

Marco Maccaferri

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3322349/publications.pdf>

Version: 2024-02-01

65
papers

8,313
citations

81743

39
h-index

128067

60
g-index

66
all docs

66
docs citations

66
times ranked

5755
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome Wide Association Study Uncovers the QTLome for Osmotic Adjustment and Related Drought Adaptive Traits in Durum Wheat. <i>Genes</i> , 2022, 13, 293.	1.0	12
2	Genetic analysis of novel resistance sources and genome-wide association mapping identified novel QTLs for resistance to <i>Zymoseptoria tritici</i> , the causal agent of septoria tritici blotch in wheat. <i>Journal of Applied Genetics</i> , 2022, 63, 429-445.	1.0	5
3	Sequence-Based Marker Assisted Selection in Wheat. , 2022, , 513-538.		3
4	Monitoring changes of lipid composition in durum wheat during grain development. <i>Journal of Cereal Science</i> , 2021, 97, 103131.	1.8	6
5	Abiotic Stress Response of Near-Isogenic Spring Durum Wheat Lines under Different Sowing Densities. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2053.	1.8	6
6	Wheat root systems as a breeding target for climate resilience. <i>Theoretical and Applied Genetics</i> , 2021, 134, 1645-1662.	1.8	74
7	High-throughput field phenotyping reveals genetic variation in photosynthetic traits in durum wheat under drought. <i>Plant, Cell and Environment</i> , 2021, 44, 2858-2878.	2.8	12
8	Back Cover Image. <i>Plant, Cell and Environment</i> , 2021, 44, .	2.8	0
9	Genome-wide association analysis unveils novel QTLs for seminal root system architecture traits in Ethiopian durum wheat. <i>BMC Genomics</i> , 2021, 22, 20.	1.2	33
10	Resequencing of 145 Landmark Cultivars Reveals Asymmetric Sub-genome Selection and Strong Founder Genotype Effects on Wheat Breeding in China. <i>Molecular Plant</i> , 2020, 13, 1733-1751.	3.9	129
11	Genomic Regions Associated with the Control of Flowering Time in Durum Wheat. <i>Plants</i> , 2020, 9, 1628.	1.6	15
12	The Global Durum Wheat Panel (GDP): An International Platform to Identify and Exchange Beneficial Alleles. <i>Frontiers in Plant Science</i> , 2020, 11, 569905.	1.7	44
13	Quantitative trait loci for agronomic traits in tetraploid wheat for enhancing grain yield in Kazakhstan environments. <i>PLoS ONE</i> , 2020, 15, e234863.	1.1	19
14	Genome-wide association mapping for grain shape and color traits in Ethiopian durum wheat (<i>Triticum</i>) Tj ETQq0 0.0 rgBT /Overlock 10	2.3	38
15	Carotenoid Pigment Content in Durum Wheat (<i>Triticum turgidum</i> L. var durum): An Overview of Quantitative Trait Loci and Candidate Genes. <i>Frontiers in Plant Science</i> , 2019, 10, 1347.	1.7	59
16	Multi-Trait, Multi-Environment Genomic Prediction of Durum Wheat With Genomic Best Linear Unbiased Predictor and Deep Learning Methods. <i>Frontiers in Plant Science</i> , 2019, 10, 1311.	1.7	47
17	Durum wheat genome highlights past domestication signatures and future improvement targets. <i>Nature Genetics</i> , 2019, 51, 885-895.	9.4	576
18	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.	1.2	7

#	ARTICLE	IF	CITATIONS
19	Exploring and exploiting the genetic variation of Fusarium head blight resistance for genomic-assisted breeding in the elite durum wheat gene pool. <i>Theoretical and Applied Genetics</i> , 2019, 132, 969-988.	1.8	57
20	Asparagine synthetase genes (AsnS1 and AsnS2) in durum wheat: structural analysis and expression under nitrogen stress. <i>Euphytica</i> , 2018, 214, 1.	0.6	21
21	Yield of chromosomally engineered durum wheat- <i>Thinopyrum ponticum</i> recombinant lines in a range of contrasting rain-fed environments. <i>Field Crops Research</i> , 2018, 228, 147-157.	2.3	11
22	Comparative Aerial and Ground Based High Throughput Phenotyping for the Genetic Dissection of NDVI as a Proxy for Drought Adaptive Traits in Durum Wheat. <i>Frontiers in Plant Science</i> , 2018, 9, 893.	1.7	117
23	Differential representation of albumins and globulins during grain development in durum wheat and its possible functional consequences. <i>Journal of Proteomics</i> , 2017, 162, 86-98.	1.2	31
24	Genome-wide association mapping for seedling and field resistance to <i>Puccinia striiformis</i> f. sp. <i>tritici</i> in elite durum wheat. <i>Theoretical and Applied Genetics</i> , 2017, 130, 649-667.	1.8	71
25	Wild emmer genome architecture and diversity elucidate wheat evolution and domestication. <i>Science</i> , 2017, 357, 93-97.	6.0	781
26	Genome-wide association mapping reveals a rich genetic architecture of stripe rust resistance loci in emmer wheat (<i>Triticum turgidum</i> ssp. <i>dicoccum</i>). <i>Theoretical and Applied Genetics</i> , 2017, 130, 2249-2270.	1.8	80
27	Novel Sources of Stripe Rust Resistance Identified by Genome-Wide Association Mapping in Ethiopian Durum Wheat (<i>Triticum turgidum</i> ssp. <i>durum</i>). <i>Frontiers in Plant Science</i> , 2017, 8, 774.	1.7	66
28	Extending the Marker × Environment Interaction Model for Genomic-Enabled Prediction and Genome-Wide Association Analysis in Durum Wheat. <i>Crop Science</i> , 2016, 56, 2193-2209.	0.8	101
29	A multiparental cross population for mapping QTL for agronomic traits in durum wheat (<i>Triticum turgidum</i> ssp. <i>durum</i>). <i>Plant Biotechnology Journal</i> , 2016, 14, 735-748.	4.1	121
30	Two major quantitative trait loci controlling the number of seminal roots in maize co-map with the root developmental genes <i>rtcs1</i> and <i>rum1</i> . <i>Journal of Experimental Botany</i> , 2016, 67, 1149-1159.	2.4	40
31	Prioritizing quantitative trait loci for root system architecture in tetraploid wheat. <i>Journal of Experimental Botany</i> , 2016, 67, 1161-1178.	2.4	206
32	Genetic variation for aerenchyma and other root anatomical traits in durum wheat (<i>Triticum durum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.8	5
33	A Genome-Wide Association Study of Resistance to Stripe Rust (<i>Puccinia striiformis</i> f. sp. <i>tritici</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5 G3: Genes, Genomes, Genetics, 2015, 5, 449-465.	0.8	356
34	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, 648-663.	4.1	386
35	Genomics Approaches to Dissect the Genetic Basis of Drought Resistance in Durum Wheat. , 2015, , 213-223.		2
36	Association Mapping Reveals Novel Stem Rust Resistance Loci in Durum Wheat at the Seedling Stage. <i>Plant Genome</i> , 2014, 7, plantgenome2013.08.0026.	1.6	67

#	ARTICLE	IF	CITATIONS
37	Association mapping for root architectural traits in durum wheat seedlings as related to agronomic performance. <i>Molecular Breeding</i> , 2014, 34, 1629-1645.	1.0	115
38	Characterization of polyploid wheat genomic diversity using a high-density 90,000 single nucleotide polymorphism array. <i>Plant Biotechnology Journal</i> , 2014, 12, 787-796.	4.1	1,828
39	QTL dissection of yield components and morpho-physiological traits in a durum wheat elite population tested in contrasting thermo-pluviometric conditions. <i>Crop and Pasture Science</i> , 2014, 65, 80.	0.7	79
40	A consensus framework map of durum wheat (<i>Triticum durum</i> Desf.) suitable for linkage disequilibrium analysis and genome-wide association mapping. <i>BMC Genomics</i> , 2014, 15, 873.	1.2	85
41	Development of COS-SNP and HRM markers for high-throughput and reliable haplotype-based detection of Lr14a in durum wheat (<i>Triticum durum</i> Desf.). <i>Theoretical and Applied Genetics</i> , 2013, 126, 1077-1101.	1.8	43
42	Searching for novel sources of field resistance to Ug99 and Ethiopian stem rust races in durum wheat via association mapping. <i>Theoretical and Applied Genetics</i> , 2013, 126, 1237-1256.	1.8	116
43	Sequence-based SNP genotyping in durum wheat. <i>Plant Biotechnology Journal</i> , 2013, 11, 809-817.	4.1	63
44	Wheat syntenome unveils new evidences of contrasted evolutionary plasticity between paleo- and neoduplicated subgenomes. <i>Plant Journal</i> , 2013, 76, 1030-1044.	2.8	99
45	Genetic analysis of Soil-Borne Cereal Mosaic Virus response in durum wheat: evidence for the role of the major quantitative trait locus QSbm.ubo-2BS and of minor quantitative trait loci. <i>Molecular Breeding</i> , 2012, 29, 973-988.	1.0	11
46	Resistance to Soil-borne cereal mosaic virus in durum wheat is controlled by a major QTL on chromosome arm 2BS and minor loci. <i>Theoretical and Applied Genetics</i> , 2011, 123, 527-544.	1.8	25
47	High-throughput SNP discovery and genotyping in durum wheat (<i>Triticum durum</i> Desf.). <i>Theoretical and Applied Genetics</i> , 2011, 123, 555-569.	1.8	120
48	Association mapping in durum wheat grown across a broad range of water regimes. <i>Journal of Experimental Botany</i> , 2011, 62, 409-438.	2.4	270
49	Association mapping of leaf rust response in durum wheat. <i>Molecular Breeding</i> , 2010, 26, 189-228.	1.0	86
50	Understanding the relationships between genetic and phenotypic structures of a collection of elite durum wheat accessions. <i>Field Crops Research</i> , 2010, 119, 91-105.	2.3	54
51	Virulence Phenotypes and Molecular Genotypes in Collections of <i>Puccinia triticina</i> from Italy. <i>Plant Disease</i> , 2010, 94, 420-424.	0.7	26
52	Genomics of Tolerance to Abiotic Stress in the Triticeae. , 2009, , 481-558.		8
53	An integrated DArT-SSR linkage map of durum wheat. <i>Molecular Breeding</i> , 2008, 22, 629-648.	1.0	97
54	A major QTL for durable leaf rust resistance widely exploited in durum wheat breeding programs maps on the distal region of chromosome arm 7BL. <i>Theoretical and Applied Genetics</i> , 2008, 117, 1225-1240.	1.8	59

#	ARTICLE	IF	CITATIONS
55	Quantitative Trait Loci for Grain Yield and Adaptation of Durum Wheat (<i>Triticum durum</i> Desf.) Across a Wide Range of Water Availability. <i>Genetics</i> , 2008, 178, 489-511.	1.2	397
56	Genetic dissection of seminal root architecture in elite durum wheat germplasm. <i>Annals of Applied Biology</i> , 2007, 151, 291-305.	1.3	115
57	Molecular Markers and QTL Analysis for Grain Quality Improvement in Wheat. , 2007, , 25-50.		2
58	Nucleotide-binding site (NBS) profiling of genetic diversity in durum wheat. <i>Genome</i> , 2006, 49, 1473-1480.	0.9	26
59	A panel of elite accessions of durum wheat (<i>Triticum durum</i> Desf.) suitable for association mapping studies. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2006, 4, 79-85.	0.4	54
60	Population structure and long-range linkage disequilibrium in a durum wheat elite collection. <i>Molecular Breeding</i> , 2005, 15, 271-290.	1.0	212
61	Validation and characterization of a major QTL affecting leaf ABA concentration in maize. <i>Molecular Breeding</i> , 2005, 15, 291-303.	1.0	59
62	Searching for quantitative trait loci controlling root traits in maize: a critical appraisal. <i>Plant and Soil</i> , 2003, 255, 35-54.	1.8	104
63	Microsatellite analysis reveals a progressive widening of the genetic basis in the elite durum wheat germplasm. <i>Theoretical and Applied Genetics</i> , 2003, 107, 783-797.	1.8	104
64	Mapping QTLs Regulating Morpho-physiological Traits and Yield: Case Studies, Shortcomings and Perspectives in Drought-stressed Maize. <i>Annals of Botany</i> , 2002, 89, 941-963.	1.4	331
65	Toward positional cloning of Vgt1, a QTL controlling the transition from the vegetative to the reproductive phase in maize. <i>Plant Molecular Biology</i> , 2002, 48, 601-613.	2.0	116