Gary J Muehlbauer

List of Publications by Year
in descending order

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114

papers

13,038

citations

28736

57

h-index

28425

109

g-index

119

all docs

119

docs citations

119

times ranked

12068

citing authors

#	ARTICLE	IF	CITATIONS
1	The Aegilops ventricosa 2NvS segment in bread wheat: cytology, genomics and breeding. Theoretical and Applied Genetics, 2021, 134, 529-542.	1.8	48
2	De Novo Genome Assembly of the Japanese Wheat Cultivar Norin 61 Highlights Functional Variation in Flowering Time and Fusarium-Resistant Genes in East Asian Genotypes. Plant and Cell Physiology, 2021, 62, 8-27.	1.5	16
3	Genetic characterization of flour quality and breadâ€making traits in a spring wheat nested association mapping population. Crop Science, 2021, 61, 1168-1183.	0.8	4
4	Genetic dissection of a pericentromeric region of barley chromosome 6H associated with Fusarium head blight resistance, grain protein content and agronomic traits. Theoretical and Applied Genetics, 2021, 134, 3963-3981.	1.8	5
5	Multiple wheat genomes reveal global variation in modern breeding. Nature, 2020, 588, 277-283.	13.7	513
6	Similar Seed Composition Phenotypes Are Observed From CRISPR-Generated In-Frame and Knockout Alleles of a Soybean KASI Ortholog. Frontiers in Plant Science, 2020, 11, 1005.	1.7	11
7	Natural Genetic Variation Underlying Tiller Development in Barley (<i>Hordeum vulgare</i> L). G3: Genes, Genomes, Genetics, 2020, 10, 1197-1212.	0.8	7
8	Genetic architecture of agronomic and quality traits in a nested association mapping population of spring wheat. Plant Genome, 2020, 13, e20051.	1.6	11
9	Sheathing the blade: Significant contribution of sheaths to daytime and nighttime gas exchange in a grass crop. Plant, Cell and Environment, 2020, 43, 1844-1861.	2.8	9
10	Genomic prediction of maize microphenotypes provides insights for optimizing selection and mining diversity. Plant Biotechnology Journal, 2020, 18, 2456-2465.	4.1	20
11	Mapping malting quality and yield characteristics in a north American two-rowed malting barley Ã— wild barley advanced backcross population. Molecular Breeding, 2019, 39, 1.	1.0	3
12	RNA Isolation and Analysis of LncRNAs from Gametophytes of Maize. Methods in Molecular Biology, 2019, 1933, 67-86.	0.4	3
13	Dense genotyping-by-sequencing linkage maps of two Synthetic W7984Ã—Opata reference populations provide insights into wheat structural diversity. Scientific Reports, 2019, 9, 1793.	1.6	28
14	Environmental Association Identifies Candidates for Tolerance to Low Temperature and Drought. G3: Genes, Genomes, Genetics, 2019, 9, 3423-3438.	0.8	18
15	Development of a Multiparent Population for Genetic Mapping and Allele Discovery in Six-Row Barley. Genetics, 2019, 213, 595-613.	1.2	23
16	A high-resolution gene expression atlas links dedicated meristem genes to key architectural traits. Genome Research, 2019, 29, 1962-1973.	2.4	35
17	TRITEX: chromosome-scale sequence assembly of Triticeae genomes with open-source tools. Genome Biology, 2019, 20, 284.	3.8	179
18	<i>ELIGULUM-A</i> Regulates Lateral Branch and Leaf Development in Barley. Plant Physiology, 2018, 176, 2750-2760.	2.3	22

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19	Circular RNAs mediated by transposons are associated with transcriptomic and phenotypic variation in maize. New Phytologist, 2018, 217, 1292-1306.	3.5	92
20	A Critical Assessment of 60 Years of Maize Intragenic Recombination. Frontiers in Plant Science, 2018, 9, 1560.	1.7	0
21	QTL Mapping of Fusarium Head Blight and Correlated Agromorphological Traits in an Elite Barley Cultivar Rasmusson. Frontiers in Plant Science, 2018, 9, 1260.	1.7	37
22	Intragenic Meiotic Crossovers Generate Novel Alleles with Transgressive Expression Levels. Molecular Biology and Evolution, 2018, 35, 2762-2772.	3.5	4
23	Molecular Mapping and Cloning of Genes and QTLs. Compendium of Plant Genomes, 2018, , 139-154.	0.3	7
24	Genetics of Whole Plant Morphology and Architecture. Compendium of Plant Genomes, 2018, , 209-231.	0.3	0
25	A barley UDP-glucosyltransferase inactivates nivalenol and provides Fusarium Head Blight resistance in transgenic wheat. Journal of Experimental Botany, 2017, 68, 2187-2197.	2.4	74
26	A chromosome conformation capture ordered sequence of the barley genome. Nature, 2017, 544, 427-433.	13.7	1,365
27	Construction of a map-based reference genome sequence for barley, Hordeum vulgare L.. Scientific Data, 2017, 4, 170044.	2.4	130
28	An Induced Chromosomal Translocation in Soybean Disrupts a <i>KASI</i> Ortholog and Is Associated with a High-Sucrose and Low-Oil Seed Phenotype. G3: Genes, Genomes, Genetics, 2017, 7, 1215-1223.	0.8	42
29	Genome-Wide Association Mapping of Stem Rust Resistance in<i>Hordeum vulgare</i>subsp.<i>spontaneum</i>. G3: Genes, Genomes, Genetics, 2017, 7, 3491-3507.	0.8	30
30	Mapping Agronomic Traits in a Wild Barley Advanced Backcrossâ€“Nested Association Mapping Population. Crop Science, 2017, 57, 1199-1210.	0.8	38
31	Fast neutron-induced structural rearrangements at a soybean NAP1 locus result in gnarled trichomes. Theoretical and Applied Genetics, 2016, 129, 1725-1738.	1.8	35
32	The Effects of Both Recent and Long-Term Selection and Genetic Drift Are Readily Evident in North American Barley Breeding Populations. G3: Genes, Genomes, Genetics, 2016, 6, 609-622.	0.8	21
33	Genomeâ€wide recombination dynamics are associated with phenotypic variation in maize. New Phytologist, 2016, 210, 1083-1094.	3.5	88
34	Examining the Transcriptional Response in Wheat <i>Fhb1</i> Nearâ€Isogenic Lines to <i>Fusarium graminearum</i> Infection and Deoxynivalenol Treatment. Plant Genome, 2016, 9, plantgenome2015.05.0032.	1.6	44
35	Co-expression network analysis of duplicate genes in maize (Zea mays L.) reveals no subgenome bias. BMC Genomics, 2016, 17, 875.	1.2	36
36	Differential transcriptomic responses to Fusarium graminearum infection in two barley quantitative trait loci associated with Fusarium head blight resistance. BMC Genomics, 2016, 17, 387.	1.2	64

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37	Exome sequencing of geographically diverse barley landraces and wild relatives gives insights into environmental adaptation. Nature Genetics, 2016, 48, 1024-1030.	9.4	259
38	Genomic analysis of 6,000-year-old cultivated grain illuminates the domestication history of barley. Nature Genetics, 2016, 48, 1089-1093.	9.4	122
39	Development and Genetic Characterization of an Advanced Backcross-Nested Association Mapping (AB-NAM) Population of Wild Ã— Cultivated Barley. Genetics, 2016, 203, 1453-1467.	1.2	73
40	Genetic control of morphometric diversity in the maize shoot apical meristem. Nature Communications, 2015, 6, 8974.	5.8	100
41	Transgenic Wheat Expressing a Barley UDP-Glucosyltransferase Detoxifies Deoxynivalenol and Provides High Levels of Resistance to <i>Fusarium graminearum</i>. Molecular Plant-Microbe Interactions, 2015, 28, 1237-1246.	1.4	120
42	The Barley <i>Uniculme4</i> Gene Encodes a BLADE-ON-PETIOLE-Like Protein That Controls Tillering and Leaf Patterning. Plant Physiology, 2015, 168, 164-174.	2.3	85
43	A whole-genome shotgun approach for assembling and anchoring the hexaploid bread wheat genome. Genome Biology, 2015, 16, 26.	3.8	256
44	Sequencing of 15Â622 geneâ€bearing BAC s clarifies the geneâ€dense regions of the barley genome. Plant Journal, 2015, 84, 216-227.	2.8	36
45	Diversity of Maize Shoot Apical Meristem Architecture and Its Relationship to Plant Morphology. G3: Genes, Genomes, Genetics, 2015, 5, 819-827.	0.8	22
46	Association Mapping of Agronomic QTLs in U.S. Spring Barley Breeding Germplasm. Plant Genome, 2014, 7, plantgenome2013.11.0037.	1.6	63
47	The USDA Barley Core Collection: Genetic Diversity, Population Structure, and Potential for Genome-Wide Association Studies. PLoS ONE, 2014, 9, e94688.	1.1	188
48	Genetic Control of Maize Shoot Apical Meristem Architecture. G3: Genes, Genomes, Genetics, 2014, 4, 1327-1337.	0.8	13
49	Genome Resilience and Prevalence of Segmental Duplications Following Fast Neutron Irradiation of Soybean. Genetics, 2014, 198, 967-981.	1.2	53
50	Genome-wide discovery and characterization of maize long non-coding RNAs. Genome Biology, 2014, 15, R40.	13.9	419
51	Barley genetic variation: implications for crop improvement. Briefings in Functional Genomics, 2014, 13, 341-350.	1.3	29
52	Two Genomic Regions Contribute Disproportionately to Geographic Differentiation in Wild Barley. G3: Genes, Genomes, Genetics, 2014, 4, 1193-1203.	0.8	38
53	Association mapping of grain hardness, polyphenol oxidase, total phenolics, amylose content, and Î²-glucan in US barley breeding germplasm. Molecular Breeding, 2014, 34, 1229-1243.	1.0	35
54	Genetics of Tillering in Rice and Barley. Plant Genome, 2014, 7, plantgenome2013.10.0032.	1.6	75

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55	eQTL Networks Reveal Complex Genetic Architecture in the Immature Soybean Seed. Plant Genome, 2014, 7, plantgenome2013.08.0027.	1.6	15
56	A Sequence-Ready Physical Map of Barley Anchored Genetically by Two Million Single-Nucleotide Polymorphisms Â Â. Plant Physiology, 2014, 164, 412-423.	2.3	77
57	Shoot and Inflorescence Architecture. Biotechnology in Agriculture and Forestry, 2014, , 55-80.	0.2	3
58	Distribution, functional impact, and origin mechanisms of copy number variation in the barley genome. Genome Biology, 2013, 14, R58.	3.8	125
59	Barley whole exome capture: a tool for genomic research in the genus <i>Hordeum</i> and beyond. Plant Journal, 2013, 76, 494-505.	2.8	260
60	Haplotype diversity and population structure in cultivated and wild barley evaluated for Fusarium head blight responses. Theoretical and Applied Genetics, 2013, 126, 619-636.	1.8	21
61	Anchoring and ordering <scp>NGS</scp> contig assemblies by population sequencing (<scp>POPSEQ</scp>). Plant Journal, 2013, 76, 718-727.	2.8	264
62	Transcriptomic characterization of two major <i><scp>F</scp>usarium</i> resistance quantitative trait loci (<scp>QTL</scp>s), <i><scp>F</scp>hb1</i> and <i><scp>Q</scp>fhs.ifaâ€‹‹scp>5A</scp></i>, identifies novel candidate genes. Molecular Plant Pathology, 2013, 14, 772-785.	2.0	132
63	Marker-trait associations in Virginia Tech winter barley identified using genome-wide mapping. Theoretical and Applied Genetics, 2013, 126, 693-710.	1.8	78
64	The barley UNICULM2 gene resides in a centromeric region and may be associated with signaling and stress responses. Functional and Integrative Genomics, 2013, 13, 33-41.	1.4	11
65	Mendelian and Non-Mendelian Regulation of Gene Expression in Maize. PLoS Genetics, 2013, 9, e1003202.	1.5	84
66	Transgenic Arabidopsis thaliana expressing a barley UDP-glucosyltransferase exhibit resistance to the mycotoxin deoxynivalenol. Journal of Experimental Botany, 2012, 63, 4731-4740.	2.4	92
67	Ontogeny of the Maize Shoot Apical Meristem. Plant Cell, 2012, 24, 3219-3234.	3.1	72
68	Soilâ€“Occupancy Effects of Invasive and Native Grassland Plant Species on Composition and Diversity of Mycorrhizal Associations. Invasive Plant Science and Management, 2012, 5, 494-505.	0.5	24
69	A physical, genetic and functional sequence assembly of the barley genome. Nature, 2012, 491, 711-716.	13.7	1,416
70	The Hordeum Toolbox: The Barley Coordinated Agricultural Project Genotype and Phenotype Resource. Plant Genome, 2012, 5, 81-91.	1.6	35
71	Effect of population size and unbalanced data sets on QTL detection using genome-wide association mapping in barley breeding germplasm. Theoretical and Applied Genetics, 2012, 124, 111-124.	1.8	77
72	Density Stress has Minimal Impacts on the Barley or Maize Seedling Transcriptome. Plant Genome, 2011, 4, .	1.6	9

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73	The Genetics of Winterhardiness in Barley: Perspectives from Genomeâ€Wide Association Mapping. Plant Genome, 2011, 4, .	1.6	62
74	An Improved Consensus Linkage Map of Barley Based on Flow-Sorted Chromosomes and Single Nucleotide Polymorphism Markers. Plant Genome, 2011, 4, 238-249.	1.6	150
75	INTERMEDIUM-C, a modifier of lateral spikelet fertility in barley, is an ortholog of the maize domestication gene TEOSINTE BRANCHED 1. Nature Genetics, 2011, 43, 169-172.	9.4	302
76	Quantitative trait loci conferring resistance to Fusarium head blight in barley respond differentially to Fusarium graminearum infection. Functional and Integrative Genomics, 2011, 11, 95-102.	1.4	12
77	Patterns of polymorphism and linkage disequilibrium in cultivated barley. Theoretical and Applied Genetics, 2011, 122, 523-531.	1.8	41
78	Phenotypic and Genomic Analyses of a Fast Neutron Mutant Population Resource in Soybean Â Â. Plant Physiology, 2011, 156, 240-253.	2.3	175
79	Population Structure and Linkage Disequilibrium in U.S. Barley Germplasm: Implications for Association Mapping. Crop Science, 2010, 50, 556-566.	0.8	106
80	Validation of a Candidate Deoxynivalenol-Inactivating UDP-Glucosyltransferase from Barley by Heterologous Expression in Yeast. Molecular Plant-Microbe Interactions, 2010, 23, 977-986.	1.4	126
81	The genetics of barley low-tillering mutants: low number of tillers-1 (lnt1). Theoretical and Applied Genetics, 2010, 121, 705-715.	1.8	45
82	Association mapping of spot blotch resistance in wild barley. Molecular Breeding, 2010, 26, 243-256.	1.0	151
83	Transcriptome analysis of a barley breeding program examines gene expression diversity and reveals target genes for malting quality improvement. BMC Genomics, 2010, 11, 653.	1.2	29
84	Genome-wide SNPs and re-sequencing of growth habit and inflorescence genes in barley: implications for association mapping in germplasm arrays varying in size and structure. BMC Genomics, 2010, 11, 707.	1.2	81
85	RNA-Seq Atlas of Glycine max: A guide to the soybean transcriptome. BMC Plant Biology, 2010, 10, 160.	1.6	634
86	Transcriptome Analysis of the Barleyâ€"Deoxynivalenol Interaction: Evidence for a Role of Glutathione in Deoxynivalenol Detoxification. Molecular Plant-Microbe Interactions, 2010, 23, 962-976.	1.4	140
87	An Integrated Resource for Barley Linkage Map and Malting Quality QTL Alignment. Plant Genome, 2009, 2, .	1.6	116
88	The emergence of whole genome association scans in barley. Current Opinion in Plant Biology, 2009, 12, 218-222.	3.5	138
89	Development and implementation of high-throughput SNP genotyping in barley. BMC Genomics, 2009, 10, 582.	1.2	570
90	The genetics of barley low-tillering mutants: absent lower laterals (als). Theoretical and Applied Genetics, 2009, 118, 1351-1360.	1.8	35

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91	Single-feature polymorphism discovery by computing probe affinity shape powers. BMC Genetics, 2009, 10, 48.	2.7	11
92	Wild barley accumulates distinct sets of transcripts in response to pathogens of different trophic lifestyles. Physiological and Molecular Plant Pathology, 2009, 74, 91-98.	1.3	9
93	Transcriptome Analysis of a Wheat Near-Isogenic Line Pair Carrying Fusarium Head Blightâ€"Resistant and â€"Susceptible Alleles. Molecular Plant-Microbe Interactions, 2009, 22, 1366-1378.	1.4	70
94	Marker Imputation in Barley Association Studies. Plant Genome, 2009, 2, .	1.6	10
95	Overexpression of the maize Teosinte Branched1 gene in wheat suppresses tiller development. Plant Cell Reports, 2008, 27, 1217-1225.	2.8	61
96	Transgenic wheat expressing a barley class II chitinase gene has enhanced resistance against Fusarium graminearum. Journal of Experimental Botany, 2008, 59, 2371-2378.	2.4	144
97	A walk on the wild side: mining wild wheat and barley collections for rust resistance genes. Australian Journal of Agricultural Research, 2007, 58, 532.	1.5	99
98	Transcriptome Analysis of Trichothecene-Induced Gene Expression in Barley. Molecular Plant-Microbe Interactions, 2007, 20, 1364-1375.	1.4	104
99	Genetic Variation in Three Native Plant Species across the State of Minnesota. Crop Science, 2007, 47, 2379-2389.	0.8	17
100	Overexpression of defense response genes in transgenic wheat enhances resistance to Fusarium head blight. Plant Cell Reports, 2007, 26, 479-488.	2.8	150
101	Development of a Fusarium graminearum Affymetrix GeneChip for profiling fungal gene expression in vitro and in planta. Fungal Genetics and Biology, 2006, 43, 316-325.	0.9	164
102	A high-density consensus map of barley linking DArT markers to SSR, RFLP and STS loci and agricultural traits. BMC Genomics, 2006, 7, 206.	1.2	305
103	A hAT superfamily transposase recruited by the cereal grass genome. Molecular Genetics and Genomics, 2006, 275, 553-563.	1.0	35
104	A model wheat cultivar for transformation to improve resistance to Fusarium Head Blight. Plant Cell Reports, 2006, 25, 313-319.	2.8	43
105	Transcriptome Analysis and Physical Mapping of Barley Genes in Wheatâ€"Barley Chromosome Addition Lines. Genetics, 2006, 172, 1277-1285.	1.2	67
106	Transcriptome Analysis of the Barley-Fusarium graminearum Interaction. Molecular Plant-Microbe Interactions, 2006, 19, 407-417.	1.4	175
107	A New Resource for Cereal Genomics: 22K Barley GeneChip Comes of Age. Plant Physiology, 2004, 134, 960-968.	2.3	287
108	Validation of quantitative trait loci for Fusarium head blight and kernel discoloration in barley. Molecular Breeding, 2004, 14, 91-104.	1.0	27

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109	Tissue specificity of the sugarcane bacilliform virus promoter in oat, barley and wheat. Molecular Breeding, 2004, 14, 331-338.	1.0	11
110	Genetic Relationship between Kernel Discoloration and Grain Protein Concentration in Barley. Crop Science, 2003, 43, 1671-1679.	0.8	38
111	Systemic expression of defense response genes in wheat spikes as a response to Fusarium graminearum infection. Physiological and Molecular Plant Pathology, 2001, 58, 1-12.	1.3	85
112	Fungal Development and Induction of Defense Response Genes During Early Infection of Wheat Spikes by Fusarium graminearum. Molecular Plant-Microbe Interactions, 2000, 13, 159-169.	1.4	271
113	Ectopic Expression of the Maize Homeobox GeneLiguleless3 Alters Cell Fates in the Leaf1. Plant Physiology, 1999, 119, 651-662.	2.3	80
114	Association between xylem vasculature size and freezing survival in winter barley. Journal of Agronomy and Crop Science, 0, , .	1.7	0