

# Maria Francesca Cardone

## List of Publications by Year in descending order

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49  
papers

2,782  
citations

279798

23  
h-index

206112

48  
g-index

51  
all docs

51  
docs citations

51  
times ranked

3808  
citing authors

#	ARTICLE	IF	CITATIONS
1	Native Vineyard Non-Saccharomyces Yeasts Used for Biological Control of Botrytis cinerea in Stored Table Grape. <i>Microorganisms</i> , 2021, 9, 457.	3.6	11
2	Color Stabilization of Apulian Red Wines through the Sequential Inoculation of <i>Starmerella bacillaris</i> and <i>Saccharomyces cerevisiae</i> . <i>Molecules</i> , 2021, 26, 907.	3.8	5
3	Novel and emerging biotechnological crop protection approaches. <i>Plant Biotechnology Journal</i> , 2021, 19, 1495-1510.	8.3	26
4	Somatic Embryogenesis in <i>Vitis</i> for Genome Editing: Optimization of Protocols for Recalcitrant Genotypes. <i>Horticulturae</i> , 2021, 7, 511.	2.8	5
5	Gene expression signature induced by grape intake in healthy subjects reveals wide-spread beneficial effects on peripheral blood mononuclear cells. <i>Journal of Functional Foods</i> , 2020, 64, 103705.	3.4	7
6	Microarray data and pathway analyses of peripheral blood mononuclear cells from healthy subjects after a three weeks grape-rich diet. <i>Data in Brief</i> , 2020, 29, 105278.	1.0	5
7	FT-NIR Analysis of Intact Table Grape Berries to Understand Consumer Preference Driving Factors. <i>Foods</i> , 2020, 9, 98.	4.3	12
8	Unraveling the Deep Genetic Architecture for Seedlessness in Grapevine and the Development and Validation of a New Set of Markers for VvAGL11-Based Gene-Assisted Selection. <i>Genes</i> , 2020, 11, 151.	2.4	12
9	Transcriptomic and genomic structural variation analyses on grape cultivars reveal new insights into the genotype-dependent responses to water stress. <i>Scientific Reports</i> , 2019, 9, 2809.	3.3	17
10	SNP genotyping elucidates the genetic diversity of Magna Graecia grapevine germplasm and its historical origin and dissemination. <i>BMC Plant Biology</i> , 2019, 19, 7.	3.6	51
11	Study of the Influence of Different Yeast Strains on Red Wine Fermentation with NIR Spectroscopy and Principal Component Analysis. <i>J</i> , 2018, 1, 133-147.	0.9	4
12	The molecular characterization by SSRs reveals a new South Italian kinship and the origin of the cultivar Uva di Troia. <i>SpringerPlus</i> , 2016, 5, 1562.	1.2	7
13	Genomics technologies to study structural variations in the grapevine genome. <i>BIO Web of Conferences</i> , 2016, 7, 01016.	0.2	0
14	Inter-variational structural variation in grapevine genomes. <i>Plant Journal</i> , 2016, 88, 648-661.	5.7	45
15	Morphological Variability in Leaves and Molecular Characterization of Novel Table Grape Candidate Cultivars ( <i>Vitis vinifera</i> L.). <i>Molecular Biotechnology</i> , 2014, 56, 557-570.	2.4	9
16	Evidences for an Alternative Genealogy of "Sangiovese"™. <i>Molecular Biotechnology</i> , 2013, 53, 278-288.	2.4	20
17	Sangiovese and Its Offspring in Southern Italy. <i>Molecular Biotechnology</i> , 2013, 54, 581-589.	2.4	10
18	Validation Assay of p3_VvAGL11 Marker in a Wide Range of Genetic Background for Early Selection of Stenospermocarpy in <i>Vitis vinifera</i> L.. <i>Molecular Biotechnology</i> , 2013, 54, 1021-1030.	2.4	37

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19	Male infertility and copy number variants (CNVs) in the dog: a two-pronged approach using Computer Assisted Sperm Analysis (CASA) and Fluorescent In Situ Hybridization (FISH). <i>BMC Genomics</i> , 2013, 14, 921.	2.8	10
20	Evolutionary history of linked D4Z4 and Beta satellite clusters at the FSHD locus (4q35). <i>Genomics</i> , 2012, 100, 289-296.	2.9	5
21	Copy number variation of individual cattle genomes using next-generation sequencing. <i>Genome Research</i> , 2012, 22, 778-790.	5.5	259
22	Real-time PCR for the detection of precise transgene copy number in durum wheat. <i>Cellular and Molecular Biology Letters</i> , 2011, 16, 652-68.	7.0	26
23	Initial analysis of copy number variations in cattle selected for resistance or susceptibility to intestinal nematodes. <i>Mammalian Genome</i> , 2011, 22, 111-121.	2.2	46
24	Genomic characteristics of cattle copy number variations. <i>BMC Genomics</i> , 2011, 12, 127.	2.8	201
25	Genome-wide characterization of centromeric satellites from multiple mammalian genomes. <i>Genome Research</i> , 2011, 21, 137-145.	5.5	78
26	Analysis of copy number variations among diverse cattle breeds. <i>Genome Research</i> , 2010, 20, 693-703.	5.5	280
27	New Insights into Centromere Organization and Evolution from the White-Cheeked Gibbon and Marmoset. <i>Molecular Biology and Evolution</i> , 2009, 26, 1889-1900.	8.9	45
28	A satellite-like sequence, representing a "clone gap" in the human genome, was likely involved in the seeding of a novel centromere in macaque. <i>Chromosoma</i> , 2009, 118, 269-277.	2.2	9
29	A burst of segmental duplications in the genome of the African great ape ancestor. <i>Nature</i> , 2009, 457, 877-881.	27.8	222
30	Primate chromosome evolution: Ancestral karyotypes, marker order and neocentromeres. <i>Chromosome Research</i> , 2008, 16, 17-39.	2.2	117
31	Stably expressed d-genome-derived HMW glutenin subunit genes transformed into different durum wheat genotypes change dough mixing properties. <i>Molecular Breeding</i> , 2008, 22, 267-279.	2.1	31
32	Evolutionary toggling of the MAPT 17q21.31 inversion region. <i>Nature Genetics</i> , 2008, 40, 1076-1083.	21.4	176
33	Hominoid chromosomal rearrangements on 17q map to complex regions of segmental duplication. <i>Genome Biology</i> , 2008, 9, R28.	9.6	25
34	Evolutionary Formation of New Centromeres in Macaque. <i>Science</i> , 2007, 316, 243-246.	12.6	136
35	Evolutionary history of chromosome 11 featuring four distinct centromere repositioning events in Catarrhini. <i>Genomics</i> , 2007, 90, 35-43.	2.9	28
36	Characterization and evolution of the novel gene family FAM90A in primates originated by multiple duplication and rearrangement events. <i>Human Molecular Genetics</i> , 2007, 16, 2572-2582.	2.9	24

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37	Ancestral reconstruction of segmental duplications reveals punctuated cores of human genome evolution. <i>Nature Genetics</i> , 2007, 39, 1361-1368.	21.4	192
38	Evolutionary genomic remodelling of the human 4q subtelomere (4q35.2). <i>BMC Evolutionary Biology</i> , 2007, 7, 39.	3.2	11
39	Independent centromere formation in a capricious, gene-free domain of chromosome 13q21 in Old World monkeys and pigs. <i>Genome Biology</i> , 2006, 7, R91.	9.6	60
40	Evolutionary movement of centromeres in horse, donkey, and zebra. <i>Genomics</i> , 2006, 87, 777-782.	2.9	100
41	The boundary of macaque rDNA is constituted by low-copy sequences conserved during evolution. <i>Genomics</i> , 2006, 88, 564-571.	2.9	6
42	A preliminary comparative analysis of primate segmental duplications shows elevated substitution rates and a great-ape expansion of intrachromosomal duplications. <i>Genome Research</i> , 2006, 16, 576-583.	5.5	82
43	Recurrent Sites for New Centromere Seeding. <i>Genome Research</i> , 2004, 14, 1696-1703.	5.5	135
44	Evolution of Beta Satellite DNA Sequences: Evidence for Duplication-Mediated Repeat Amplification and Spreading. <i>Molecular Biology and Evolution</i> , 2004, 21, 1792-1799.	8.9	22
45	Evolutionary History of Chromosome 20. <i>Molecular Biology and Evolution</i> , 2004, 22, 360-366.	8.9	21
46	Refinement of a chimpanzee pericentric inversion breakpoint to a segmental duplication cluster. <i>Genome Biology</i> , 2003, 4, R50.	9.6	107
47	Localization of a new highly repeated DNA sequence of Lemur catta ( <i>Lemuridae</i> , <i>Strepsirhini</i> ). <i>Genome</i> , 2002, 45, 973-976.	2.0	0
48	Analysis of chromosome conservation in Lemur catta studied by chromosome paints and BAC/PAC probes. <i>Chromosoma</i> , 2002, 111, 348-356.	2.2	26
49	Characterization of a highly repeated DNA sequence family in five species of the genus <i>Eulemur</i> . <i>Gene</i> , 2001, 275, 305-310.	2.2	9