Diane E Mather

List of Publications by Year
in descending order

104 papers	6,146 citations	101543 36 h-index	74163 75 g-index
106 all docs	106 docs citations	106 times ranked	5379 citing authors

#	Article	IF	Citations
1	Identification of Sclerotinia stem rot resistance quantitative trait loci in a chickpea (Cicer arietinum) recombinant inbred line population. Functional Plant Biology, 2022, , .	2.1	1
2	Three-dimensional imaging reveals that positions of cyst nematode feeding sites relative to xylem vessels differ between susceptible and resistant wheat. Plant Cell Reports, 2021, 40, 393-403.	5.6	8
3	Dormancy and dormancy release in white-grained wheat (Triticum aestivum L.). Planta, 2021, 253, 5.	3.2	4
4	Lipoxygenase in Wheat: Genetic Control and Impact on Stability of Lutein and Lutein Esters. Foods, 2021, 10, 1149.	4.3	8
5	Analysis of Genetic Diversity in the Traditional Chinese Medicine Plant â€˜Kushenâ€™ (Sophora flavescens) Tj ETQq1 1 0.784314 rgBT /O	3.6	2
6	A QTL on the Ca7 chromosome of chickpea affects resistance to the root-lesion nematode Pratylenchus thornei. Molecular Breeding, 2021, 41, 1.	2.1	32
7	Accumulation of mutations in genes associated with sexual reproduction contributed to the domestication of a vegetatively propagated staple crop, enset. Horticulture Research, 2020, 7, 185.	6.3	10
8	The Global Durum Wheat Panel (GDP): An International Platform to Identify and Exchange Beneficial Alleles. Frontiers in Plant Science, 2020, 11, 569905.	3.6	44
9	Infection by cyst nematodes induces rapid remodelling of developing xylem vessels in wheat roots. Scientific Reports, 2020, 10, 9025.	3.3	7
10	Variation among S-locus haplotypes and among stylar RNases in almond. Scientific Reports, 2020, 10, 583.	3.3	8
11	Laser ablation tomography for visualization of root colonization by edaphic organisms. Journal of Experimental Botany, 2019, 70, 5327-5342.	4.8	62
12	A GDSL Esterase/Lipase Catalyzes the Esterification of Lutein in Bread Wheat. Plant Cell, 2019, 31, 3092-3112.	6.6	74
13	Fine mapping of Rha2 in barley reveals candidate genes for resistance against cereal cyst nematode. Theoretical and Applied Genetics, 2019, 132, 1309-1320.	3.6	2
14	Genome-wide association mapping of grain yield in a diverse collection of spring wheat (Triticum) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	2.5	108
15	Large expert-curated database for benchmarking document similarity detection in biomedical literature search. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	15
16	Genotyping by Sequencing in Almond: SNP Discovery, Linkage Mapping, and Marker Design. G3: Genes, Genomes, Genetics, 2018, 8, 161-172.	1.8	28
17	A locus on barley chromosome 5H affects adult plant resistance to powdery mildew. Molecular Breeding, 2018, 38, 103.	2.1	11
18	Mapping of novel salt tolerance QTL in an Excaliburâ€‰Ã—â€‰Kukri doubled haploid wheat population. Theoretical and Applied Genetics, 2018, 131, 2179-2196.	3.6	60

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19	Loci on chromosomes 1A and 2A affect resistance to tan (yellow) spot in wheat populations not segregating for tsn1. Theoretical and Applied Genetics, 2017, 130, 2637-2654.	3.6	14
20	A QTL on the short arm of wheat (Triticum aestivum L.) chromosome 3B affects the stability of grain weight in plants exposed to a brief heat shock early in grain filling. BMC Plant Biology, 2016, 16, 100.	3.6	62
21	The dynamics of cereal cyst nematode infection differ between susceptible and resistant barley cultivars and lead to changes in (1,3;1,4)â€Î²â€glucan levels and <scp>HvCslF</scp> gene transcript abundance. New Phytologist, 2015, 207, 135-147.	7.3	40
22	Detection of QTL for metabolic and agronomic traits in wheat with adjustments for variation at genetic loci that affect plant phenology. Plant Science, 2015, 233, 143-154.	3.6	72
23	Genetic mapping of the Cre8 locus for resistance against cereal cyst nematode (Heterodera avenae) Tj ETQq1 1 0.784314 rgBT /Overlo	2.1	15
24	Addition of rye chromosome 4R to wheat increases anther length and pollen grain number. Theoretical and Applied Genetics, 2015, 128, 953-964.	3.6	38
25	Genetic control of lutein esterification in wheat (Triticum aestivum L.) grain. Journal of Cereal Science, 2015, 64, 109-115.	3.7	31
26	Genetic control of grain protein, dough rheology traits and loaf traits in a bread wheat population grown in three environments. Journal of Cereal Science, 2015, 64, 147-152.	3.7	20
27	Differential expression of the HvCslF6 gene late in grain development may explain quantitative differences in (1,3;1,4)-Î²-glucan concentration in barley. Molecular Breeding, 2015, 35, 20.	2.1	17
28	Morphological, physiological and yield responses of durum wheat to pre-anthesis water-deficit stress are genotype-dependent. Crop and Pasture Science, 2015, 66, 1024.	1.5	63
29	A Genome-Wide Association Study for Culm Cellulose Content in Barley Reveals Candidate Genes Co-Expressed with Members of the CELLULOSE SYNTHASE A Gene Family. PLoS ONE, 2015, 10, e0130890.	2.5	24
30	Genome-Wide Identification of MicroRNAs in Leaves and the Developing Head of Four Durum Genotypes during Water Deficit Stress. PLoS ONE, 2015, 10, e0142799.	2.5	43
31	Characterization of polyploid wheat genomic diversity using a highâ€density 90Â000 single nucleotide polymorphism array. Plant Biotechnology Journal, 2014, 12, 787-796.	8.3	1,828
32	From Genes to Markers: Exploiting Gene Sequence Information to Develop Tools for Plant Breeding. Methods in Molecular Biology, 2014, 1145, 21-36.	0.9	4
33	Use of specific differential isolates of Rhynchosporium commune to detect minor gene resistance to leaf scald in barley seedlings. Australasian Plant Pathology, 2014, 43, 197-203.	1.0	9
34	Genetic control of grain yield and grain physical characteristics in a bread wheat population grown under a range of environmental conditions. Theoretical and Applied Genetics, 2014, 127, 1607-1624.	3.6	85
35	Post-anthesis heat and a Gpc-B1 introgression have similar but non-additive effects in bread wheat. Functional Plant Biology, 2014, 41, 1002.	2.1	17
36	Genetic control of processing quality in a bread wheat mapping population grown in water-limited environments. Journal of Cereal Science, 2013, 57, 304-311.	3.7	21

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37	A cysteine in the repetitive domain of a high-molecular-weight glutenin subunit interferes with the mixing properties of wheat dough. Amino Acids, 2013, 44, 1061-1071.	2.7	10
38	Multi-environment analysis and improved mapping of a yield-related QTL on chromosome 3B of wheat. Theoretical and Applied Genetics, 2013, 126, 747-761.	3.6	77
39	Whole-Genome Mapping of Agronomic and Metabolic Traits to Identify Novel Quantitative Trait Loci in Bread Wheat Grown in a Water-Limited Environment. Plant Physiology, 2013, 162, 1266-1281.	4.8	115
40	Genetic mapping and marker development for resistance of wheat against the root lesion nematode Pratylenchus neglectus. BMC Plant Biology, 2013, 13, 230.	3.6	35
41	Variation in tolerance to radiant frost at reproductive stages in field pea germplasm. Euphytica, 2012, 186, 831-845.	1.2	17
42	Clusters of genes encoding fructan biosynthesizing enzymes in wheat and barley. Plant Molecular Biology, 2012, 80, 299-314.	3.9	29
43	A second â€˜overexpressionâ€™ allele at the Glu-B1 high-molecular-weight glutenin locus of wheat: sequence characterisation and functional effects. Theoretical and Applied Genetics, 2012, 124, 333-343.	3.6	32
44	Raising yield potential of wheat. I. Overview of a consortium approach and breeding strategies. Journal of Experimental Botany, 2011, 62, 439-452.	4.8	262
45	Genetic mapping and QTL analysis of disease resistance traits in the barley population BaudinÃ—AC Metcalfe. Crop and Pasture Science, 2011, 62, 152.	1.5	33
46	An informative set of SNP markers for molecular characterisation of Australian barley germplasm. Crop and Pasture Science, 2010, 61, 70.	1.5	15
47	Novel allelic variants encoded at the Glu-D3 locus in bread wheat. Journal of Cereal Science, 2009, 49, 254-261.	3.7	34
48	QTL detection with bidirectional and unidirectional selective genotyping: marker-based and trait-based analyses. Theoretical and Applied Genetics, 2009, 118, 347-358.	3.6	60
49	Development and assessment of simple PCR markers for SNP genotyping in barley. Theoretical and Applied Genetics, 2009, 119, 939-951.	3.6	28
50	Temperature Switch PCR (TSP): Robust assay design for reliable amplification and genotyping of SNPs. BMC Genomics, 2009, 10, 580.	2.8	47
51	Analytical Approaches and Population Types for Finding and Utilizing QTL in Complex Plant Populations. Crop Science, 2009, 49, 363-380.	1.8	53
52	Quantitative trait loci for grain fructan concentration in wheat (Triticum aestivum L.). Theoretical and Applied Genetics, 2008, 117, 701-709.	3.6	54
53	Genotypic variation in wheat grain fructan content revealed by a simplified HPLC method. Journal of Cereal Science, 2008, 48, 369-378.	3.7	95
54	The Genetics and Transcriptional Profiles of the Cellulose Synthase-Like HvCslF Gene Family in Barley. Plant Physiology, 2008, 146, 1821-1833.	4.8	204

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55	Black point formation in barley: environmental influences and quantitative trait loci. Australian Journal of Agricultural Research, 2008, 59, 1021.	1.5	10
56	QTL analysis of malting quality traits in two barley populations. Australian Journal of Agricultural Research, 2007, 58, 858.	1.5	54
57	Exact word matches in rice pseudomolecules. Genome, 2006, 49, 1047-1051.	2.0	15
58	Effect of population size on the estimation of QTL: a test using resistance to barley stripe rust. Theoretical and Applied Genetics, 2005, 111, 1260-1270.	3.6	185
59	Pedigree selection for Gibberella ear rot resistance in maize. Euphytica, 2005, 143, 1-8.	1.2	24
60	Responses to Divergent Phenotypic Selection for Fiber Traits in Timothy. Crop Science, 2005, 45, 1017-1022.	1.8	7
61	Leaf and Stem Characteristics of Timothy Plants Divergently Selected for the Ratio of Lignin to Cellulose. Crop Science, 2005, 45, 2425-2429.	1.8	15
62	Metabolic profiling and factor analysis to discriminate quantitative resistance in wheat cultivars against fusarium head blight. Physiological and Molecular Plant Pathology, 2005, 66, 119-133.	2.5	101
63	EC_oligos: automated and whole-genome primer design for exons within one or between two genomes. Bioinformatics, 2004, 20, 3668-3669.	4.1	5
64	Quantitative trait loci affecting germination traits and malt friability in a two-rowed by six-rowed barley cross. Journal of Cereal Science, 2004, 39, 283-290.	3.7	36
65	Genetic diversity for quantitatively inherited agronomic and malting quality traits. Developments in Plant Genetics and Breeding, 2003, 7, 201-226.	0.6	51
66	Genetic Control of Quantitative Grain and Malt Quality Traits in Barley. The Journal of Crop Improvement: Innovations in Practiceory and Research, 2002, 5, 131-164.	0.4	25
67	Effectiveness of selective genotyping for detection of quantitative trait loci: an analysis of grain and malt quality traits in three barley populations. Genome, 2002, 45, 1116-1124.	2.0	28
68	QTLs affecting kernel size and shape in a two-rowed by six-rowed barley cross. Theoretical and Applied Genetics, 2002, 105, 237-247.	3.6	79
69	Anatomical features at the disarticulation zone in florets of fatuoid and nonfatuoid oat (<i>Avena) Tj ETQq1 1 0.784314 rgBT /Overlo	1.1	5
70	Leafy Reducedâ€Stature Maize Hybrids for Shortâ€Season Environments. Crop Science, 1999, 39, 1106-1110.	1.8	39
71	Verifications of a Quantitative Trait Locus Affecting Agronomic Traits in Twoâ€Row Barley. Crop Science, 1999, 39, 248-252.	1.8	27
72	Mapping Quantitative Trait Loci for Starch Granule Traits in Barley. Journal of Cereal Science, 1999, 29, 153-160.	3.7	37

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73	Title is missing!. Euphytica, 1999, 107, 185-192.	1.2	20
74	Plant Population Density Effects on Maize Inbred Lines Grown in Shortâ€Season Environments. Crop Science, 1998, 38, 104-108.	1.8	38
75	Application of Geostatistical and Neighbor Analyses to Data from Plant Breeding Trials. Crop Science, 1998, 38, 1545-1553.	1.8	22
76	Mapping of Disease Resistance Loci in Barley on the Basis of Visual Assessment of Naturally Occurring Symptoms. Crop Science, 1998, 38, 843-850.	1.8	67
77	Perspectives in Development for Maize Production in the Caribbean: A Case Study of Trinidad and Tobago. Canadian Journal of Development Studies, 1997, 18, 613-627.	2.8	0
78	Assessment of ear rot symptom development in maize hybrids inoculated withFusarium graminearum. Canadian Journal of Plant Pathology, 1997, 19, 390-396.	1.4	9
79	Regions of the Genome That Affect Grain and Malt Quality in a North American Twoâ€Row Barley Cross. Crop Science, 1997, 37, 544-554.	1.8	160
80	Leafy reduced-stature maize for short-season environments: morphological aspects of inbred lines. Euphytica, 1997, 96, 301-309.	1.2	17
81	Maize landraces of the St. Lawrence-Great Lakes region of North America. Euphytica, 1997, 98, 141-148.	1.2	8
82	Regions of the Genome that Affect Agronomic Performance in Twoâ€Row Barley. Crop Science, 1996, 36, 1053-1062.	1.8	191
83	Hill plots for yield evaluation in a doubled haploid recurrent selection program in barley (Hordeum) Tj ETQq1 1 0.784314 rgBT /Overlo	0.9	4
84	Heritability of ?-glucan, groat percentage, and crown rust resistance in two oat crosses. Euphytica, 1996, 91, 359-364.	1.2	19
85	Inheritance of Kernel Resistance to Fusarium graminearum in Maize. Journal of Heredity, 1996, 87, 382-385.	2.4	30
86	Comparison of Techniques for Inoculating Maize Silk, Kernel, and Cob Tissues withFusarium graminearum. Plant Disease, 1996, 80, 81.	1.4	33
87	Distribution of Deoxynivalenol in Fusarium graminearum-Infected Maize Ears. Phytopathology, 1996, 86, 110.	2.2	35
88	Effect of Macroconidial Suspension Volume and Concentration on Expression of Resistance toFusarium graminearumin Maize.. Plant Disease, 1995, 79, 461.	1.4	34
89	Nitrogen Fertilizer Application and Seeding Date Effects on Oat Grain Milling Quality. Agronomy Journal, 1994, 86, 838-843.	1.8	13
90	Screening for Partial Resistance to an Isolate of Crown Rust (Puccinia coronataf.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 67 Td (sp. 1994, 16, 49-55.	1.4	12

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91	Nitrogen Fertilizer and Seeding Date Induced Changes in Protein, Oil and Î²-Glucan Contents of Four Oat Cultivars. Journal of Cereal Science, 1994, 20, 283-290.	3.7	42
92	Pooled DNA for linkage analysis: practical and statistical considerations. Genome, 1994, 37, 999-1004.	2.0	9
93	A method for detecting DNA polymorphism in large populations. Genome, 1994, 37, 506-508.	2.0	10
94	Evidence for a Gene for Silk Resistance toFusarium graminearumSchw. Ear Rot of Maize. Journal of Heredity, 1994, 85, 118-121.	2.4	31
95	Random amplified polymorphic DNA and pedigree relationships in spring barley. Theoretical and Applied Genetics, 1993, 85, 976-984.	3.6	223
96	Genetic improvement of spring barley cultivars grown in eastern Canada from 1910 to 1988. Euphytica, 1993, 71, 35-48.	1.2	56
97	GREGOR: Software for Genetic Simulation. Journal of Heredity, 1993, 84, 237-237.	2.4	13
98	KIN: Software for Computing Kinship Coefficients. Journal of Heredity, 1993, 84, 238-238.	2.4	52
99	Resistance of Maize Hybrids and Inbreds Following Silk Inoculation with Three Isolates ofFusarium graminearum. Plant Disease, 1993, 77, 1248.	1.4	25
100	Effect of silk age on resistance of maize toFusarium graminearum. Canadian Journal of Plant Pathology, 1992, 14, 293-298.	1.4	58
101	Genotypic differences in the resistance of maize silk toFusarium graminearum. Canadian Journal of Plant Pathology, 1992, 14, 211-214.	1.4	52
102	Evaluation of yield stability of cowpea under sole and intercrop management in Nigeria. Euphytica, 1991, 61, 193-201.	1.2	13
103	Estimation of phenotypic selection differentials for predicting genetic responses to ratio-based selection. Genome, 1988, 30, 838-843.	2.0	8
104	Protein and carbohydrate accumulation in normal and high-lysine barley in spike culture. Physiologia Plantarum, 1984, 60, 75-80.	5.2	10