

# Antonio JosÃ© Monforte

## List of Publications by Year in descending order

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114  
papers

9,156  
citations

50276

46  
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42399

92  
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docs citations

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times ranked

8332  
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#	ARTICLE	IF	CITATIONS
1	A cryptic variation in a member of the Ovate Family Proteins is underlying the melon fruit shape QTL fsqs8.1. <i>Theoretical and Applied Genetics</i> , 2022, 135, 785-801.	3.6	12
2	European traditional tomatoes galore: a result of farmers' selection of a few diversity-rich loci. <i>Journal of Experimental Botany</i> , 2022, 73, 3431-3445.	4.8	11
3	Genetic Control of Reproductive Traits under Different Temperature Regimes in Inbred Line Populations Derived from Crosses between <i>S. pimpinellifolium</i> and <i>S. lycopersicum</i> Accessions. <i>Plants</i> , 2022, 11, 1069.	3.5	5
4	Transcriptomic analysis of a near-isogenic line of melon with high fruit flesh firmness during ripening. <i>Journal of the Science of Food and Agriculture</i> , 2021, 101, 754-777.	3.5	9
5	Analysis of aroma-related volatile compounds affected by Ginsen Makuwa genomic regions introgressed in Vedranta melon background. <i>Scientia Horticulturae</i> , 2021, 276, 109664.	3.6	5
6	Identification of tomato accessions as source of new genes for improving heat tolerance: from controlled experiments to field. <i>BMC Plant Biology</i> , 2021, 21, 345.	3.6	18
7	Heterosis goes underground. <i>Journal of Experimental Botany</i> , 2021, 72, 6081-6083.	4.8	3
8	Combined Stress Conditions in Melon Induce Non-additive Effects in the Core miRNA Regulatory Network. <i>Frontiers in Plant Science</i> , 2021, 12, 769093.	3.6	3
9	Characterization of a repertoire of tomato fruit genetic variants in the San marzano genetic background. <i>Scientia Horticulturae</i> , 2020, 261, 108927.	3.6	12
10	Time to exploit phenotypic plasticity. <i>Journal of Experimental Botany</i> , 2020, 71, 5295-5297.	4.8	11
11	Evidence of the Role of QTL Epistatic Interactions in the Increase of Melon Fruit Flesh Content during Domestication. <i>Agronomy</i> , 2020, 10, 1064.	3.0	3
12	Genetic Control of Reproductive Traits in Tomatoes Under High Temperature. <i>Frontiers in Plant Science</i> , 2020, 11, 326.	3.6	32
13	A comprehensive genome variation map of melon identifies multiple domestication events and loci influencing agronomic traits. <i>Nature Genetics</i> , 2019, 51, 1607-1615.	21.4	153
14	New melon introgression lines in a Piel de Sapo genetic background with desirable agronomical traits from dudaim melons. <i>Euphytica</i> , 2019, 215, 1.	1.2	7
15	CmVPS41 Is a General Gatekeeper for Resistance to Cucumber Mosaic Virus Phloem Entry in Melon. <i>Frontiers in Plant Science</i> , 2019, 10, 1219.	3.6	16
16	Fine mapping of wmv1551, a resistance gene to Watermelon mosaic virus in melon. <i>Molecular Breeding</i> , 2019, 39, 1.	2.1	6
17	Re-evaluation of the role of Indian germplasm as center of melon diversification based on genotyping-by-sequencing analysis. <i>BMC Genomics</i> , 2019, 20, 448.	2.8	35
18	A common genetic mechanism underlies morphological diversity in fruits and other plant organs. <i>Nature Communications</i> , 2018, 9, 4734.	12.8	146

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19	Repeated domestication of melon ( <i>Cucumis melo</i> ) in Africa and Asia and a new close relative from India. <i>American Journal of Botany</i> , 2018, 105, 1662-1671.	1.7	59
20	Identification, introgression, and validation of fruit volatile QTLs from a red-fruited wild tomato species. <i>Journal of Experimental Botany</i> , 2017, 68, erw455.	4.8	61
21	A chemical genetic roadmap to improved tomato flavor. <i>Science</i> , 2017, 355, 391-394.	12.6	561
22	An SNP-based saturated genetic map and QTL analysis of fruit-related traits in Zucchini using Genotyping-by-sequencing. <i>BMC Genomics</i> , 2017, 18, 94.	2.8	93
23	New tools for breeding cantaloupe melons: first introgression line collection of makuwa melons into Charentais genetic background. <i>Acta Horticulturae</i> , 2017, , 75-80.	0.2	0
24	A new introgression line collection to improve "Piel de Sapo" melons. <i>Acta Horticulturae</i> , 2017, , 81-86.	0.2	2
25	<i>ETHQV6.3</i> is involved in melon climacteric fruit ripening and is encoded by a <i>NAC</i> domain transcription factor. <i>Plant Journal</i> , 2017, 91, 671-683.	5.7	71
26	Uncovering tomato quantitative trait loci and candidate genes for fruit cuticular lipid composition using the <i>Solanum pennellii</i> introgression line population. <i>Journal of Experimental Botany</i> , 2017, 68, 2703-2716.	4.8	41
27	Quantitative trait loci analysis of melon ( <i>Cucumis melo</i> L.) domestication-related traits. <i>Theoretical and Applied Genetics</i> , 2017, 130, 1837-1856.	3.6	37
28	The genetic control of fruit morphology in <i>Cucumis melo</i> L.. <i>Acta Horticulturae</i> , 2017, , 1-4.	0.2	1
29	"MAK-10": A Long Shelf-life Charentais Breeding Line Developed by Introgression of a Genomic Region from Makuwa Melon. <i>Hortscience: A Publication of the American Society for Horticultural Science</i> , 2017, 52, 1633-1638.	1.0	11
30	Use of Natural Diversity and Biotechnology to Increase the Quality and Nutritional Content of Tomato and Grape. <i>Frontiers in Plant Science</i> , 2017, 8, 652.	3.6	60
31	QTL Analyses in Multiple Populations Employed for the Fine Mapping and Identification of Candidate Genes at a Locus Affecting Sugar Accumulation in Melon ( <i>Cucumis melo</i> L.). <i>Frontiers in Plant Science</i> , 2017, 8, 1679.	3.6	32
32	Exploring New Alleles Involved in Tomato Fruit Quality in an Introgression Line Library of <i>Solanum pimpinellifolium</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 1172.	3.6	50
33	Genetic Mapping of Complex Traits in Cucurbits. <i>Plant Genetics and Genomics: Crops and Models</i> , 2016, , 269-290.	0.3	3
34	Mapping QTLs associated with fruit quality traits in peach [ <i>Prunus persica</i> (L.) Batsch] using SNP maps. <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	1.6	60
35	A new genomic library of melon introgression lines in a cantaloupe genetic background for dissecting desirable agronomical traits. <i>BMC Plant Biology</i> , 2016, 16, 154.	3.6	48
36	QTL ANALYSIS OF FRUIT QUALITY TRAITS IN PEACH [ <i>PRUNUS PERSICA</i> (L.) BATSCH] USING DENSE SNP MAPS. <i>Acta Horticulturae</i> , 2015, , 703-710.	0.2	4

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37	Snapmelon ( <i>Cucumis melo</i> L. <i>Momordica</i> group), an indigenous cucurbit from India with immense value for melon breeding. <i>Acta Horticulturae</i> , 2015, , 99-108.	0.2	6
38	Variability of candidate genes, genetic structure and association with sugar accumulation and climacteric behavior in a broad germplasm collection of melon ( <i>Cucumis melo</i> L.). <i>BMC Genetics</i> , 2015, 16, 28.	2.7	72
39	Anchoring the consensus ICuGI genetic map to the melon ( <i>Cucumis melo</i> L.) genome. <i>Molecular Breeding</i> , 2015, 35, 1.	2.1	24
40	AN ANALYSIS IN THE STRUCTURE OF A GENETICALLY CHARACTERIZED MELON GERMPLASM COLLECTION FOR CLIMACTERIC - NON-CLIMACTERIC RIPENING BEHAVIOUR. <i>Acta Horticulturae</i> , 2015, , 95-98.	0.2	0
41	Mapping and Introgression of QTL Involved in Fruit Shape Transgressive Segregation into "Piel de Sapo"™ Melon ( <i>Cucumis melo</i> L.). <i>PLoS ONE</i> , 2014, 9, e104188.	2.5	58
42	Diversity among melon ( <i>Cucumis melo</i> L.) landraces from the Indo-Gangetic plains of India and their genetic relationship with USA melon cultivars. <i>Genetic Resources and Crop Evolution</i> , 2014, 61, 1189-1208.	1.6	23
43	The complex resistance to cucumber mosaic cucumovirus (CMV) in the melon accession PI161375 is governed by one gene and at least two quantitative trait loci. <i>Molecular Breeding</i> , 2014, 34, 351-362.	2.1	31
44	Genetic diversity in <i>Vicia faba</i> L. populations cultivated in Tunisia revealed by simple sequence repeat analysis. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2014, 12, 278-285.	0.8	7
45	Highly efficient genomics-assisted development of a library of introgression lines of <i>Solanum pimpinellifolium</i> . <i>Molecular Breeding</i> , 2014, 34, 1817-1831.	2.1	34
46	The peach volatilome modularity is reflected at the genetic and environmental response levels in a QTL mapping population. <i>BMC Plant Biology</i> , 2014, 14, 137.	3.6	29
47	Quantitative trait loci affecting reproductive phenology in peach. <i>BMC Plant Biology</i> , 2014, 14, 52.	3.6	73
48	An integrative "omics" approach identifies new candidate genes to impact aroma volatiles in peach fruit. <i>BMC Genomics</i> , 2013, 14, 343.	2.8	48
49	Interaction between QTLs induces an advance in ethylene biosynthesis during melon fruit ripening. <i>Theoretical and Applied Genetics</i> , 2013, 126, 1531-1544.	3.6	56
50	SNP genotyping in melons: genetic variation, population structure, and linkage disequilibrium. <i>Theoretical and Applied Genetics</i> , 2013, 126, 1285-1303.	3.6	85
51	The genetic basis of fruit morphology in horticultural crops: lessons from tomato and melon. <i>Journal of Experimental Botany</i> , 2013, 65, 4625-4637.	4.8	188
52	The expanded tomato fruit volatile landscape. <i>Journal of Experimental Botany</i> , 2013, 65, 4613-4623.	4.8	155
53	Genetic diversity of Spanish <i>Cucurbita pepo</i> landraces: an unexploited resource for summer squash breeding. <i>Genetic Resources and Crop Evolution</i> , 2012, 59, 1169-1184.	1.6	47
54	High-throughput SNP genotyping in <i>Cucurbita pepo</i> for map construction and quantitative trait loci mapping. <i>BMC Genomics</i> , 2012, 13, 80.	2.8	110

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55	The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 2012, 485, 635-641.	27.8	2,860
56	Wild melon diversity in India (Punjab State). <i>Genetic Resources and Crop Evolution</i> , 2012, 59, 755-767.	1.6	48
57	A Non-Targeted Approach Unravels the Volatile Network in Peach Fruit. <i>PLoS ONE</i> , 2012, 7, e38992.	2.5	63
58	Variation in melon ( <i>Cucumis melo</i> ) landraces adapted to the humid tropics of southern India. <i>Genetic Resources and Crop Evolution</i> , 2011, 58, 225-243.	1.6	62
59	A consensus linkage map for molecular markers and Quantitative Trait Loci associated with economically important traits in melon ( <i>Cucumis melo</i> L.). <i>BMC Plant Biology</i> , 2011, 11, 111.	3.6	156
60	Towards a TILLING platform for functional genomics in Piel de Sapo melons. <i>BMC Research Notes</i> , 2011, 4, 289.	1.4	59
61	Parthenogenic Haploids in Melon: Generation and Molecular Characterization of a Doubled Haploid Line Population. <i>Journal of the American Society for Horticultural Science</i> , 2011, 136, 145-154.	1.0	25
62	FLESH CAROTENOID PROFILE IN CLIMACTERIC NEAR-ISOGENIC LINES OF MELON OBTAINED FROM NON-CLIMACTERIC PARENTALS: IMPLICATIONS FOR FRUIT DESIGN. <i>Acta Horticulturae</i> , 2010, , 43-49.	0.2	0
63	Shaping melons: agronomic and genetic characterization of QTLs that modify melon fruit morphology. <i>Theoretical and Applied Genetics</i> , 2010, 121, 931-940.	3.6	39
64	Aroma profile of a collection of near-isogenic lines of melon ( <i>Cucumis melo</i> L.). <i>Food Chemistry</i> , 2010, 118, 815-822.	8.2	43
65	Using genetic variability available in the breeder's pool to engineer fruit quality. <i>GM Crops</i> , 2010, 1, 120-127.	1.9	5
66	Uncommon disorders and decay in near-isogenic lines of melon and reference cultivars. <i>Horticultura Brasileira</i> , 2009, 27, 505-514.	0.5	1
67	On the Genetic Control of Heterosis for Fruit Shape in Melon ( <i>Cucumis Melo</i> L.). <i>Journal of Heredity</i> , 2009, 100, 229-235.	2.4	20
68	Phenotypic and molecular diversity among landraces of snapmelon ( <i>Cucumis melo</i> var. <i>momordica</i> ) adapted to the hot and humid tropics of eastern India. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2009, 7, 291-300.	0.8	32
69	Postharvest firmness behaviour of near-isogenic lines of melon. <i>Postharvest Biology and Technology</i> , 2009, 51, 320-326.	6.0	19
70	Aroma volatiles associated with the senescence of climacteric or non-climacteric melon fruit. <i>Postharvest Biology and Technology</i> , 2009, 52, 146-155.	6.0	43
71	A set of EST-SNPs for map saturation and cultivar identification in melon. <i>BMC Plant Biology</i> , 2009, 9, 90.	3.6	90
72	Discrimination of climacteric and non-climacteric melon fruit at harvest or at the senescence stage by quality traits. <i>Journal of the Science of Food and Agriculture</i> , 2009, 89, 1743-1753.	3.5	15

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73	Dissection of the oligogenic resistance to Cucumber mosaic virus in the melon accession PI 161375. <i>Theoretical and Applied Genetics</i> , 2009, 118, 275-284.	3.6	47
74	Identification of QTLs related to sugar and organic acid composition in melon using near-isogenic lines. <i>Scientia Horticulturae</i> , 2009, 121, 425-433.	3.6	47
75	Genetic Diversity and Population Structure of Traditional Greek and Cypriot Melon Cultigens ( <i>Cucumis melo</i> L.) Based on Simple Sequence Repeat Variability. <i>Hortscience: A Publication of the American Society for Horticultural Science</i> , 2009, 44, 1820-1824.	1.0	22
76	Candidate genes and QTLs for fruit ripening and softening in melon. <i>Theoretical and Applied Genetics</i> , 2008, 116, 589-602.	3.6	97
77	Exploiting synteny in <i>Cucumis</i> for mapping of Psm: a unique locus controlling paternal mitochondrial sorting. <i>Theoretical and Applied Genetics</i> , 2008, 117, 523-529.	3.6	13
78	Bin mapping of genomic and EST-derived SSRs in melon ( <i>Cucumis melo</i> L.). <i>Theoretical and Applied Genetics</i> , 2008, 118, 139-150.	3.6	115
79	Identification of QTLs for resistance to powdery mildew and SSR markers diagnostic for powdery mildew resistance genes in melon ( <i>Cucumis melo</i> L.). <i>Theoretical and Applied Genetics</i> , 2008, 118, 165-175.	3.6	85
80	Climacteric or non-climacteric behavior in melon fruit. <i>Postharvest Biology and Technology</i> , 2008, 49, 27-37.	6.0	126
81	Climacteric and non-climacteric behavior in melon fruit. <i>Postharvest Biology and Technology</i> , 2008, 50, 125-134.	6.0	34
82	Identification of Melon Fruit Quality Quantitative Trait Loci Using Near-isogenic Lines. <i>Journal of the American Society for Horticultural Science</i> , 2008, 133, 139-151.	1.0	59
83	Genetics of Root System Architecture Using Near-isogenic Lines of Melon. <i>Journal of the American Society for Horticultural Science</i> , 2008, 133, 448-458.	1.0	20
84	FIRST ATTEMPTS OF LINKING MODELLING, POSTHARVEST BEHAVIOUR AND MELON GENETICS. <i>Acta Horticulturae</i> , 2008, , 401-408.	0.2	0
85	Morphological variation in tomato: a comprehensive study of quantitative trait loci controlling fruit shape and development. <i>Journal of Experimental Botany</i> , 2007, 58, 1339-1349.	4.8	85
86	HORTICULTURAL AND MOLECULAR CHARACTERIZATION OF LANDRACES OF INDIAN SNAPMELON ( <i>CUCUMIS</i> ) Tj ETQq0 0 0 rgBT /Overl 0.2	0.2	1
87	Diversity among landraces of Indian snapmelon ( <i>Cucumis melo</i> var. <i>momordica</i> ). <i>Genetic Resources and Crop Evolution</i> , 2007, 54, 1267-1283.	1.6	89
88	Creating climacteric melon fruit from nonclimacteric parentals: postharvest quality implications. , 2007, , 197-205.		8
89	Estimating the Genetic Architecture of Fruit Quality Traits in Melon Using a Genomic Library of Near Isogenic Lines. <i>Journal of the American Society for Horticultural Science</i> , 2007, 132, 80-89.	1.0	91
90	Mapping Fruit Susceptibility to Postharvest Physiological Disorders and Decay Using a Collection of Near-isogenic Lines of Melon. <i>Journal of the American Society for Horticultural Science</i> , 2007, 132, 739-748.	1.0	24

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91	THE SPANISH MELON GENOMICS INITIATIVE. <i>Acta Horticulturae</i> , 2007, , 47-54.	0.2	3
92	IDENTIFICATION OF QTLs ASSOCIATED WITH COMMERCIAL POSTHARVEST QUALITY TRAITS AND DISORDERS USING A COLLECTION OF NEAR ISOGENIC LINES OF MELON. <i>Acta Horticulturae</i> , 2007, , 309-317.	0.2	1
93	Simple-sequence repeat markers used in merging linkage maps of melon ( <i>Cucumis melo</i> L.). <i>Theoretical and Applied Genetics</i> , 2005, 110, 802-811.	3.6	170
94	Development of a genomic library of near isogenic lines (NILs) in melon ( <i>Cucumis melo</i> L.) from the exotic accession PI161375. <i>Theoretical and Applied Genetics</i> , 2005, 112, 139-148.	3.6	98
95	Inheritance mode of fruit traits in melon: Heterosis for fruit shape and its correlation with genetic distance. <i>Euphytica</i> , 2005, 144, 31-38.	1.2	48
96	Mapping With a Few Plants: Using Selective Mapping for Microsatellite Saturation of the <i>Prunus</i> Reference Map. <i>Genetics</i> , 2005, 171, 1305-1309.	2.9	180
97	Phylogenetic relationships among <i>Cucumis</i> species based on the ribosomal internal transcribed spacer sequence and microsatellite markers. <i>Plant Systematics and Evolution</i> , 2004, 248, 191.	0.9	42
98	Identification of quantitative trait loci involved in fruit quality traits in melon ( <i>Cucumis melo</i> L.). <i>Theoretical and Applied Genetics</i> , 2004, 108, 750-758.	3.6	159
99	Single-nucleotide polymorphisms detected in expressed sequence tags of melon ( <i>Cucumis</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 1	2.0	45
100	Genetic variability in melon based on microsatellite variation. <i>Plant Breeding</i> , 2003, 122, 153-157.	1.9	92
101	Identification and Characterization of Aluminum Tolerance Loci in <i>Arabidopsis</i> ( <i>Landsberg erecta</i> Å—) Tj ETQq1 1 0.784314 rgBT /Overlock 1 <i>Plant Physiology</i> , 2003, 132, 936-948.	4.8	147
102	Comparison of a set of allelic QTL-NILs for chromosome 4 of tomato: Deductions about natural variation and implications for germplasm utilization. <i>Theoretical and Applied Genetics</i> , 2001, 102, 572-590.	3.6	87
103	Fine mapping of a quantitative trait locus (QTL) from <i>Lycopersicon hirsutum</i> chromosome 1 affecting fruit characteristics and agronomic traits: breaking linkage among QTLs affecting different traits and dissection of heterosis for yield. <i>Theoretical and Applied Genetics</i> , 2000, 100, 471-479.	3.6	126
104	Genetic Control and Evolution of Sesquiterpene Biosynthesis in <i>Lycopersicon esculentum</i> and <i>L. hirsutum</i> . <i>Plant Cell</i> , 2000, 12, 2283-2294.	6.6	87
105	Development of a set of near isogenic and backcross recombinant inbred lines containing most of the <i>Lycopersicon hirsutum</i> genome in a <i>L. esculentum</i> genetic background: A tool for gene mapping and gene discovery. <i>Genome</i> , 2000, 43, 803-813.	2.0	178
106	Development of a set of near isogenic and backcross recombinant inbred lines containing most of the <i>Lycopersicon hirsutum</i> genome in a <i>L. esculentum</i> genetic background: A tool for gene mapping and gene discovery. <i>Genome</i> , 2000, 43, 803-813.	2.0	91
107	Salt tolerance in <i>Lycopersicon</i> spp. VII. Pleiotropic action of genes controlling earliness on fruit yield. <i>Theoretical and Applied Genetics</i> , 1999, 98, 593-601.	3.6	30
108	Citrus and <i>Prunus</i> -like retrotransposons. <i>Theoretical and Applied Genetics</i> , 1999, 99, 503-510.	3.6	46

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109	Salt tolerance in <i>Lycopersicon</i> species. V. Does genetic variability at quantitative trait loci affect their analysis?. <i>Theoretical and Applied Genetics</i> , 1997, 95, 284-293.	3.6	70
110	Salt tolerance in <i>Lycopersicon</i> species VI. Genotype-by-salinity interaction in quantitative trait loci detection: constitutive and response QTLs. <i>Theoretical and Applied Genetics</i> , 1997, 95, 706-713.	3.6	67
111	Salt tolerance in <i>Lycopersicon</i> species. IV. Efficiency of marker-assisted selection for salt tolerance improvement. <i>Theoretical and Applied Genetics</i> , 1996, 93-93, 765-772.	3.6	36
112	Characterization of the length polymorphism in the A+T-rich region of the <i>Drosophila obscura</i> group species. <i>Journal of Molecular Evolution</i> , 1993, 36, 214-223.	1.8	47
113	La tomata "Valenciana"™ del Perell: comparaci3 de les seues caracteristiques gen3tiques i fenot3piques amb el conjunt de tomates tradicionals europees.. , 0, , .		0
114	Mapeo de un gen implicado en segregaci3n distorsionada en poblaciones interespecíficas de tomate. <i>Agronomy Mesoamerican</i> , 0, , 419-431.	0.2	0