

# Maria Teresa Dettori

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7433616/publications.pdf>

Version: 2024-02-01

15  
papers

2,217  
citations

623734

14  
h-index

996975

15  
g-index

15  
all docs

15  
docs citations

15  
times ranked

2388  
citing authors

#	ARTICLE	IF	CITATIONS
1	The high-quality draft genome of peach ( <i>Prunus persica</i> ) identifies unique patterns of genetic diversity, domestication and genome evolution. <i>Nature Genetics</i> , 2013, 45, 487-494.	21.4	1,031
2	The Peach v2.0 release: high-resolution linkage mapping and deep resequencing improve chromosome-scale assembly and contiguity. <i>BMC Genomics</i> , 2017, 18, 225.	2.8	342
3	Construction of a saturated linkage map for <i>Prunus</i> using an almond–peach F2 progeny. <i>Theoretical and Applied Genetics</i> , 1998, 97, 1034-1041.	3.6	202
4	Whole-Genome Analysis of Diversity and SNP-Major Gene Association in Peach Germplasm. <i>PLoS ONE</i> , 2015, 10, e0136803.	2.5	98
5	A peach linkage map integrating RFLPs, SSRs, RAPDs, and morphological markers. <i>Genome</i> , 2001, 44, 783-790.	2.0	89
6	A Unique Mutation in a MYB Gene Cosegregates with the Nectarine Phenotype in Peach. <i>PLoS ONE</i> , 2014, 9, e90574.	2.5	86
7	Integrated QTL detection for key breeding traits in multiple peach progenies. <i>BMC Genomics</i> , 2017, 18, 404.	2.8	75
8	A set of EST-SSRs isolated from peach fruit transcriptome and their transportability across <i>Prunus</i> species. <i>Molecular Ecology Notes</i> , 2007, 7, 307-310.	1.7	56
9	Permanent Genetic Resources added to Molecular Ecology Resources Database 1 December 2009–31 January 2010. <i>Molecular Ecology Resources</i> , 2010, 10, 576-579.	4.8	56
10	Mining microsatellites in the peach genome: development of new long-core SSR markers for genetic analyses in five <i>Prunus</i> species. <i>SpringerPlus</i> , 2015, 4, 337.	1.2	44
11	Microsatellite and AFLP markers in the <i>Prunus persica</i> [L. (Batsch)]– <i>P. ferganensis</i> BC1 linkage map: saturation and coverage improvement. <i>Theoretical and Applied Genetics</i> , 2005, 111, 1013-1021.	3.6	42
12	The peach ( <i>Prunus persica</i> L. Batsch) genome harbours 10 KNOX genes, which are differentially expressed in stem development, and the class 1 KNOPE1 regulates elongation and lignification during primary growth. <i>Journal of Experimental Botany</i> , 2012, 63, 5417-5435.	4.8	33
13	High-density genetic map and QTL analysis of soluble solid content, maturity date, and mealiness in peach using genotyping by sequencing. <i>Scientia Horticulturae</i> , 2019, 257, 108734.	3.6	30
14	Identification of <i>Feijoa sellowiana</i> Berg accessions by RAPD markers. <i>Scientia Horticulturae</i> , 2000, 86, 279-290.	3.6	20
15	Transcriptome reprogramming of resistant and susceptible peach genotypes during <i>Xanthomonas arboricola</i> pv. <i>pruni</i> early leaf infection. <i>PLoS ONE</i> , 2018, 13, e0196590.	2.5	13