Physiology, 2020, 164, 65-72.	1.6	21
52	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
53	Bar-HRM: a reliable and fast method for species identification of ginseng (Panax ginseng,) Tj ETQq1 1 0.784314 rgBT /Overlock e7660.	0.9	21
54	Molecular basis of Cyperus difformis cross-resistance to ALS-inhibiting herbicides. Pesticide Biochemistry and Physiology, 2016, 127, 38-45.	1.6	19

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55	Species identification approach for both raw materials and end products of herbal supplements from Tinospora species. BMC Complementary and Alternative Medicine, 2018, 18, 111.	3.7	19
56	Microsatellites: Evolution and Contribution. Methods in Molecular Biology, 2013, 1006, 1-13.	0.4	18
57	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
58	Genetic diversity of Barbary fig (Opuntia ficus-indica) collection in Greece with ISSR molecular markers. Plant Gene, 2015, 2, 29-33.	1.4	18
59	RNA sequencing-based transcriptome analysis of kiwifruit infected by Botrytis cinerea. Physiological and Molecular Plant Pathology, 2020, 111, 101514.	1.3	18
60	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
61	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
62	Trp574 substitution in the acetolactate synthase of Sinapis arvensis confers cross-resistance to tribenuron and imazamox. Pesticide Biochemistry and Physiology, 2017, 142, 9-14.	1.6	17
63	Over-expression of CsGSTU promotes tolerance to the herbicide alachlor and resistance to Pseudomonas syringae pv. tabaci in transgenic tobacco. Biologia Plantarum, 2017, 61, 169-177.	1.9	17
64	Evaluation of a DNA-based method for spice/herb authentication, so you do not have to worry about what is in your curry, buon appetito!. PLoS ONE, 2017, 12, e0186283.	1.1	17
65	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
66	HRM and 16S rRNA gene sequencing reveal the cultivable microbiota of the European sea bass during ice storage. International Journal of Food Microbiology, 2020, 327, 108658.	2.1	17
67	Metabarcoding reveals low fidelity and presence of toxic species in short chain-of-commercialization of herbal products. Journal of Food Composition and Analysis, 2021, 97, 103767.	1.9	17
68	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
69	Sequence Characterization and Expression Analysis of Three APETALA2-like Genes from Saffron Crocus. Plant Molecular Biology Reporter, 2012, 30, 443-452.	1.0	16
70	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
71	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
72	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

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73	High-Resolution Melting approaches towards plant fungal molecular diagnostics. Phytoparasitica, 2015, 43, 265-272.	0.6	15
74	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
75	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
76	Non-polar secondary metabolites and essential oil of ex situ propagated and cultivated Sideritis syriaca L. subsp. syriaca (Lamiaceae) with consolidated identity (DNA Barcoding): towards a potential new industrial crop. Industrial Crops and Products, 2020, 158, 112957.	2.5	15
77	Detection and quantification of cashew in commercial tea products using High Resolution Melting (HRM) analysis. Journal of Food Science, 2020, 85, 1629-1634.	1.5	15
78	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
79	De novo transcriptome assembly of two contrasting pumpkin cultivars. Genomics Data, 2016, 7, 200-201.	1.3	14
80	Cosmeceutical Properties of Two Cultivars of Red Raspberry Grown under Different Conditions. Cosmetics, 2018, 5, 20.	1.5	14
81	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
82	Hybrid analysis (barcode-high resolution melting) for authentication of Thai herbal products, Andrographis paniculata (Burm.f.) Wall.ex Nees. Pharmacognosy Magazine, 2016, 12, 71.	0.3	14
83	Introducing an RNA editing requirement into a plastid-localised transgene reduces but does not eliminate functional gene transfer to the nucleus. Plant Molecular Biology, 2011, 76, 299-309.	2.0	13
84	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
85	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
86	Phenotypic and molecular characterization of apple (Malus Ã— domestica Borkh) genetic resources in Greece. Scientia Agricola, 2018, 75, 509-518.	0.6	13
87	Tolerance of Transplastomic Tobacco Plants Overexpressing a Theta Class Glutathione Transferase to Abiotic and Oxidative Stresses. Frontiers in Plant Science, 2018, 9, 1861.	1.7	13
88	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
89	Should DNA sequence be incorporated with other taxonomical data for routine identifying of plant species?. BMC Complementary and Alternative Medicine, 2017, 17, 437.	3.7	12
90	Expanding the Plant GSTome Through Directed Evolution: DNA Shuffling for the Generation of New Synthetic Enzymes With Engineered Catalytic and Binding Properties. Frontiers in Plant Science, 2018, 9, 1737.	1.7	12

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91	Structure and Antioxidant Catalytic Function of Plant Glutathione Transferases. Current Chemical Biology, 2011, 5, 64-74.	0.2	11
92	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
93	Expression of an HCV Core Antigen Coding Gene in Tobacco (N. tabacumL.). Preparative Biochemistry and Biotechnology, 2008, 38, 411-421.	1.0	10
94	Overexpression of A Biotic Stress-Inducible Pvgstu Gene Activates Early Protective Responses in Tobacco under Combined Heat and Drought. International Journal of Molecular Sciences, 2021, 22, 2352.	1.8	10
95	Fruit Quality Traits and Genotypic Characterization in a Pomegranate Ex Situ (Punica granatum L.) Collection in Greece. Agriculture (Switzerland), 2021, 11, 482.	1.4	10
96	Protoplast Isolation, Fusion, Culture and Transformation in the Woody Plant Jasminum spp.. Agriculture (Switzerland), 2021, 11, 699.	1.4	10
97	Plant Glutathione Transferases: Structure, Antioxidant Catalytic Function and in planta Protective Role in Biotic and Abiotic Stress. Current Chemical Biology, 2015, 8, 58-75.	0.2	10
98	Glyphosate resistance of molecularly identified Conyza albida and Conyza bonariensis populations. Crop Protection, 2014, 65, 207-215.	1.0	9
99	Structure, Evolution and Functional Roles of Plant Glutathione Transferases. , 2017, , 195-213.		9
100	HRM analysis as a tool to facilitate identification of bacteria from mussels during storage at 4â€¯Â°C. Food Microbiology, 2020, 85, 103304.	2.1	9
101	DNA Fingerprinting and Species Identification Uncovers the Genetic Diversity of Katsouni Pea in the Greek Islands Amorgos and Schinoussa. Plants, 2020, 9, 479.	1.6	9
102	Biosolid-Amended Soil Enhances Defense Responses in Tomato Based on Metagenomic Profile and Expression of Pathogenesis-Related Genes. Plants, 2021, 10, 2789.	1.6	9
103	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
104	Effect of different factors on regeneration and transformation efficiency of tomato (Lycopersicum) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.4	8
105	Resistance of Rapistrum rugosum to tribenuron and imazamox due to Trp574 or Pro197 substitution in the acetolactate synthase. Pesticide Biochemistry and Physiology, 2019, 154, 1-6.	1.6	8
106	Simple and Efficient Removal of Marker Genes From Plastids by Homologous Recombination. , 2005, 286, 255-270.		7
107	Expression of the yeast cpd1 gene in tobacco confers resistance to the fungal toxin cercosporin. New Biotechnology, 2007, 24, 245-251.	2.7	7
108	Expression of SOD transgene in pepper confer stress tolerance and improve shoot regeneration. Electronic Journal of Biotechnology, 2009, 12, .	1.2	7

#	Article	IF	Citations
109	Genotyping ofListeria monocytogenesisolates from poultry carcasses using high resolution melting (HRM) analysis. Biotechnology and Biotechnological Equipment, 2014, 28, 107-111.	0.5	7
110	Rapid analysis for the identification of the seagrass Halophila ovalis (Hydrocharitaceae). African Journal of Biotechnology, 2015, 14, 649-656.	0.3	7
111	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
112	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
113	Novel authentication approach for coffee beans and the brewed beverage using a nuclear-based species-specific marker coupled with high resolution melting analysis. LWT - Food Science and Technology, 2021, 137, 110336.	2.5	7
114	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
115	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
116	Multiuse of Bar-HRM for Ophiocordyceps sinensis identification and authentication. Scientific Reports, 2018, 8, 12770.	1.6	5
117	Towards sweet cherry (Prunus avium L.) breeding: phenotyping evaluation of newly developed hybrids. Euphytica, 2018, 214, 1.	0.6	5
118	Metagenome data of bacterial diversity in pear (Pyrus communis L.) rhizospheres associated with Phytophthora infection and amino acid treatment. Data in Brief, 2019, 26, 104396.	0.5	5
119	Molecular screening of domestic apple cultivars for scab resistance genes in Greece. Czech Journal of Genetics and Plant Breeding, 2020, 56, 165-169.	0.4	5
120	Galium spurium and G. aparine Resistance to ALS-Inhibiting Herbicides in Northern Greece. Planta Daninha, 0, 37, .	0.5	5
121	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
122	Quantifying an online wildlife trade using a web crawler. Biodiversity and Conservation, 2022, 31, 855-869.	1.2	5
123	Microsatellite high-resolution melting (SSR-HRM) analysis for identification of sweet cherry rootstocks in Greece. Plant Genetic Resources: Characterisation and Utilisation, 2014, 12, 160-163.	0.4	4
124	Identification of Phytophthora species by a high resolution melting analysis: an innovative tool for rapid differentiation. Plant Protection Science, 2016, 52, 176-181.	0.7	4
125	Comparative Genomics of Botrytis cinerea Strains with Differential Multi-Drug Resistance. Frontiers in Plant Science, 2016, 7, 554.	1.7	4
126	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

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127	In silico analysis of the LRR receptor-like serine threonine kinases subfamily in Morus notabilis. Plant OMICS, 2016, 9, 319-326.	0.4	4
128	Development and Fertility Restoration of CMS Eggplant Lines Carrying the Cytoplasm of Solanum violaceum. Journal of Agricultural Science, 2016, 8, 10.	0.1	3
129	Identification and evidence of positive selection upon resistance gene analogs in cotton (Gossypium) Tj ETQq1 1 0.784314 rgBT /Ove	1.4	3
130	Evaluation of suitable DNA regions for molecular identification of high value medicinal plants in genus Kaempferia. Nucleosides, Nucleotides and Nucleic Acids, 2017, 36, 726-735.	0.4	3
131	Development of a Simple and Low-Resource Regeneration System of Two Greek Tomato Varieties. Agriculture (Switzerland), 2021, 11, 412.	1.4	3
132	Exploring plant diversity through soil DNA in Thai national parks for influencing land reform and agriculture planning. PeerJ, 2021, 9, e11753.	0.9	3
133	A New Accurate Genotyping HRM Method for Alternaria Species Related to Fruit Rot Diseases of Apple and Pomegranate. International Journal of Phytopathology, 2016, 4, 159-165.	0.1	3
134	Metataxonomic Analysis of Bacteria Entrapped in a Stalactiteâ€™s Core and Their Possible Environmental Origins. Microorganisms, 2021, 9, 2411.	1.6	3
135	DNA-Based Identification of Eurasian Vicia Species Using Chloroplast and Nuclear DNA Barcodes. Plants, 2022, 11, 947.	1.6	3
136	Environmental DNA detection of giant snakehead in Thailandâ€™s major rivers for wild stock assessment. PLoS ONE, 2022, 17, e0267667.	1.1	3
137	Rapid discrimination between four seagrass species using hybrid analysis. Genetics and Molecular Research, 2015, 14, 3957-3963.	0.3	2
138	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
139	Plant Adaptation to Stress Conditions: The Case of Glutathione S-Transferases (GSTs). , 2018, , 173-202.		2
140	Comparison of hierarchical clustering methods for binary data from molecular markers. International Journal of Data Analysis Techniques and Strategies, 2020, 12, 190.	0.2	2
141	Genomics Opportunities and Breeding Strategies Towards Improvement of Climate-Smart Traits and Disease Resistance Against Pathogens in Sweet Cherry. , 2020, , 385-404.		2
142	Excision of Plastid Marker Genes Using Directly Repeated DNA Sequences. Methods in Molecular Biology, 2014, 1132, 107-123.	0.4	2
143	Adaptive response of Pinus monticola driven by positive selection upon resistance gene analogs (RGAs) of the TIR-NBS-LRR subfamily. IForest, 2017, 10, 237-241.	0.5	2
144	Sequence-related amplified polymorphism (SRAP) markers, an efficient and affordable tool for evaluation genetic diversity in forest areas. Silva Balcanica, 2020, 21, 41-46.	0.2	2

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145	The Identification of Several Dipterocarpaceae and Fagaceae Trees by Barcode DNA Coupled with High-Resolution Melting Analysis. Forests, 2021, 12, 1466.	0.9	2
146	Genotypic differentiation of Monilinia spp. populations in Serbia using a high-resolution melting (HRM) analysis. Plant Protection Science, 2020, 57, 38-46.	0.7	2
147	Multiple resistance of silky windgrass to acetolactate synthase- and acetyl-CoA synthaseâ€“inhibiting herbicides. Weed Technology, 2022, 36, 334-343.	0.4	2
148	Bar-HRM for Species Confirmation of Native Plants Used in Forest Restoration in Northern Thailand. Forests, 2022, 13, 997.	0.9	2
149	Identification of Uvaria sp by barcoding coupled with high-resolution melting analysis (Bar-HRM). Genetics and Molecular Research, 2016, 15, .	0.3	1
150	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.	0.8	1
151	Growth rate and genetic structure of Sinapis arvensis susceptible and herbicide resistant populations originating from Greece. Euphytica, 2020, 216, 1.	0.6	1
152	â€˜Tsolakeikoâ€™: A Greek Sweet Cherry Cultivar. Hortscience: A Publication of the American Society for Hortcultural Science, 2015, 50, 1591-1592.	0.5	1
153	Comparison of hierarchical clustering methods for binary data from molecular markers. International Journal of Data Analysis Techniques and Strategies, 2020, 12, 190.	0.2	1
154	Comparison of Hierarchical Clustering Methods for Binary Data From SSR andÂISSR Molecular Markers. Studies in Classification, Data Analysis, and Knowledge Organization, 2021, , 233-241.	0.1	0
155	Marker-Free Transplastomic Plants by Excision of Plastid Marker Genes Using Directly Repeated DNA Sequences. Methods in Molecular Biology, 2021, 2317, 95-107.	0.4	0
156	Perspectives of Genome Editing in Plant Breeding. Advances in Plants & Agriculture Research, 2016, 3, .	0.3	0