

Michele Morgante

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

125
papers

20,199
citations

59
h-index

126
g-index

126
ext. papers

24,088
ext. citations

9
avg, IF

6.06
L-index

#	Paper	IF	Citations
125	ddRAD-seq reveals the genetic structure and detects signals of selection in Italian brown trout.. <i>Genetics Selection Evolution</i> , 2022 , 54, 8	4.9	1
124	The genomes of 204 <i>Vitis vinifera</i> accessions reveal the origin of European wine grapes.. <i>Nature Communications</i> , 2021 , 12, 7240	17.4	6
123	Open chromatin in grapevine marks candidate CREs and with other chromatin features correlates with gene expression. <i>Plant Journal</i> , 2021 , 107, 1631-1647	6.9	1
122	A draft genome of sweet cherry (<i>Prunus avium</i> L.) reveals genome-wide and local effects of domestication. <i>Plant Journal</i> , 2020 , 103, 1420-1432	6.9	6
121	A single polyploidization event at the origin of the tetraploid genome of <i>Coffea arabica</i> is responsible for the extremely low genetic variation in wild and cultivated germplasm. <i>Scientific Reports</i> , 2020 , 10, 4642	4.9	32
120	Genetic and Genomic Approaches for Adaptation of Grapevine to Climate Change 2020 , 157-270		7
119	Gene duplication and transposition of mobile elements drive evolution of the Rpv3 resistance locus in grapevine. <i>Plant Journal</i> , 2020 , 101, 529-542	6.9	14
118	Two-omics data revealed commonalities and differences between Rpv12- and Rpv3-mediated resistance in grapevine. <i>Scientific Reports</i> , 2020 , 10, 12193	4.9	9
117	Physiological and RNA sequencing data of white lupin plants grown under Fe and P deficiency. <i>Data in Brief</i> , 2019 , 25, 104069	1.2	5
116	Physiological and transcriptomic data highlight common features between iron and phosphorus acquisition mechanisms in white lupin roots. <i>Plant Science</i> , 2019 , 285, 110-121	5.3	18
115	Genetic, epigenetic and genomic effects on variation of gene expression among grape varieties. <i>Plant Journal</i> , 2019 , 99, 895-909	6.9	11
114	Genomic tools for durum wheat breeding: de novo assembly of Svevo transcriptome and SNP discovery in elite germplasm. <i>BMC Genomics</i> , 2019 , 20, 278	4.5	4
113	Single primer enrichment technology as a tool for massive genotyping: a benchmark on black poplar and maize. <i>Annals of Botany</i> , 2019 , 124, 543-552	4.1	14
112	Genetic Mapping of the Incompatibility Locus in Olive and Development of a Linked Sequence-Tagged Site Marker. <i>Frontiers in Plant Science</i> , 2019 , 10, 1760	6.2	7
111	Common and specific responses to iron and phosphorus deficiencies in roots of apple tree (<i>Malus domestica</i>). <i>Plant Molecular Biology</i> , 2019 , 101, 129-148	4.6	4
110	Optimizing ddRADseq in Non-Model Species: A Case Study in <i>Eucalyptus dunnii</i> Maiden. <i>Agronomy</i> , 2019 , 9, 484	3.6	17
109	Transgenerational Response to Nitrogen Deprivation in. <i>International Journal of Molecular Sciences</i> , 2019 , 20,	6.3	2

108	The genetic background modulates the intensity of Rpv3-dependent downy mildew resistance in grapevine. <i>Plant Breeding</i> , 2018 , 137, 220-228	2.4	16
107	Grapevine field experiments reveal the contribution of genotype, the influence of environment and the effect of their interaction (GE) on the berry transcriptome. <i>Plant Journal</i> , 2018 , 93, 1143-1159	6.9	37
106	InDel markers for monitoring the introgression of downy mildew resistance from wild relatives into grape varieties. <i>Molecular Breeding</i> , 2018 , 38, 1	3.4	6
105	Genes and gene clusters related to genotype and drought-induced variation in saccharification potential, lignin content and wood anatomical traits in <i>Populus nigra</i> . <i>Tree Physiology</i> , 2018 , 38, 320-339 ^{4.2}	4.2	24
104	Reduction of heterozygosity (ROH) as a method to detect mosaic structural variation. <i>Plant Biotechnology Journal</i> , 2017 , 15, 791-793	11.6	8
103	De novo assembly, functional annotation, and analysis of the giant reed (<i>L.</i>) leaf transcriptome provide tools for the development of a biofuel feedstock. <i>Biotechnology for Biofuels</i> , 2017 , 10, 138	7.8	28
102	A PLAG1 mutation contributed to stature recovery in modern cattle. <i>Scientific Reports</i> , 2017 , 7, 17140	4.9	32
101	Regeneration of the entire human epidermis using transgenic stem cells. <i>Nature</i> , 2017 , 551, 327-332	50.4	379
100	Identifying Genetic Signatures of Natural Selection Using Pooled Population Sequencing in <i>Picea abies</i> . <i>G3: Genes, Genomes, Genetics</i> , 2016 , 6, 1979-89	3.2	19
99	Genome-wide analysis of LTR-retrotransposon expression in leaves of <i>Populus trichocarpa</i> water-deprived plants. <i>Tree Genetics and Genomes</i> , 2016 , 12, 1	2.1	16
98	Biomass traits and candidate genes for bioenergy revealed through association genetics in coppiced European <i>Populus nigra</i> (L.). <i>Biotechnology for Biofuels</i> , 2016 , 9, 195	7.8	24
97	The limits and potential of paleogenomic techniques for reconstructing grapevine domestication. <i>Journal of Archaeological Science</i> , 2016 , 72, 57-70	2.9	31
96	A Homolog of Blade-On-Petiole 1 and 2 (BOP1/2) Controls Internode Length and Homeotic Changes of the Barley Inflorescence. <i>Plant Physiology</i> , 2016 , 171, 1113-27	6.6	31
95	Genome Sequencing, Transcriptomics, and Proteomics. <i>Compendium of Plant Genomes</i> , 2016 , 141-161	0.8	8
94	Characterization of the Poplar Pan-Genome by Genome-Wide Identification of Structural Variation. <i>Molecular Biology and Evolution</i> , 2016 , 33, 2706-19	8.3	66
93	LTR retrotransposon dynamics in the evolution of the olive (<i>Olea europaea</i>) genome. <i>DNA Research</i> , 2015 , 22, 91-100	4.5	34
92	Transposon Insertions, Structural Variations, and SNPs Contribute to the Evolution of the Melon Genome. <i>Molecular Biology and Evolution</i> , 2015 , 32, 2760-74	8.3	50
91	A high-density, SNP-based consensus map of tetraploid wheat as a bridge to integrate durum and bread wheat genomics and breeding. <i>Plant Biotechnology Journal</i> , 2015 , 13, 648-63	11.6	196

90	Genetic properties of the MAGIC maize population: a new platform for high definition QTL mapping in <i>Zea mays</i> . <i>Genome Biology</i> , 2015 , 16, 167	18.3	144
89	Physical Mapping of Bread Wheat Chromosome 5A: An Integrated Approach. <i>Plant Genome</i> , 2015 , 8, eplantgenome2015.03.0011	4.4	9
88	The Ty1-copia LTR retroelement family PARTC is highly conserved in conifers over 200 MY of evolution. <i>Gene</i> , 2015 , 568, 89-99	3.8	22
87	Sequencing of diverse mandarin, pummelo and orange genomes reveals complex history of admixture during citrus domestication. <i>Nature Biotechnology</i> , 2014 , 32, 656-62	44.5	413
86	Structural variation and genome complexity: is dispensable really dispensable?. <i>Current Opinion in Plant Biology</i> , 2014 , 18, 31-6	9.9	72
85	A <i>Picea abies</i> linkage map based on SNP markers identifies QTLs for four aspects of resistance to <i>Heterobasidion parviporum</i> infection. <i>PLoS ONE</i> , 2014 , 9, e101049	3.7	39
84	The peculiar landscape of repetitive sequences in the olive (<i>Olea europaea</i> L.) genome. <i>Genome Biology and Evolution</i> , 2014 , 6, 776-91	3.9	51
83	Characterization of polyploid wheat genomic diversity using a high-density 90,000 single nucleotide polymorphism array. <i>Plant Biotechnology Journal</i> , 2014 , 12, 787-96	11.6	1136
82	Genetic Diversity in the Grapevine Germplasm 2014 , 683-704		7
81	Three distinct mutational mechanisms acting on a single gene underpin the origin of yellow flesh in peach. <i>Plant Journal</i> , 2013 , 76, 175-87	6.9	115
80	The Hypomethylated Partial Restriction (HMPR) method reduces the repetitive content of genomic libraries in Norway spruce (<i>Picea abies</i>). <i>Tree Genetics and Genomes</i> , 2013 , 9, 601-612	2.1	3
79	The repetitive component of the sunflower genome as shown by different procedures for assembling next generation sequencing reads. <i>BMC Genomics</i> , 2013 , 14, 686	4.5	46
78	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, 487-94	36.3	777
77	The Norway spruce genome sequence and conifer genome evolution. <i>Nature</i> , 2013 , 497, 579-84	50.4	983
76	Breeding with rare defective alleles (BRDA): a natural <i>Populus nigra</i> HCT mutant with modified lignin as a case study. <i>New Phytologist</i> , 2013 , 198, 765-776	9.8	73
75	Historical introgression of the downy mildew resistance gene Rpv12 from the Asian species <i>Vitis amurensis</i> into grapevine varieties. <i>PLoS ONE</i> , 2013 , 8, e61228	3.7	83
74	An extensive evaluation of read trimming effects on Illumina NGS data analysis. <i>PLoS ONE</i> , 2013 , 8, e85034	3.7	252
73	Selective sweep at the Rpv3 locus during grapevine breeding for downy mildew resistance. <i>Theoretical and Applied Genetics</i> , 2012 , 124, 277-86	6	84

72	High resolution mapping of Dense spike-ar (dsp.ar) to the genetic centromere of barley chromosome 7H. <i>Theoretical and Applied Genetics</i> , 2012 , 124, 373-84	6	33
71	Accelerating the domestication of forest trees in a changing world. <i>Trends in Plant Science</i> , 2012 , 17, 64-72	13.1	85
70	Whole genome comparisons of <i>Fragaria</i> , <i>Prunus</i> and <i>Malus</i> reveal different modes of evolution between Rosaceous subfamilies. <i>BMC Genomics</i> , 2012 , 13, 129	4.5	62
69	Phenotypic plasticity, QTL mapping and genomic characterization of bud set in black poplar. <i>BMC Plant Biology</i> , 2012 , 12, 47	5.3	32
68	Disentangling the roles of history and local selection in shaping clinal variation of allele frequencies and gene expression in Norway spruce (<i>Picea abies</i>). <i>Genetics</i> , 2012 , 191, 865-81	4	112
67	Analysis of the barley bract suppression gene <i>Trd1</i> . <i>Theoretical and Applied Genetics</i> , 2012 , 125, 33-45	6	28
66	The quest for rare variants: pooled multiplexed next generation sequencing in plants. <i>Frontiers in Plant Science</i> , 2012 , 3, 133	6.2	13
65	Development and evaluation of a 9K SNP array for peach by internationally coordinated SNP detection and validation in breeding germplasm. <i>PLoS ONE</i> , 2012 , 7, e35668	3.7	164
64	Large-scale detection of rare variants via pooled multiplexed next-generation sequencing: towards next-generation Ecotilling. <i>Plant Journal</i> , 2011 , 67, 736-45	6.9	55
63	Bud set in poplar--genetic dissection of a complex trait in natural and hybrid populations. <i>New Phytologist</i> , 2011 , 189, 106-21	9.8	97
62	Forest ecosystem genomics and adaptation: EVOLTREE conference report. <i>Tree Genetics and Genomes</i> , 2011 , 7, 869-875	2.1	7
61	Nucleotide diversity and linkage disequilibrium in <i>Populus nigra</i> cinnamyl alcohol dehydrogenase (<i>CAD4</i>) gene. <i>Tree Genetics and Genomes</i> , 2011 , 7, 1011-1023	2.1	82
60	Genetic dissection of barley morphology and development. <i>Plant Physiology</i> , 2011 , 155, 617-27	6.6	145
59	Exploiting induced variation to dissect quantitative traits in barley. <i>Biochemical Society Transactions</i> , 2010 , 38, 683-8	5.1	8
58	Analysis of transposons and repeat composition of the sunflower (<i>Helianthus annuus</i> L.) genome. <i>Theoretical and Applied Genetics</i> , 2010 , 120, 491-508	6	41
57	The SSR-based molecular profile of 1005 grapevine (<i>Vitis vinifera</i> L.) accessions uncovers new synonymy and parentages, and reveals a large admixture amongst varieties of different geographic origin. <i>Theoretical and Applied Genetics</i> , 2010 , 121, 1569-85	6	157
56	Correction: High throughput approaches reveal splicing of primary microRNA transcripts and tissue specific expression of mature microRNAs in <i>Vitis vinifera</i> . <i>BMC Genomics</i> , 2010 , 11, 109	4.5	44
55	Physical mapping in highly heterozygous genomes: a physical contig map of the Pinot Noir grapevine cultivar. <i>BMC Genomics</i> , 2010 , 11, 204	4.5	15

54	Expansion and subfunctionalisation of flavonoid 3 β 5Hydroxylases in the grapevine lineage. <i>BMC Genomics</i> , 2010 , 11, 562	4.5	76
53	Automated FingerPrint Background removal: FPB. <i>BMC Bioinformatics</i> , 2009 , 10, 127	3.6	8
52	High throughput approaches reveal splicing of primary microRNA transcripts and tissue specific expression of mature microRNAs in <i>Vitis vinifera</i> . <i>BMC Genomics</i> , 2009 , 10, 558	4.5	52
51	Recombinant near-isogenic lines: a resource for the mendelization of heterotic QTL in maize. <i>Molecular Genetics and Genomics</i> , 2009 , 281, 447-57	3.1	12
50	QTL detection in maize testcross progenies as affected by related and unrelated testers. <i>Theoretical and Applied Genetics</i> , 2009 , 118, 993-1004	6	29
49	Resistance to <i>Plasmopara viticola</i> in grapevine BiancaSis controlled by a major dominant gene causing localised necrosis at the infection site. <i>Theoretical and Applied Genetics</i> , 2009 , 120, 163-76	6	149
48	The powdery mildew resistance gene REN1 co-segregates with an NBS-LRR gene cluster in two Central Asian grapevines. <i>BMC Genetics</i> , 2009 , 10, 89	2.6	73
47	Asymmetric allele-specific expression in relation to developmental variation and drought stress in barley hybrids. <i>Plant Journal</i> , 2009 , 59, 14-26	6.9	45
46	Reply: A unified classification system for eukaryotic transposable elements should reflect their phylogeny. <i>Nature Reviews Genetics</i> , 2009 , 10, 276-276	30.1	22
45	A universal classification of eukaryotic transposable elements implemented in Repbase. <i>Nature Reviews Genetics</i> , 2008 , 9, 414-414	30.1	4
44	A set of microsatellite markers with long core repeat optimized for grape (<i>Vitis</i> spp.) genotyping. <i>BMC Plant Biology</i> , 2008 , 8, 127	5.3	81
43	A physical map of the heterozygous grapevine Cabernet Sauvignon allows mapping candidate genes for disease resistance. <i>BMC Plant Biology</i> , 2008 , 8, 66	5.3	53
42	Annotating genomes with massive-scale RNA sequencing. <i>Genome Biology</i> , 2008 , 9, R175	18.3	186
41	Control of steric hindrance on restriction enzyme reactions with surface-bound DNA nanostructures. <i>Nano Letters</i> , 2008 , 8, 4140-5	11.5	45
40	A unified classification system for eukaryotic transposable elements. <i>Nature Reviews Genetics</i> , 2007 , 8, 973-82	30.1	1776
39	The grapevine genome sequence suggests ancestral hexaploidization in major angiosperm phyla. <i>Nature</i> , 2007 , 449, 463-7	50.4	2675
38	Global expression analysis of nucleotide binding site-leucine rich repeat-encoding and related genes in <i>Arabidopsis</i> . <i>BMC Plant Biology</i> , 2007 , 7, 56	5.3	124
37	Transposable elements and the plant pan-genomes. <i>Current Opinion in Plant Biology</i> , 2007 , 10, 149-55	9.9	175

36	Conserved noncoding genomic sequences associated with a flowering-time quantitative trait locus in maize. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 11376-81	11.5	429
35	Classical genetic and quantitative trait loci analyses of heterosis in a maize hybrid between two elite inbred lines. <i>Genetics</i> , 2007 , 176, 625-44	4	135
34	A dense single-nucleotide polymorphism-based genetic linkage map of grapevine (<i>Vitis vinifera</i> L.) anchoring Pinot Noir bacterial artificial chromosome contigs. <i>Genetics</i> , 2007 , 176, 2637-50	4	109
33	Multilocus patterns of nucleotide diversity, linkage disequilibrium and demographic history of Norway spruce [<i>Picea abies</i> (L.) Karst]. <i>Genetics</i> , 2006 , 174, 2095-105	4	205
32	Plant genome organisation and diversity: the year of the junk!. <i>Current Opinion in Biotechnology</i> , 2006 , 17, 168-73	11.4	64
31	Population genetics of Norway spruce (<i>Picea abies</i> Karst.) at regional scale: sensitivity of different microsatellite motif classes in detecting differentiation. <i>Annals of Forest Science</i> , 2006 , 63, 485-491	3.1	24
30	Gene duplication and exon shuffling by helitron-like transposons generate intraspecies diversity in maize. <i>Nature Genetics</i> , 2005 , 37, 997-1002	36.3	403
29	Analysis of the distribution of marker classes in a genetic linkage map: a case study in Norway spruce (<i>Picea abies</i> karst). <i>Tree Genetics and Genomes</i> , 2005 , 1, 93-102	2.1	15
28	Structured motifs search. <i>Journal of Computational Biology</i> , 2005 , 12, 1065-82	1.7	28
27	Evolution of DNA sequence nonhomologies among maize inbreds. <i>Plant Cell</i> , 2005 , 17, 343-60	11.6	255
26	Long-range patterns of diversity and linkage disequilibrium surrounding the maize Y1 gene are indicative of an asymmetric selective sweep. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 9885-90	11.5	169
25	Anchoring 9,371 maize expressed sequence tagged unigenes to the bacterial artificial chromosome contig map by two-dimensional overgo hybridization. <i>Plant Physiology</i> , 2004 , 134, 1317-26	6.6	88
24	Mapping and sequencing complex genomes: let's get physical!. <i>Nature Reviews Genetics</i> , 2004 , 5, 578-88	30.1	72
23	Corn and humans: recombination and linkage disequilibrium in two genomes of similar size. <i>Trends in Genetics</i> , 2004 , 20, 103-11	8.5	180
22	Linkage disequilibrium and sequence diversity in a 500-kbp region around the <i>adh1</i> locus in elite maize germplasm. <i>Theoretical and Applied Genetics</i> , 2004 , 109, 681-9	6	63
21	From plant genomics to breeding practice. <i>Current Opinion in Biotechnology</i> , 2003 , 14, 214-9	11.4	168
20	Monitoring genome-wide changes in gene expression in response to endogenous cytokinin reveals targets in <i>Arabidopsis thaliana</i> . <i>FEBS Letters</i> , 2003 , 554, 373-80	3.8	67
19	Contrasting effects of selection on sequence diversity and linkage disequilibrium at two phytoene synthase loci. <i>Plant Cell</i> , 2003 , 15, 1795-806	11.6	214

18	SNP frequency, haplotype structure and linkage disequilibrium in elite maize inbred lines. <i>BMC Genetics</i> , 2002 , 3, 19	2.6	345
17	TIR-X and TIR-NBS proteins: two new families related to disease resistance TIR-NBS-LRR proteins encoded in Arabidopsis and other plant genomes. <i>Plant Journal</i> , 2002 , 32, 77-92	6.9	201
16	Microsatellites are preferentially associated with nonrepetitive DNA in plant genomes. <i>Nature Genetics</i> , 2002 , 30, 194-200	36.3	836
15	Comparative genomic mapping between a 754 kb region flanking DREB1A in Arabidopsis thaliana and maize. <i>Plant Molecular Biology</i> , 2002 , 48, 741-50	4.6	15
14	Genome-wide gene expression profiling in Arabidopsis thaliana reveals new targets of abscisic acid and largely impaired gene regulation in the abi1-1 mutant. <i>Journal of Cell Science</i> , 2002 , 115, 4891-900	5.3	264
13	Abundance, distribution, and transcriptional activity of repetitive elements in the maize genome. <i>Genome Research</i> , 2001 , 11, 1660-76	9.7	316
12	Analysis of the genus Zea (Poaceae) using polymorphic chloroplast simple sequence repeats. <i>Plant Systematics and Evolution</i> , 1999 , 218, 245-256	1.3	18
11	Intimate association of microsatellite repeats with retrotransposons and other dispersed repetitive elements in barley. <i>Plant Journal</i> , 1999 , 17, 415-25	6.9	147
10	Identification of Microsatellite Markers and Their Application to Population Genetics of Venturia inaequalis. <i>Phytopathology</i> , 1999 , 89, 748-53	3.8	180
9	Pcr-based multiplex DNA fingerprinting techniques for the analysis of conifer genomes. <i>Molecular Breeding</i> , 1998 , 4, 173-177	3.4	33
8	Comparative analysis of genetic similarity among maize inbred lines detected by RFLPs, RAPDs, SSRs, and AFLPs. <i>Theoretical and Applied Genetics</i> , 1998 , 97, 1248-1255	6	363
7	Cross-species amplification of soybean (Glycine max) simple sequence repeats (SSRs) within the genus and other legume genera: implications for the transferability of SSRs in plants. <i>Molecular Biology and Evolution</i> , 1998 , 15, 1275-87	8.3	334
6	Identification and characterization of microsatellites in Norway spruce (Picea abies K.). <i>Genome</i> , 1997 , 40, 411-9	2.4	130
5	Molecular technologies for biodiversity evaluation: opportunities and challenges. <i>Nature Biotechnology</i> , 1997 , 15, 625-8	44.5	108
4	A first linkage map of Cichorium intybus L. using a one-way pseudo-testcross and PCR-derived markers. <i>Molecular Breeding</i> , 1997 , 3, 415-425	3.4	22
3	The comparison of RFLP, RAPD, AFLP and SSR (microsatellite) markers for germplasm analysis. <i>Molecular Breeding</i> , 1996 , 2, 225-238	3.4	1574
2	Paternal inheritance of plastids in interspecific hybrids of the genus Actinidia revealed by PCR-amplification of chloroplast DNA fragments. <i>Molecular Genetics and Genomics</i> , 1995 , 247, 693-7		28
1	Polymorphic simple sequence repeat regions in chloroplast genomes: applications to the population genetics of pines. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995 , 92, 7759-63	11.5	360

