Mallikarjuna Aradhya

List of Publications by Year
in descending order

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Version: 2024-02-01

40	3,133	159358	301761
papers	citations	30	39
		h-index	g-index

42	42	42	3276
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Co-located quantitative trait loci mediate resistance to Agrobacterium tumefaciens, Phytophthora cinnamomi, and P. pini in Juglans microcarpa Ã— J. regia hybrids. Horticulture Research, 2021, 8, 111.	2.9	4
2	A fineâ€scale genetic linkage map reveals genomic regions associated with economic traits in walnut (Juglans regia). Plant Breeding, 2019, 138, 635-646.	1.0	10
3	Temperate Nut Crops: Chestnut, Hazelnut, Pecan, Pistachio, and Walnut. , 2019, , 417-449.		3
4	Sequencing a Juglans regiaâ€‰Ã—â€‰J. microcarpa hybrid yields high-quality genome assemblies of parental species. Horticulture Research, 2019, 6, 55.	2.9	67
5	DNA profiling of figs (Ficus carica L.) from Slovenia and Californian USDA collection revealed the uniqueness of some North Adriatic varieties. Genetic Resources and Crop Evolution, 2018, 65, 1503-1516.	0.8	5
6	Genetic diversity analysis of cultivated and wild grapevine (Vitis vinifera L.) accessions around the Mediterranean basin and Central Asia. BMC Plant Biology, 2018, 18, 137.	1.6	118
7	Patterns of genomic and phenomic diversity in wine and table grapes. Horticulture Research, 2017, 4, 17035.	2.9	87
8	Genotyping by Sequencing for SNP-Based Linkage Analysis and Identification of QTLs Linked to Fruit Quality Traits in Japanese Plum (Prunus salicina Lindl.). Frontiers in Plant Science, 2017, 8, 476.	1.7	74
9	Genetic and ecological insights into glacial refugia of walnut (Juglans regia L.). PLoS ONE, 2017, 12, e0185974.	1.1	57
10	Genome-wide identification of microRNAs in pomegranate (Punica granatum L.) by high-throughput sequencing. BMC Plant Biology, 2016, 16, 122.	1.6	57
11	Evolutionary Genomics of Peach and Almond Domestication. G3: Genes, Genomes, Genetics, 2016, 6, 3985-3993.	0.8	59
12	The walnut (Juglans regia) genome sequence reveals diversity in genes coding for the biosynthesis of nonâ€structural polyphenols. Plant Journal, 2016, 87, 507-532.	2.8	233
13	Synteny analysis in Rosids with a walnut physical map reveals slow genome evolution in long-lived woody perennials. BMC Genomics, 2015, 16, 707.	1.2	83
14	A Modern Ampelography: A Genetic Basis for Leaf Shape and Venation Patterning in Grape. Plant Physiology, 2014, 164, 259-272.	2.3	233
15	Multiple loss-of-function 5-O-glucosyltransferase alleles revealed in Vitis vinifera, but not in other Vitis species. Theoretical and Applied Genetics, 2014, 127, 2433-2451.	1.8	12
16	Vitis Phylogenomics: Hybridization Intensities from a SNP Array Outperform Genotype Calls. PLoS ONE, 2013, 8, e78680.	1.1	55
17	Genomics Assisted Ancestry Deconvolution in Grape. PLoS ONE, 2013, 8, e80791.	1.1	43
18	Genome-wide SNP discovery in walnut with an AGSNP pipeline updated for SNP discovery in allogamous organisms. BMC Genomics, 2012, 13, 354.	1.2	47

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19	Characterizing the walnut genome through analyses of BAC end sequences. Plant Molecular Biology, 2012, 78, 95-107.	2.0	27
20	Genetic structure and domestication history of the grape. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 3530-3535.	3.3	684
21	Molecular characterization of genetic diversity, structure, and differentiation in the olive (Olea) Tj ETQq1 1 0.784314 rgBT /Overlock 10 and Crop Evolution, 2011, 58, 519-531.	0.8	39
22	Genetic structure and differentiation in cultivated fig (Ficus carica L.). Genetica, 2010, 138, 681-694.	0.5	58
23	Genetic variation in walnuts (Juglans regia and J. sigillata; Juglandaceae): Species distinctions, human impacts, and the conservation of agrobiodiversity in Yunnan, China. American Journal of Botany, 2010, 97, 660-671.	0.8	87
24	Molecular phylogeny of Juglans (Juglandaceae): a biogeographic perspective. Tree Genetics and Genomes, 2007, 3, 363-378.	0.6	105
25	Characterization of 14 Microsatellite Markers for Genetic Analysis and Cultivar Identification of Walnut. Journal of the American Society for Horticultural Science, 2005, 130, 348-354.	0.5	124
26	Molecular characterization of variability and relationships among seven cultivated and selected wild species of Prunus L. using amplified fragment length polymorphism. Scientia Horticulturae, 2004, 103, 131-144.	1.7	33
27	Genetic structure and differentiation in cultivated grape, Vitis vinifera L.. Genetical Research, 2003, 81, 179-192.	0.3	253
28	Genetic variability in the pistachio late blight fungus, Alternaria alternata. Mycological Research, 2001, 105, 300-306.	2.5	44
29	Title is missing!. Genetic Resources and Crop Evolution, 1999, 46, 579-586.	0.8	59
30	Genetic variability in Macadamia. Genetic Resources and Crop Evolution, 1998, 45, 19-32.	0.8	34
31	Enzyme polymorphisms in Canarium. Scientia Horticulturae, 1997, 68, 197-206.	1.7	4
32	Allozyme Variation In Spineless Pejibaye (bactris Gasipaes Palmae). Economic Botany, 1997, 51, 149-157.	0.8	14
33	Genetic diversity inNepheliumas revealed by isozyme polymorphism. The Journal of Horticultural Science, 1996, 71, 847-857.	0.3	2
34	Lack of association between allozyme heterozygosity and juvenile traits in Eucalyptus. New Forests, 1995, 9, 97-110.	0.7	5
35	Isozyme variation in lychee (Litchi chinensis Sonn.). Scientia Horticulturae, 1995, 63, 21-35.	1.7	32
36	Isozyme variation in cultivated and wild pineapple. Euphytica, 1994, 79, 87-99.	0.6	37

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37	Genetic relationships among cultivated bananas and plantains from Asia and the Pacific. Euphytica, 1993, 67, 163-175.	0.6	64
38	Genetic structure and differentiation inMetrosideros polymorpha(Myrtaceae) along altitudinal gradients in Maui, Hawaii. Genetical Research, 1993, 61, 159-170.	0.3	34
39	Genetic evidence for recent and incipient speciation in the evolution of Hawaiian Metrosideros (Myrtaceae). Heredity, 1991, 67, 129-138.	1.2	43
40	Isozyme variation in taro (Colocasia esculenta (L.) Schott) from Asia and Oceania. Euphytica, 1991, 56, 55-66.	0.6	104