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List of Publications by Year
in descending order

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36	753	516215 16	552369 26
papers	citations	h-index	g-index

36	36	36	1044
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Effect Î¿f Genotype and Growing Year on the Nutritional, Phytochemical, and Antioxidant Properties of Industrial Hemp (Cannabis sativa L.) Seeds. Antioxidants, 2019, 8, 491.	2.2	113
2	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
3	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
4	The study of the E-class SEPALLATA3-like MADS-box genes in wild-type and mutant flowers of cultivated saffron crocus (Crocus sativus L.) and its putative progenitors. Journal of Plant Physiology, 2011, 168, 1675-1684.	1.6	36
5	Multiplex HRM analysis as a tool for rapid molecular authentication of nine herbal teas. Food Control, 2016, 60, 113-116.	2.8	34
6	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
7	Performance and Hydroponic Tomato Crop Quality Characteristics in a Novel Greenhouse Using Dye-Sensitized Solar Cell Technology for Covering Material. Horticulturae, 2019, 5, 42.	1.2	32
8	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
9	Heterotopic expression of B-class floral homeotic genesPISTILLATA/GLOBOSAsupports a modified model for crocus (Crocus sativusL.) flower formation. DNA Sequence, 2007, 18, 120-130.	0.7	28
10	Fibre and Seed Productivity of Industrial Hemp (Cannabis sativa L.) Varieties under Mediterranean Conditions. Agronomy, 2021, 11, 171.	1.3	28
11	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
12	Tepal formation and expression pattern of B-class paleoAP3-like MADS-box genes in crocus (Crocus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.7	25
13	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
14	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
15	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
16	Genetic diversity of Barbary fig (Opuntia ficus-indica) collection in Greece with ISSR molecular markers. Plant Gene, 2015, 2, 29-33.	1.4	18
17	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
18	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

#	Article	IF	Citations
19	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
20	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
21	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
22	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
23	Cloning, Structural Characterization, and Phylogenetic Analysis of Flower MADS-Box Genes from Crocus (Crocus sativusL.). Scientific World Journal, The, 2007, 7, 1047-1062.	0.8	11
24	Characterization of PROFILIN genes from allotetraploid (Gossypium hirsutum) cotton and its diploid progenitors and expression analysis in cotton genotypes differing in fiber characteristics. Molecular Biology Reports, 2012, 39, 3523-3532.	1.0	11
25	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
26	Isolation, Characterization, and Expression Analysis of an NAP-Like cDNA from Crocus (Crocus sativus) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.6	10
27	Promoting Lifelong Learning and Satisfying Farmers' Social and Psychological Needs Through Farmer Field Schools: Views From Rural Greece. Journal of Agricultural and Food Information, 2018, 19, 66-74.	1.1	9
28	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
29	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
30	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
31	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
32	Identification and evidence of positive selection upon resistance gene analogs in cotton (Gossypium) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.4	3
33	Utilization of Tomato Landraces to Improve Seedling Performance under Salt Stress. Stresses, 2021, 1, 238-252.	1.8	3
34	famRCA-RACE: A ROLLING CIRCLE AMPLIFICATION RACE FOR ISOLATING A FAMILY OF HOMOLOGOUS cDNAs IN ONE REACTION AND ITS APPLICATION TO OBTAIN NAC GENES TRANSCRIPTION FACTORS FROM CROCUS (CROCUS SATIVUS) FLOWER. Preparative Biochemistry and Biotechnology, 2010, 40, 177-187.	1.0	2
35	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
36	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