

Gary J Muehlbauer

List of Publications by Year in descending order

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114
papers

13,038
citations

25034

57
h-index

24982

109
g-index

119
all docs

119
docs citations

119
times ranked

10860
citing authors

#	ARTICLE	IF	CITATIONS
1	A physical, genetic and functional sequence assembly of the barley genome. <i>Nature</i> , 2012, 491, 711-716.	27.8	1,416
2	A chromosome conformation capture ordered sequence of the barley genome. <i>Nature</i> , 2017, 544, 427-433.	27.8	1,365
3	RNA-Seq Atlas of <i>Glycine max</i> : A guide to the soybean transcriptome. <i>BMC Plant Biology</i> , 2010, 10, 160.	3.6	634
4	Development and implementation of high-throughput SNP genotyping in barley. <i>BMC Genomics</i> , 2009, 10, 582.	2.8	570
5	Multiple wheat genomes reveal global variation in modern breeding. <i>Nature</i> , 2020, 588, 277-283.	27.8	513
6	Genome-wide discovery and characterization of maize long non-coding RNAs. <i>Genome Biology</i> , 2014, 15, R40.	9.6	419
7	A high-density consensus map of barley linking DArT markers to SSR, RFLP and STS loci and agricultural traits. <i>BMC Genomics</i> , 2006, 7, 206.	2.8	305
8	INTERMEDIUM-C, a modifier of lateral spikelet fertility in barley, is an ortholog of the maize domestication gene TEOSINTE BRANCHED 1. <i>Nature Genetics</i> , 2011, 43, 169-172.	21.4	302
9	A New Resource for Cereal Genomics: 22K Barley GeneChip Comes of Age. <i>Plant Physiology</i> , 2004, 134, 960-968.	4.8	287
10	Fungal Development and Induction of Defense Response Genes During Early Infection of Wheat Spikes by <i>Fusarium graminearum</i> . <i>Molecular Plant-Microbe Interactions</i> , 2000, 13, 159-169.	2.6	271
11	Anchoring and ordering <sc>NGS</sc> contig assemblies by population sequencing (<sc>POPSEQ</sc>). <i>Plant Journal</i> , 2013, 76, 718-727.	5.7	264
12	Barley whole exome capture: a tool for genomic research in the genus <i>Hordeum</i> and beyond. <i>Plant Journal</i> , 2013, 76, 494-505.	5.7	260
13	Exome sequencing of geographically diverse barley landraces and wild relatives gives insights into environmental adaptation. <i>Nature Genetics</i> , 2016, 48, 1024-1030.	21.4	259
14	A whole-genome shotgun approach for assembling and anchoring the hexaploid bread wheat genome. <i>Genome Biology</i> , 2015, 16, 26.	8.8	256
15	The USDA Barley Core Collection: Genetic Diversity, Population Structure, and Potential for Genome-Wide Association Studies. <i>PLoS ONE</i> , 2014, 9, e94688.	2.5	188
16	TRITEX: chromosome-scale sequence assembly of Triticeae genomes with open-source tools. <i>Genome Biology</i> , 2019, 20, 284.	8.8	179
17	Transcriptome Analysis of the Barley- <i>Fusarium graminearum</i> Interaction. <i>Molecular Plant-Microbe Interactions</i> , 2006, 19, 407-417.	2.6	175
18	Phenotypic and Genomic Analyses of a Fast Neutron Mutant Population Resource in Soybean. <i>Plant Physiology</i> , 2011, 156, 240-253.	4.8	175

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19	Development of a <i>Fusarium graminearum</i> Affymetrix GeneChip for profiling fungal gene expression in vitro and in planta. <i>Fungal Genetics and Biology</i> , 2006, 43, 316-325.	2.1	164
20	Association mapping of spot blotch resistance in wild barley. <i>Molecular Breeding</i> , 2010, 26, 243-256.	2.1	151
21	Overexpression of defense response genes in transgenic wheat enhances resistance to <i>Fusarium head blight</i> . <i>Plant Cell Reports</i> , 2007, 26, 479-488.	5.6	150
22	An Improved Consensus Linkage Map of Barley Based on Flow-Sorted Chromosomes and Single Nucleotide Polymorphism Markers. <i>Plant Genome</i> , 2011, 4, 238-249.	2.8	150
23	Transgenic wheat expressing a barley class II chitinase gene has enhanced resistance against <i>Fusarium graminearum</i> . <i>Journal of Experimental Botany</i> , 2008, 59, 2371-2378.	4.8	144
24	Transcriptome Analysis of the Barley–Deoxynivalenol Interaction: Evidence for a Role of Glutathione in Deoxynivalenol Detoxification. <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 962-976.	2.6	140
25	The emergence of whole genome association scans in barley. <i>Current Opinion in Plant Biology</i> , 2009, 12, 218-222.	7.1	138
26	Transcriptomic characterization of two major <i>Fusarium</i> resistance quantitative trait loci (QTLs), <i>Fhb1</i> and <i>Qfhs.5A</i> , identifies novel candidate genes. <i>Molecular Plant Pathology</i> , 2013, 14, 772-785.	4.2	132
27	Construction of a map-based reference genome sequence for barley, <i>Hordeum vulgare</i> L.. <i>Scientific Data</i> , 2017, 4, 170044.	5.3	130
28	Validation of a Candidate Deoxynivalenol-Inactivating UDP-Glucosyltransferase from Barley by Heterologous Expression in Yeast. <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 977-986.	2.6	126
29	Distribution, functional impact, and origin mechanisms of copy number variation in the barley genome. <i>Genome Biology</i> , 2013, 14, R58.	8.8	125
30	Genomic analysis of 6,000-year-old cultivated grain illuminates the domestication history of barley. <i>Nature Genetics</i> , 2016, 48, 1089-1093.	21.4	122
31	Transgenic Wheat Expressing a Barley UDP-Glucosyltransferase Detoxifies Deoxynivalenol and Provides High Levels of Resistance to <i>Fusarium graminearum</i> . <i>Molecular Plant-Microbe Interactions</i> , 2015, 28, 1237-1246.	2.6	120
32	An Integrated Resource for Barley Linkage Map and Malting Quality QTL Alignment. <i>Plant Genome</i> , 2009, 2, .	2.8	116
33	Population Structure and Linkage Disequilibrium in U.S. Barley Germplasm: Implications for Association Mapping. <i>Crop Science</i> , 2010, 50, 556-566.	1.8	106
34	Transcriptome Analysis of Trichothecene-Induced Gene Expression in Barley. <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 1364-1375.	2.6	104
35	Genetic control of morphometric diversity in the maize shoot apical meristem. <i>Nature Communications</i> , 2015, 6, 8974.	12.8	100
36	A walk on the wild side: mining wild wheat and barley collections for rust resistance genes. <i>Australian Journal of Agricultural Research</i> , 2007, 58, 532.	1.5	99

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37	Transgenic <i>Arabidopsis thaliana</i> expressing a barley UDP-glucosyltransferase exhibit resistance to the mycotoxin deoxynivalenol. <i>Journal of Experimental Botany</i> , 2012, 63, 4731-4740.	4.8	92
38	Circular RNAs mediated by transposons are associated with transcriptomic and phenotypic variation in maize. <i>New Phytologist</i> , 2018, 217, 1292-1306.	7.3	92
39	Genome-wide recombination dynamics are associated with phenotypic variation in maize. <i>New Phytologist</i> , 2016, 210, 1083-1094.	7.3	88
40	Systemic expression of defense response genes in wheat spikes as a response to <i>Fusarium graminearum</i> infection. <i>Physiological and Molecular Plant Pathology</i> , 2001, 58, 1-12.	2.5	85
41	The Barley <i>Ucn4</i> Gene Encodes a BLADE-ON-PETIOLE-Like Protein That Controls Tillering and Leaf Patterning. <i>Plant Physiology</i> , 2015, 168, 164-174.	4.8	85
42	Mendelian and Non-Mendelian Regulation of Gene Expression in Maize. <i>PLoS Genetics</i> , 2013, 9, e1003202.	3.5	84
43	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. <i>BMC Genomics</i> , 2010, 11, 707.	2.8	81
44	Ectopic Expression of the Maize Homeobox Gene <i>Liguleless3</i> Alters Cell Fates in the Leaf1. <i>Plant Physiology</i> , 1999, 119, 651-662.	4.8	80
45	Marker-trait associations in Virginia Tech winter barley identified using genome-wide mapping. <i>Theoretical and Applied Genetics</i> , 2013, 126, 693-710.	3.6	78
46	Effect of population size and unbalanced data sets on QTL detection using genome-wide association mapping in barley breeding germplasm. <i>Theoretical and Applied Genetics</i> , 2012, 124, 111-124.	3.6	77
47	A Sequence-Ready Physical Map of Barley Anchored Genetically by Two Million Single-Nucleotide Polymorphisms. <i>Plant Physiology</i> , 2014, 164, 412-423.	4.8	77
48	Genetics of Tillering in Rice and Barley. <i>Plant Genome</i> , 2014, 7, plantgenome2013.10.0032.	2.8	75
49	A barley UDP-glucosyltransferase inactivates nivalenol and provides <i>Fusarium</i> Head Blight resistance in transgenic wheat. <i>Journal of Experimental Botany</i> , 2017, 68, 2187-2197.	4.8	74
50	Development and Genetic Characterization of an Advanced Backcross-Nested Association Mapping (AB-NAM) Population of Wild – Cultivated Barley. <i>Genetics</i> , 2016, 203, 1453-1467.	2.9	73
51	Ontogeny of the Maize Shoot Apical Meristem. <i>Plant Cell</i> , 2012, 24, 3219-3234.	6.6	72
52	Transcriptome Analysis of a Wheat Near-Isogenic Line Pair Carrying <i>Fusarium</i> Head Blight-Resistant and -Susceptible Alleles. <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 1366-1378.	2.6	70
53	Transcriptome Analysis and Physical Mapping of Barley Genes in Wheat-Barley Chromosome Addition Lines. <i>Genetics</i> , 2006, 172, 1277-1285.	2.9	67
54	Differential transcriptomic responses to <i>Fusarium graminearum</i> infection in two barley quantitative trait loci associated with <i>Fusarium</i> head blight resistance. <i>BMC Genomics</i> , 2016, 17, 387.	2.8	64

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55	Association Mapping of Agronomic QTLs in U.S. Spring Barley Breeding Germplasm. <i>Plant Genome</i> , 2014, 7, plantgenome2013.11.0037.	2.8	63
56	The Genetics of Winterhardiness in Barley: Perspectives from Genome-Wide Association Mapping. <i>Plant Genome</i> , 2011, 4, .	2.8	62
57	Overexpression of the maize Teosinte Branched1 gene in wheat suppresses tiller development. <i>Plant Cell Reports</i> , 2008, 27, 1217-1225.	5.6	61
58	Genome Resilience and Prevalence of Segmental Duplications Following Fast Neutron Irradiation of Soybean. <i>Genetics</i> , 2014, 198, 967-981.	2.9	53
59	The <i>Aegilops ventricosa</i> 2NvS segment in bread wheat: cytology, genomics and breeding. <i>Theoretical and Applied Genetics</i> , 2021, 134, 529-542.	3.6	48
60	The genetics of barley low-tillering mutants: low number of tillers-1 (Int1). <i>Theoretical and Applied Genetics</i> , 2010, 121, 705-715.	3.6	45
61	Examining the Transcriptional Response in Wheat <i><i>Fhb1</i></i> Near-Isogenic Lines to <i><i>Fusarium graminearum</i></i> Infection and Deoxynivalenol Treatment. <i>Plant Genome</i> , 2016, 9, plantgenome2015.05.0032.	2.8	44
62	A model wheat cultivar for transformation to improve resistance to Fusarium Head Blight. <i>Plant Cell Reports</i> , 2006, 25, 313-319.	5.6	43
63	An Induced Chromosomal Translocation in Soybean Disrupts a <i><i>KASI</i></i> Ortholog and Is Associated with a High-Sucrose and Low-Oil Seed Phenotype. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1215-1223.	1.8	42
64	Patterns of polymorphism and linkage disequilibrium in cultivated barley. <i>Theoretical and Applied Genetics</i> , 2011, 122, 523-531.	3.6	41
65	Genetic Relationship between Kernel Discoloration and Grain Protein Concentration in Barley. <i>Crop Science</i> , 2003, 43, 1671-1679.	1.8	38
66	Two Genomic Regions Contribute Disproportionately to Geographic Differentiation in Wild Barley. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1193-1203.	1.8	38
67	Mapping Agronomic Traits in a Wild Barley Advanced Backcross "Nested Association Mapping Population. <i>Crop Science</i> , 2017, 57, 1199-1210.	1.8	38
68	QTL Mapping of Fusarium Head Blight and Correlated Agromorphological Traits in an Elite Barley Cultivar Rasmusson. <i>Frontiers in Plant Science</i> , 2018, 9, 1260.	3.6	37
69	Sequencing of 15,622 gene-bearing BACs clarifies the gene-dense regions of the barley genome. <i>Plant Journal</i> , 2015, 84, 216-227.	5.7	36
70	Co-expression network analysis of duplicate genes in maize (<i>Zea mays</i> L.) reveals no subgenome bias. <i>BMC Genomics</i> , 2016, 17, 875.	2.8	36
71	A hAT superfamily transposase recruited by the cereal grass genome. <i>Molecular Genetics and Genomics</i> , 2006, 275, 553-563.	2.1	35
72	The genetics of barley low-tillering mutants: absent lower laterals (als). <i>Theoretical and Applied Genetics</i> , 2009, 118, 1351-1360.	3.6	35

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73	The Hordeum Toolbox: The Barley Coordinated Agricultural Project Genotype and Phenotype Resource. <i>Plant Genome</i> , 2012, 5, 81-91.	2.8	35
74	Association mapping of grain hardness, polyphenol oxidase, total phenolics, amylose content, and β -glucan in US barley breeding germplasm. <i>Molecular Breeding</i> , 2014, 34, 1229-1243.	2.1	35
75	Fast neutron-induced structural rearrangements at a soybean NAP1 locus result in gnarled trichomes. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1725-1738.	3.6	35
76	A high-resolution gene expression atlas links dedicated meristem genes to key architectural traits. <i>Genome Research</i> , 2019, 29, 1962-1973.	5.5	35
77	Genome-Wide Association Mapping of Stem Rust Resistance in <i>Hordeum vulgare</i> subsp. <i>spontaneum</i> . <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3491-3507.	1.8	30
78	Transcriptome analysis of a barley breeding program examines gene expression diversity and reveals target genes for malting quality improvement. <i>BMC Genomics</i> , 2010, 11, 653.	2.8	29
79	Barley genetic variation: implications for crop improvement. <i>Briefings in Functional Genomics</i> , 2014, 13, 341-350.	2.7	29
80	Dense genotyping-by-sequencing linkage maps of two Synthetic W7984—Opata reference populations provide insights into wheat structural diversity. <i>Scientific Reports</i> , 2019, 9, 1793.	3.3	28
81	Validation of quantitative trait loci for Fusarium head blight and kernel discoloration in barley. <i>Molecular Breeding</i> , 2004, 14, 91-104.	2.1	27
82	Soil—Occupancy Effects of Invasive and Native Grassland Plant Species on Composition and Diversity of Mycorrhizal Associations. <i>Invasive Plant Science and Management</i> , 2012, 5, 494-505.	1.1	24
83	Development of a Multiparent Population for Genetic Mapping and Allele Discovery in Six-Row Barley. <i>Genetics</i> , 2019, 213, 595-613.	2.9	23
84	Diversity of Maize Shoot Apical Meristem Architecture and Its Relationship to Plant Morphology. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 819-827.	1.8	22
85	<i>ELIGULUM-A</i> Regulates Lateral Branch and Leaf Development in Barley. <i>Plant Physiology</i> , 2018, 176, 2750-2760.	4.8	22
86	Haplotype diversity and population structure in cultivated and wild barley evaluated for Fusarium head blight responses. <i>Theoretical and Applied Genetics</i> , 2013, 126, 619-636.	3.6	21
87	The Effects of Both Recent and Long-Term Selection and Genetic Drift Are Readily Evident in North American Barley Breeding Populations. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 609-622.	1.8	21
88	Genomic prediction of maize microphenotypes provides insights for optimizing selection and mining diversity. <i>Plant Biotechnology Journal</i> , 2020, 18, 2456-2465.	8.3	20
89	Environmental Association Identifies Candidates for Tolerance to Low Temperature and Drought. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3423-3438.	1.8	18
90	Genetic Variation in Three Native Plant Species across the State of Minnesota. <i>Crop Science</i> , 2007, 47, 2379-2389.	1.8	17

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91	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. <i>Plant and Cell Physiology</i> , 2021, 62, 8-27.	3.1	16
92	eQTL Networks Reveal Complex Genetic Architecture in the Immature Soybean Seed. <i>Plant Genome</i> , 2014, 7, plantgenome2013.08.0027.	2.8	15
93	Genetic Control of Maize Shoot Apical Meristem Architecture. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1327-1337.	1.8	13
94	Quantitative trait loci conferring resistance to Fusarium head blight in barley respond differentially to Fusarium graminearum infection. <i>Functional and Integrative Genomics</i> , 2011, 11, 95-102.	3.5	12
95	Tissue specificity of the sugarcane bacilliform virus promoter in oat, barley and wheat. <i>Molecular Breeding</i> , 2004, 14, 331-338.	2.1	11
96	Single-feature polymorphism discovery by computing probe affinity shape powers. <i>BMC Genetics</i> , 2009, 10, 48.	2.7	11
97	The barley UNICULM2 gene resides in a centromeric region and may be associated with signaling and stress responses. <i>Functional and Integrative Genomics</i> , 2013, 13, 33-41.	3.5	11
98	Similar Seed Composition Phenotypes Are Observed From CRISPR-Generated In-Frame and Knockout Alleles of a Soybean KASI Ortholog. <i>Frontiers in Plant Science</i> , 2020, 11, 1005.	3.6	11
99	Genetic architecture of agronomic and quality traits in a nested association mapping population of spring wheat. <i>Plant Genome</i> , 2020, 13, e20051.	2.8	11
100	Marker Imputation in Barley Association Studies. <i>Plant Genome</i> , 2009, 2, .	2.8	10
101	Wild barley accumulates distinct sets of transcripts in response to pathogens of different trophic lifestyles. <i>Physiological and Molecular Plant Pathology</i> , 2009, 74, 91-98.	2.5	9
102	Density Stress has Minimal Impacts on the Barley or Maize Seedling Transcriptome. <i>Plant Genome</i> , 2011, 4, .	2.8	9
103	Sheathing the blade: Significant contribution of sheaths to daytime and nighttime gas exchange in a grass crop. <i>Plant, Cell and Environment</i> , 2020, 43, 1844-1861.	5.7	9
104	Molecular Mapping and Cloning of Genes and QTLs. <i>Compendium of Plant Genomes</i> , 2018, , 139-154.	0.5	7
105	Natural Genetic Variation Underlying Tiller Development in Barley (<i>Hordeum vulgare</i> L). <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1197-1212.	1.8	7
106	Genetic dissection of a pericentromeric region of barley chromosome 6H associated with Fusarium head blight resistance, grain protein content and agronomic traits. <i>Theoretical and Applied Genetics</i> , 2021, 134, 3963-3981.	3.6	5
107	Intragenic Meiotic Crossovers Generate Novel Alleles with Transgressive Expression Levels. <i>Molecular Biology and Evolution</i> , 2018, 35, 2762-2772.	8.9	4
108	Genetic characterization of flour quality and bread-making traits in a spring wheat nested association mapping population. <i>Crop Science</i> , 2021, 61, 1168-1183.	1.8	4

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109	Mapping malting quality and yield characteristics in a north American two-rowed malting barley Æ— wild barley advanced backcross population. <i>Molecular Breeding</i> , 2019, 39, 1.	2.1	3
110	RNA Isolation and Analysis of LncRNAs from Gametophytes of Maize. <i>Methods in Molecular Biology</i> , 2019, 1933, 67-86.	0.9	3
111	Shoot and Inflorescence Architecture. <i>Biotechnology in Agriculture and Forestry</i> , 2014, , 55-80.	0.2	3
112	A Critical Assessment of 60 Years of Maize Intragenic Recombination. <i>Frontiers in Plant Science</i> , 2018, 9, 1560.	3.6	0
113	Genetics of Whole Plant Morphology and Architecture. <i>Compendium of Plant Genomes</i> , 2018, , 209-231.	0.5	0
114	Association between xylem vasculature size and freezing survival in winter barley. <i>Journal of Agronomy and Crop Science</i> , 0, , .	3.5	0