Daniele Bassi

List of Publications by Year
in descending order

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64	3,235	159585 30	155660 55
papers	citations	h-index	g-index

64	64	64	2919
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The Peach v2.0 release: high-resolution linkage mapping and deep resequencing improve chromosome-scale assembly and contiguity. BMC Genomics, 2017, 18, 225.	2.8	342
2	Simultaneous determination of soluble sugars and organic acids as their trimethylsilyl derivatives in apricot fruits by gas-liquid chromatography. Journal of Chromatography A, 1997, 758, 99-107.	3.7	174
3	Sugars in peach fruit: a breeding perspective. Horticulture Research, 2016, 3, 15067.	6.3	159
4	Influence of cultivar and site of cultivation on levels of lipophilic and hydrophilic antioxidants in virgin olive oils (Olea Europea L.) and correlations with oxidative stability. Scientia Horticulturae, 2007, 112, 108-119.	3.6	156
5	QTL analysis of fruit quality traits in two peach intraspecific populations and importance of maturity date pleiotropic effect. Tree Genetics and Genomes, 2011, 7, 323-335.	1.6	154
6	Geographical Characterization of Italian Extra Virgin Olive Oils Using High-Field1H NMR Spectroscopy. Journal of Agricultural and Food Chemistry, 2001, 49, 2687-2696.	5.2	147
7	Fine mapping and identification of a candidate gene for a major locus controlling maturity date in peach. BMC Plant Biology, 2013, 13, 166.	3.6	113
8	Genetic dissection of aroma volatile compounds from the essential oil of peach fruit: QTL analysis and identification of candidate genes using dense SNP maps. Tree Genetics and Genomes, 2013, 9, 189-204.	1.6	105
9	Identification of key odor volatile compounds in the essential oil of nine peach accessions. Journal of the Science of Food and Agriculture, 2010, 90, 1146-1154.	3.5	100
10	Whole-Genome Analysis of Diversity and SNP-Major Gene Association in Peach Germplasm. PLoS ONE, 2015, 10, e0136803.	2.5	98
11	An integrated approach for increasing breeding efficiency in apple and peach in Europe. Horticulture Research, 2018, 5, 11.	6.3	98
12	Varietal discrimination of extra virgin olive oils by near and mid infrared spectroscopy. Food Research International, 2010, 43, 2126-2131.	6.2	86
13	A Unique Mutation in a MYB Gene Cosegregates with the Nectarine Phenotype in Peach. PLoS ONE, 2014, 9, e90574.	2.5	86
14	Changes in endopolygalacturonase levels and characterization of a putative endoâ€PG gene during fruit softening in peach genotypes with nonmelting and melting flesh fruit phenotypes. New Phytologist, 2006, 171, 315-328.	7.3	81
15	Integrated QTL detection for key breeding traits in multiple peach progenies. BMC Genomics, 2017, 18, 404.	2.8	75
16	Brown Rot Strikes Prunus Fruit: An Ancient Fight Almost Always Lost. Journal of Agricultural and Food Chemistry, 2016, 64, 4029-4047.	5.2	72
17	QTL mapping for brown rot (Monilinia fructigena) resistance in an intraspecific peach (Prunus persica) Tj ETQq1 1 0.784314 rgBT /Ov	1.6	64
18	Development of a new SSR-based linkage map in apricot and analysis of synteny with existing Prunus maps. Tree Genetics and Genomes, 2007, 3, 239-249.	1.6	61

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19	Cultivar influence on virgin olive (Olea europea L.) oil flavor based on aromatic compounds and sensorial profile. Scientia Horticulturae, 2008, 118, 139-148.	3.6	60
20	The use of AFLP markers for cultivar identification in apricot. Plant Breeding, 2003, 122, 526-531.	1.9	59
21	Evaluation of Three Electronic Noses for Detecting Incipient Wood Decay. Sensors, 2010, 10, 1062-1092.	3.8	57
22	Comparative transcript profiling of apricot (Prunus armeniaca L.) fruit development and on-tree ripening. Tree Genetics and Genomes, 2011, 7, 609-616.	1.6	53
23	Genetic dissection of fruit weight and size in an F2 peach (Prunus persica (L.) Batsch) progeny. Molecular Breeding, 2015, 35, 1.	2.1	48
24	Genome-enabled predictions for fruit weight and quality from repeated records in European peach progenies. BMC Genomics, 2017, 18, 432.	2.8	44
25	Peach. , 2012, , 505-569.		44
26	Identification of QTL for resistance to plum pox virus strains M and D in Lito and Harcot apricot cultivars. Molecular Breeding, 2011, 27, 289-299.	2.1	43
27	Deletion of the miR172 target site in a <scp>TOE</scp>â€type gene is a strong candidate variant for dominant doubleâ€flower trait in Rosaceae. Plant Journal, 2018, 96, 358-371.	5.7	43
28	Agronomic and molecular analyses for the characterisation of accessions in Tunisian olive germplasm collections. Electronic Journal of Biotechnology, 2006, 9, 0-0.	2.2	42
29	Melting of â€˜Big Topâ€™ Nectarine Fruit: Some Physiological, Biochemical, and Molecular Aspects. Journal of the American Society for Horticultural Science, 2011, 136, 61-68.	1.0	41
30	Growth and mineral nutrition of pear rootstocks in lime soils. Scientia Horticulturae, 1993, 54, 13-22.	3.6	35
31	Selecting with markers linked to the PPVres major QTL is not sufficient to predict resistance to Plum Pox Virus (PPV) in apricot. Tree Genetics and Genomes, 2014, 10, 1161-1170.	1.6	34
32	Identifying SNP markers tightly associated with six major genes in peach [Prunus persica (L.) Batsch] using a high-density SNP array with an objective of marker-assisted selection (MAS). Tree Genetics and Genomes, 2016, 12, 1.	1.6	28
33	Genetic Interactions of Pillar (Columnar), Compact, and Dwarf Peach Tree Genotypes. Journal of the American Society for Horticultural Science, 2002, 127, 254-261.	1.0	28
34	Fighting Sharka in Peach: Current Limitations and Future Perspectives. Frontiers in Plant Science, 2016, 7, 1290.	3.6	26
35	Evaluation of a portable MOS electronic nose to detect root rots in shade tree species. Computers and Electronics in Agriculture, 2013, 96, 117-125.	7.7	25
36	Characterization of fruit quality traits for organic acids content and profile in a large peach germplasm collection. Scientia Horticulturae, 2021, 278, 109865.	3.6	24

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37	Olive Fertility as Affected by Cross-Pollination and Boron. Scientific World Journal, The, 2012, 2012, 1-8.	2.1	23
38	Integrative genomics approaches validate PpYUC11-like as candidate gene for the stony hard trait in peach (P. persica L. Batsch). BMC Plant Biology, 2018, 18, 88.	3.6	21
39	Mutations in orthologous PETALOSA TOE-type genes cause a dominant double-flower phenotype in phylogenetically distant eudicots. Journal of Experimental Botany, 2020, 71, 2585-2595.	4.8	20
40	Genetic dissection of Sharka disease tolerance in peach (P. persica L. Batsch). BMC Plant Biology, 2017, 17, 192.	3.6	19
41	High-density multi-population consensus genetic linkage map for peach. PLoS ONE, 2018, 13, e0207724.	2.5	19
42	Environmental and seasonal influence on virgin olive (Olea europaea L.) oil volatiles in northern Italy. Scientia Horticulturae, 2009, 122, 385-392.	3.6	18
43	Bitterness inheritance in apricot (P. armeniaca L.) seeds. Tree Genetics and Genomes, 2008, 4, 767-776.	1.6	16
44	Phenotyping Brown Rot Susceptibility in Stone Fruit: A Literature Review with Emphasis on Peach. Horticulturae, 2021, 7, 115.	2.8	16
45	Identification and characterization of transcripts differentially expressed during development of apricot (Prunus armeniaca L.) fruit. Tree Genetics and Genomes, 2005, 1, 69-78.	1.6	15
46	Regional and cultivar comparison of Italian single cultivar olive oils according to flavor profiling. European Journal of Lipid Science and Technology, 2013, 115, 196-210.	1.5	14
47	FTâ€NIR Spectroscopy for the Quality Characterization of Apricots (Prunus Armeniaca L.). Journal of Food Science, 2010, 75, E462-8.	3.1	13
48	Identification of a melting type variant among peach (P. persica L. Batsch) fruit textures by a digital penetrometer. Journal of Texture Studies, 2018, 49, 370-377.	2.5	12
49	PeachVar-DB: A Curated Collection of Genetic Variations for the Interactive Analysis of Peach Genome Data. Plant and Cell Physiology, 2018, 59, e2-e2.	3.1	12
50	The Multisite PeachRefPop Collection: A True Cultural Heritage and International Scientific Tool for Fruit Trees. Plant Physiology, 2020, 184, 632-646.	4.8	12
51	PEACH (Prunus persica (L.) Batsch). , 2016, , 535-571.		11
52	Development of a high-resolution melting approach for reliable and cost-effective genotyping of PPVres locus in apricot (P. armeniaca). Molecular Breeding, 2017, 37, 1.	2.1	11
53	SSR Marker Based DNA Fingerprinting of Tunisian Olive (Olea europaeaL.) Varieties. Journal of Agronomy, 2008, 7, 176-181.	0.4	11
54	CHARACTERIZATION BY MOLECULAR MARKERS OF 'POMPIA', A NATURAL CITRUS HYBRID CULTIVATED IN SARDINIA. Acta Horticulturae, 2015, , 165-172.	0.2	10

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55	Linkage and association mapping for the slow softening (SwS) trait in peach (P. persica L. Batsch) fruit. Tree Genetics and Genomes, 2018, 14, 1.	1.6	9
56	Resistance to Sharka in Apricot: Comparison of Phase-Reconstructed Resistant and Susceptible Haplotypes of â€˜Litoâ€™ Chromosome 1 and Analysis of Candidate Genes. Frontiers in Plant Science, 2019, 10, 1576.	3.6	8
57	Genetic and phenotypic analyses reveal major quantitative loci associated to fruit size and shape traits in a non-flat peach collection (P. persica L. Batsch). Horticulture Research, 2021, 8, 232.	6.3	8
58	A qNMR approach for bitterness phenotyping and QTL identification in an F1 apricot progeny. Journal of Biotechnology, 2012, 159, 312-319.	3.8	7
59	TheDi2/petVariant in thePETALOSAGene Underlies a Major Heat Requirement-Related QTL for Blooming Date in Peach [Prunus persica(L.) Batsch]. Plant and Cell Physiology, 2021, 62, 356-365.	3.1	7
60	Evaluation of a large apricot germplasm collection for fruit skin and flesh acidity and organic acids composition. Scientia Horticulturae, 2022, 294, 110780.	3.6	6
61	Preliminary phenotypic characterization of Sorbus domestica and S. torminalis under selection for timber production. Agroforestry Systems, 2018, 92, 589-597.	2.0	4
62	Development of an HRMA-Based Marker Assisted Selection (MAS) Approach for Cost-Effective Genotyping of S and M Loci Controlling Self-Compatibility in Apricot (Prunus armeniaca L.). Genes, 2022, 13, 548.	2.4	3
63	Quantitative Trait Loci Mapping and Identification of Candidate Genes Linked to Fruit Acidity in Apricot (Prunus armeniaca L.). Frontiers in Plant Science, 2022, 13, 838370.	3.6	3
64	Less is more: natural variation disrupting a miR172 gene at the di locus underlies the recessive double-flower trait in peach (P. persica L. Batsch). BMC Plant Biology, 2022, 22, .	3.6	2