

Cathrine L McIntyre

List of Publications by Year in descending order

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105
papers

7,618
citations

36303

51
h-index

54911

84
g-index

108
all docs

108
docs citations

108
times ranked

6142
citing authors

#	ARTICLE	IF	CITATIONS
1	Articulating the effect of food systems innovation on the Sustainable Development Goals. <i>Lancet Planetary Health</i> , The, 2021, 5, e50-e62.	11.4	135
2	Genotypic variation for lodging tolerance in spring wheat: wider and deeper root plates, a feature of low lodging, high yielding germplasm. <i>Field Crops Research</i> , 2020, 258, 107942.	5.1	18
3	Innovation can accelerate the transition towards a sustainable food system. <i>Nature Food</i> , 2020, 1, 266-272.	14.0	285
4	Overexpression of <i>TaCML20</i> , a calmodulin-like gene, enhances water soluble carbohydrate accumulation and yield in wheat. <i>Physiologia Plantarum</i> , 2019, 165, 790-799.	5.2	17
5	Heat shock factor C2a serves as a proactive mechanism for heat protection in developing grains in wheat via an ABA-mediated regulatory pathway. <i>Plant, Cell and Environment</i> , 2018, 41, 79-98.	5.7	102
6	Overexpression of a predominantly root-expressed NAC transcription factor in wheat roots enhances root length, biomass and drought tolerance. <i>Plant Cell Reports</i> , 2018, 37, 225-237.	5.6	77
7	Mapping QTLs associated with agronomic and physiological traits under terminal drought and heat stress conditions in wheat (<i>Triticum aestivum</i> L.). <i>Genome</i> , 2017, 60, 26-45.	2.0	106
8	A strong root-specific expression system for stable transgene expression in bread wheat. <i>Plant Cell Reports</i> , 2016, 35, 469-481.	5.6	14
9	Drought-Up-Regulated TaNAC69-1 is a Transcriptional Repressor of <i>TaSHY2</i> and <i>TaAA7</i> , and Enhances Root Length and Biomass in Wheat. <i>Plant and Cell Physiology</i> , 2016, 57, 2076-2090.	3.1	44
10	Abiotic stress upregulated TaZFP34 represses the expression of type-B response regulator and SHY2 genes and enhances root to shoot ratio in wheat. <i>Plant Science</i> , 2016, 252, 88-102.	3.6	41
11	An Assessment of Heavy Ion Irradiation Mutagenesis for Reverse Genetics in Wheat (<i>Triticum aestivum</i>) Tj ETQq1 1,0784314,rgBT/Ove	2.5	23
12	Characterisation of alleles of the sucrose phosphate synthase gene family in sugarcane and their association with sugar-related traits. <i>Molecular Breeding</i> , 2015, 35, 1.	2.1	12
13	Brachypodium as an emerging model for cereal-pathogen interactions. <i>Annals of Botany</i> , 2015, 115, 717-731.	2.9	60
14	TaHsfA6f is a transcriptional activator that regulates a suite of heat stress protection genes in wheat (<i>Triticum aestivum</i> L.) including previously unknown Hsf targets. <i>Journal of Experimental Botany</i> , 2015, 66, 1025-1039.	4.8	153
15	More fertile florets and grains per spike can be achieved at higher temperature in wheat lines with high spike biomass and sugar content at booting. <i>Functional Plant Biology</i> , 2014, 41, 482.	2.1	64
16	The heat shock factor family from <i>Triticum aestivum</i> in response to heat and other major abiotic stresses and their role in regulation of heat shock protein genes. <i>Journal of Experimental Botany</i> , 2014, 65, 539-557.	4.8	208
17	Preferential retention of chromosome regions in derived synthetic wheat lines: a source of novel alleles for wheat improvement. <i>Crop and Pasture Science</i> , 2014, 65, 125.	1.5	8
18	Major QTL for Fusarium crown rot resistance in a barley landrace. <i>Theoretical and Applied Genetics</i> , 2013, 126, 2511-2520.	3.6	31

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19	QTL for yield and associated traits in the Seri/Babax population grown across several environments in Mexico, in the West Asia, North Africa, and South Asia regions. <i>Theoretical and Applied Genetics</i> , 2013, 126, 971-984.	3.6	119
20	Dissecting the molecular basis of the contribution of source strength to high fructan accumulation in wheat. <i>Plant Molecular Biology</i> , 2013, 81, 71-92.	3.9	26
21	TaMYB13-1, a R2R3 MYB transcription factor, regulates the fructan synthetic pathway and contributes to enhanced fructan accumulation in bread wheat. <i>Journal of Experimental Botany</i> , 2013, 64, 3681-3696.	4.8	47
22	A Novel and Major Quantitative Trait Locus for Fusarium Crown Rot Resistance in a Genotype of Wild Barley (<i>Hordeum spontaneum</i> L.). <i>PLoS ONE</i> , 2013, 8, e58040.	2.5	42
23	Characterization of a QTL affecting spike morphology on the long arm of chromosome 3H in barley (<i>Hordeum vulgare</i> L.) based on near isogenic lines and a NIL-derived population. <i>Theoretical and Applied Genetics</i> , 2012, 125, 1385-1392.	3.6	38
24	Assessment of the genetic diversity in a collection of <i>Erianthus arundinaceus</i> . <i>Genetic Resources and Crop Evolution</i> , 2012, 59, 1483-1491.	1.6	16
25	Genotypic variation in the accumulation of water soluble carbohydrates in wheat. <i>Functional Plant Biology</i> , 2012, 39, 560.	2.1	29
26	Overexpression of TaNAC69 Leads to Enhanced Transcript Levels of Stress Up-Regulated Genes and Dehydration Tolerance in Bread Wheat. <i>Molecular Plant</i> , 2011, 4, 697-712.	8.3	233
27	TaMYB13 is a transcriptional activator of fructosyltransferase genes involved in linked fructan synthesis in wheat. <i>Plant Journal</i> , 2011, 68, 857-870.	5.7	70
28	TaNf-YB3 is involved in the regulation of photosynthesis genes in <i>Triticum aestivum</i> . <i>Functional and Integrative Genomics</i> , 2011, 11, 327-340.	3.5	74
29	Linked gene networks involved in nitrogen and carbon metabolism and levels of water-soluble carbohydrate accumulation in wheat stems. <i>Functional and Integrative Genomics</i> , 2011, 11, 585-597.	3.5	20
30	Molecular detection of genomic regions associated with grain yield and yield-related components in an elite bread wheat cross evaluated under irrigated and rainfed conditions. <i>Theoretical and Applied Genetics</i> , 2010, 120, 527-541.	3.6	151
31	Heat and drought adaptive QTL in a wheat population designed to minimize confounding agronomic effects. <i>Theoretical and Applied Genetics</i> , 2010, 121, 1001-1021.	3.6	484
32	Construction of a high-density composite map and comparative mapping of segregation distortion regions in barley. <i>Molecular Genetics and Genomics</i> , 2010, 284, 319-331.	2.1	55
33	TaNf-YC11, one of the light-upregulated NF-YC members in <i>Triticum aestivum</i> , is co-regulated with photosynthesis-related genes. <i>Functional and Integrative Genomics</i> , 2010, 10, 265-276.	3.5	38
34	Molecular mapping of adult plant stripe rust resistance in wheat and identification of pyramided QTL genotypes. <i>Euphytica</i> , 2010, 176, 251-260.	1.2	112
35	Members of the Dof transcription factor family in <i>Triticum aestivum</i> are associated with light-mediated gene regulation. <i>Functional and Integrative Genomics</i> , 2009, 9, 485-498.	3.5	99
36	The Complex Genetic Structure of Sugarcane Limits Identification of Additional SNP-Defined Simplex Alleles in Microsatellite Loci. <i>Tropical Plant Biology</i> , 2009, 2, 133-142.	1.9	1

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37	Genetic control of wheat quality: interactions between chromosomal regions determining protein content and composition, dough rheology, and sponge and dough baking properties. <i>Theoretical and Applied Genetics</i> , 2009, 118, 1519-1537.	3.6	85
38	Use of dry matter content as a rapid and low-cost estimate for ranking genotypic differences in water-soluble carbohydrate concentrations in the stem and leaf sheath of <i>Triticum aestivum</i> . <i>Crop and Pasture Science</i> , 2009, 60, 51.	1.5	31
39	Use of expression analysis to dissect alterations in carbohydrate metabolism in wheat leaves during drought stress. <i>Plant Molecular Biology</i> , 2008, 67, 197-214.	3.9	131
40	Comparative genetics in sugarcane enables structured map enhancement and validation of marker-trait associations. <i>Molecular Breeding</i> , 2008, 21, 233-247.	2.1	32
41	Identification of QTL for sugar-related traits in a sweet-grain sorghum (<i>Sorghum bicolor</i> L. Moench) recombinant inbred population. <i>Molecular Breeding</i> , 2008, 22, 367-384.	2.1	138
42	QTL analysis of ergot resistance in sorghum. <i>Theoretical and Applied Genetics</i> , 2008, 117, 369-382.	3.6	46
43	Multi-environment QTL mixed models for drought stress adaptation in wheat. <i>Theoretical and Applied Genetics</i> , 2008, 117, 1077-1091.	3.6	160
44	Genetic control of yield related stalk traits in sugarcane. <i>Theoretical and Applied Genetics</i> , 2008, 117, 1191-1203.	3.6	82
45	Molecular characterization of the waxy locus in sorghum. <i>Genome</i> , 2008, 51, 524-533.	2.0	46
46	Molecular Dissection of Variation in Carbohydrate Metabolism Related to Water-Soluble Carbohydrate Accumulation in Stems of Wheat. <i>Plant Physiology</i> , 2008, 146, 323-324.	4.8	157
47	Construction of a genetic linkage map for <i>Saccharum officinarum</i> incorporating both simplex and duplex markers to increase genome coverage. <i>Genome</i> , 2007, 50, 742-756.	2.0	52
48	Genome-wide identification and expression analysis of the NF-Y family of transcription factors in <i>Triticum aestivum</i> . <i>Plant Molecular Biology</i> , 2007, 65, 77-92.	3.9	176
49	An assessment of the genetic relationship between sweet and grain sorghums, within <i>Sorghum bicolor</i> ssp. <i>bicolor</i> (L.) Moench, using AFLP markers. <i>Euphytica</i> , 2007, 157, 161-176.	1.2	83
50	Identification of common root-lesion nematode (<i>Pratylenchus thornei</i> Sher et Allen) loci in bread wheat. <i>Genome</i> , 2006, 49, 1319-1323.	2.0	28
51	Genetic Components of Variance and the Role of Pollen Traits in Sorghum Ergot Resistance. <i>Crop Science</i> , 2006, 46, 2387-2395.	1.8	15
52	AFLP analysis of genetic diversity within <i>Saccharum officinarum</i> and comparison with sugarcane cultivars. <i>Australian Journal of Agricultural Research</i> , 2006, 57, 1167.	1.5	45
53	TaNAC69 from the NAC superfamily of transcription factors is up-regulated by abiotic stresses in wheat and recognises two consensus DNA-binding sequences. <i>Functional Plant Biology</i> , 2006, 33, 43.	2.1	81
54	Differential gene expression of wheat progeny with contrasting levels of transpiration efficiency. <i>Plant Molecular Biology</i> , 2006, 61, 863-881.	3.9	44

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55	The identification and characterisation of alleles of sucrose phosphate synthase gene family III in sugarcane. <i>Molecular Breeding</i> , 2006, 18, 39-50.	2.1	39
56	Quantitative trait loci identified for sugar related traits in a sugarcane (<i>Saccharum</i> spp.) cultivar— <i>Saccharum officinarum</i> population. <i>Theoretical and Applied Genetics</i> , 2006, 112, 1306-1317.	3.6	85
57	Characterisation of single nucleotide polymorphisms in sugarcane ESTs. <i>Theoretical and Applied Genetics</i> , 2006, 113, 331-343.	3.6	58
58	Associations between DNA markers and resistance to diseases in sugarcane and effects of population substructure. <i>Theoretical and Applied Genetics</i> , 2006, 114, 155-164.	3.6	97
59	Analysing diversity in sugarcane resistance gene analogues. <i>Australasian Plant Pathology</i> , 2006, 35, 631.	1.0	4
60	Quantitative trait loci for root lesion nematode (<i>Pratylenchus thornei</i>) resistance in Middle-Eastern landraces and their potential for introgression into Australian bread wheat. <i>Australian Journal of Agricultural Research</i> , 2005, 56, 1059.	1.5	34
61	Relationships between hard-seededness and seed weight in mungbean (<i>Vigna radiata</i>) assessed by QTL analysis. <i>Plant Breeding</i> , 2005, 124, 292-298.	1.9	57
62	Verification of the introgression of <i>Erianthus arundinaceus</i> germplasm into sugarcane using molecular markers. <i>Plant Breeding</i> , 2005, 124, 322-328.	1.9	66
63	A combination of AFLP and SSR markers provides extensive map coverage and identification of homo(eo)logous linkage groups in a sugarcane cultivar. <i>Theoretical and Applied Genetics</i> , 2005, 110, 789-801.	3.6	174
64	A "Chinese Spring" wheat (<i>Triticum aestivum</i> L.) bacterial artificial chromosome library and its use in the isolation of SSR markers for targeted genome regions. <i>Theoretical and Applied Genetics</i> , 2005, 111, 1489-1494.	3.6	17
65	Characterisation of genome regions incorporated from an important wild relative into Australian sugarcane. <i>Molecular Breeding</i> , 2005, 15, 367-381.	2.1	47
66	Identification and Validation of Molecular Markers Associated with Pachymetra Root Rot and Brown Rust Resistance in Sugarcane Using Map- and Association-based Approaches. <i>Molecular Breeding</i> , 2005, 16, 151-161.	2.1	29
67	Resistance gene analogues in sugarcane and sorghum and their association with quantitative trait loci for rust resistance. <i>Genome</i> , 2005, 48, 391-400.	2.0	66
68	Genomics approaches for the identification of genes determining important traits in sugarcane. <i>Field Crops Research</i> , 2005, 92, 137-147.	5.1	70
69	Identification of differentially expressed genes in wheat undergoing gradual water deficit stress using a subtractive hybridisation approach. <i>Plant Science</i> , 2005, 168, 661-670.	3.6	23
70	A preliminary assessment of the genetic relationship between <i>Erianthus rockii</i> and the "Saccharum complex" using microsatellite (SSR) and AFLP markers. <i>Plant Science</i> , 2005, 169, 976-984.	3.6	54
71	Identification of Differentially Expressed Transcripts from Maturing Stem of Sugarcane by in silico Analysis of Stem Expressed Sequence Tags and Gene Expression Profiling. <i>Plant Molecular Biology</i> , 2004, 54, 503-517.	3.9	110
72	Homologues of the maize rust resistance gene Rp1-D are genetically associated with a major rust resistance QTL in sorghum. <i>Theoretical and Applied Genetics</i> , 2004, 109, 875-883.	3.6	29

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73	Markers associated with stalk number and suckering in sugarcane colocate with tillering and rhizomatousness QTLs in sorghum. <i>Genome</i> , 2004, 47, 988-993.	2.0	37
74	Identification of a novel sugar transporter homologue strongly expressed in maturing stem vascular tissues of sugarcane by expressed sequence tag and microarray analysis. <i>Plant Molecular Biology</i> , 2003, 52, 371-386.	3.9	126
75	Prediction of hybrid performance in grain sorghum using RFLP markers. <i>Theoretical and Applied Genetics</i> , 2003, 106, 559-567.	3.6	109
76	Identifications of two different mechanisms for sorghum midge resistance through QTL mapping. <i>Theoretical and Applied Genetics</i> , 2003, 107, 116-122.	3.6	67
77	Identification of a major locus conferring resistance to powdery mildew (<i>Erysiphe polygoni</i> DC) in mungbean (<i>Vigna radiata</i> L. Wilczek) by QTL analysis. <i>Genome</i> , 2003, 46, 738-744.	2.0	63
78	Development of a mungbean (<i>Vigna radiata</i>) RFLP linkage map and its comparison with lablab (<i>Lablab</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T Genetics, 2002, 105, 160-166.	3.6	97
79	Microsatellite markers from sugarcane (<i>Saccharum</i> spp.) ESTs cross transferable to erianthus and sorghum. <i>Plant Science</i> , 2001, 160, 1115-1123.	3.6	384
80	Low level of selfing found in a sample of crosses in Australian sugarcane breeding programs. <i>Euphytica</i> , 2001, 117, 245-249.	1.2	28
81	Molecular analyses suggest a need for a significant rearrangement of Rutaceae subfamilies and a minor reassessment of species relationships within Flindersia. <i>Plant Systematics and Evolution</i> , 2000, 223, 15-27.	0.9	57
82	Identification of genomic regions associated with stay green in sorghum by testing RILs in multiple environments. <i>Theoretical and Applied Genetics</i> , 2000, 100, 1225-1232.	3.6	166
83	Title is missing!. <i>Euphytica</i> , 1998, 102, 1-7.	1.2	43
84	Identification of genomic regions for rust resistance in sorghum. <i>Euphytica</i> , 1998, 103, 287-292.	1.2	39
85	Assessing genetic diversity in a sugarcane germplasm collection using an automated AFLP analysis. <i>Genetica</i> , 1998, 104, 143-153.	1.1	62
86	Construction of a genetic map in a sorghum recombinant inbred line using probes from different sources and its comparison with other sorghum maps. <i>Australian Journal of Agricultural Research</i> , 1998, 49, 729.	1.5	43
87	Isolation and characterisation of repeated DNA sequences from <i>Erianthus</i> spp. (Saccharinae:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	2.0	1
88	Using genomic slot blot hybridization to assess intergeneric <i>Saccharum</i> x <i>Erianthus</i> hybrids (Andropogoneae æ“ Saccharinae). <i>Genome</i> , 1997, 40, 428-432.	2.0	22
89	Title is missing!. <i>Euphytica</i> , 1997, 93, 283-292.	1.2	52
90	Strategies for the suppression of peroxidase gene expression in tobacco. I. Designing efficient ribozymes. <i>Transgenic Research</i> , 1996, 5, 257-262.	2.4	3

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91	Strategies for the suppression of peroxidase gene expression in tobacco. II. In vivo suppression of peroxidase activity in transgenic tobacco using ribozyme and antisense constructs. <i>Transgenic Research</i> , 1996, 5, 263-270.	2.4	29
92	Ribosomal DNA variations in <i>Erianthus</i> , a wild sugarcane relative (Andropogoneae-Saccharinae). <i>Theoretical and Applied Genetics</i> , 1996, 92, 733-743.	3.6	37
93	Cloning and Sequence of a cDNA Encoding Phenylalanine Ammonia-Lyase from the Tropical Forage Legume <i>Stylosanthes humilis</i> . <i>Plant Physiology</i> , 1995, 108, 1301-1302.	4.8	12
94	Differential Expression of Peroxidase Isogenes During the Early Stages of Infection of the Tropical Forage Legume <i>Stylosanthes humilis</i> by <i>Colletotrichum gloeosporioides</i> . <i>Molecular Plant-Microbe Interactions</i> , 1995, 8, 398.	2.6	50
95	Analysis of phylogenetic relationships in the Triticeae tribe using RFLPs. <i>Theoretical and Applied Genetics</i> , 1993, 86, 649-655.	3.6	58
96	A strain-specific cyclin homolog in the fungal phytopathogen <i>Colletotrichum gloeosporioides</i> . <i>Gene</i> , 1993, 133, 141-145.	2.2	12
97	An RFLP species-specific DNA sequence for the A genome of rice. <i>Genome</i> , 1993, 36, 445-448.	2.0	4
98	Characterization of minisatellite sequences from <i>Oryza sativa</i> . <i>Genome</i> , 1993, 36, 978-983.	2.0	42
99	Relationships between <i>Oryza</i> species (Poaceae) based on 5S DNA sequences. <i>Plant Systematics and Evolution</i> , 1992, 183, 249-264.	0.9	18
100	Physical mapping of a low-copy DNA sequence in rye (<i>Secale cereale</i> L.). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1990, 87, 1899-1902.	7.1	87
101	Evolution and systematic relationships in the Triticeae (Poaceae). <i>Plant Systematics and Evolution</i> , 1988, 160, 1-28.	0.9	27
102	Amplification and dispersion of repeated DNA sequences in the Triticeae. <i>Plant Systematics and Evolution</i> , 1988, 160, 39-59.	0.9	86
103	DNA sequence analyses of the ribosomal spacer regions in the Triticeae. <i>Plant Systematics and Evolution</i> , 1988, 160, 91-104.	0.9	23
104	Frequent duplication and deletion events in the 5S RNA genes and the associated spacer regions of the Triticeae. <i>Plant Systematics and Evolution</i> , 1988, 160, 105-122.	0.9	133
105	Variation at isozyme loci in Triticeae. <i>Plant Systematics and Evolution</i> , 1988, 160, 123-142.	0.9	58