

Martin Mascher

List of Publications by Year in descending order

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Version: 2024-02-01

110
papers

14,463
citations

50170

46
h-index

25716

108
g-index

133
all docs

133
docs citations

133
times ranked

11058
citing authors

#	ARTICLE	IF	CITATIONS
1	Population genomic analysis of <i>Aegilops tauschii</i> identifies targets for bread wheat improvement. <i>Nature Biotechnology</i> , 2022, 40, 422-431.	9.4	102
2	The barley mutant <i>multiflorus2.b</i> reveals quantitative genetic variation for new spikelet architecture. <i>Theoretical and Applied Genetics</i> , 2022, 135, 571-590.	1.8	7
3	Genome sequences of three <i>Aegilops</i> species of the section <i>Sitopsis</i> reveal phylogenetic relationships and provide resources for wheat improvement. <i>Plant Journal</i> , 2022, 110, 179-192.	2.8	46
4	Physical geography, isolation by distance and environmental variables shape genomic variation of wild barley (<i>Hordeum vulgare</i> L. ssp. <i>spontaneum</i>) in the Southern Levant. <i>Heredity</i> , 2022, 128, 107-119.	1.2	10
5	The Barley and Wheat Pan-Genomes. <i>Methods in Molecular Biology</i> , 2022, 2443, 147-159.	0.4	2
6	Chromosome-scale assembly of barley cv. "Haruna Nijo"™ as a resource for barley genetics. <i>DNA Research</i> , 2022, 29, .	1.5	6
7	Cherish your weeds. <i>Molecular Plant</i> , 2022, 15, 396-397.	3.9	1
8	<i>Aegilops sharonensis</i> genome-assisted identification of stem rust resistance gene Sr62. <i>Nature Communications</i> , 2022, 13, 1607.	5.8	48
9	A reference-guided TILLING by amplicon-sequencing platform supports forward and reverse genetics in barley. <i>Plant Communications</i> , 2022, 3, 100317.	3.6	15
10	Prospects of telomere-to-telomere assembly in barley: Analysis of sequence gaps in the MorexV3 reference genome. <i>Plant Biotechnology Journal</i> , 2022, 20, 1373-1386.	4.1	24
11	The barley leaf rust resistance gene <i>Rph3</i> encodes a predicted membrane protein and is induced upon infection by avirulent pathotypes of <i>Puccinia hordei</i> . <i>Nature Communications</i> , 2022, 13, 2386.	5.8	12
12	Advancing Grain Legumes Domestication and Evolution Studies with Genomics. <i>Plant and Cell Physiology</i> , 2022, 63, 1540-1553.	1.5	6
13	A catalogue of resistance gene homologs and a chromosome-scale reference sequence support resistance gene mapping in winter wheat. <i>Plant Biotechnology Journal</i> , 2022, 20, 1730-1742.	4.1	21
14	The mosaic oat genome gives insights into a uniquely healthy cereal crop. <i>Nature</i> , 2022, 606, 113-119.	13.7	70
15	Genome analysis in <i>Avena sativa</i> reveals hidden breeding barriers and opportunities for oat improvement. <i>Communications Biology</i> , 2022, 5, 474.	2.0	23
16	High-Resolution Mapping of Barley mild mosaic virus Resistance Gene <i>rym15</i> . <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	1
17	Recombination Landscape Divergence Between Populations is Marked by Larger Low-Recombining Regions in Domesticated Rye. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	5
18	Six-rowed wild-growing barleys are hybrids of diverse origins. <i>Plant Journal</i> , 2022, 111, 849-858.	2.8	1

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19	The <i>Aegilops ventricosa</i> 2NvS segment in bread wheat: cytology, genomics and breeding. <i>Theoretical and Applied Genetics</i> , 2021, 134, 529-542.	1.8	48
20	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.	1.5	16
21	A highly differentiated region of wheat chromosome 7AL encodes a <i>Pm1a</i> immune receptor that recognizes its corresponding <i>AvrPm1a</i> effector from <i>Blumeria graminis</i> . <i>New Phytologist</i> , 2021, 229, 2812-2826.	3.5	72
22	Genome Assembly of the Canadian two-row Malting Barley cultivar AAC Synergy. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	6
23	Chromosome-scale genome assembly provides insights into rye biology, evolution and agronomic potential. <i>Nature Genetics</i> , 2021, 53, 564-573.	9.4	138
24	Long-read sequence assembly: a technical evaluation in barley. <i>Plant Cell</i> , 2021, 33, 1888-1906.	3.1	180
25	Transcriptional landscapes of floral meristems in barley. <i>Science Advances</i> , 2021, 7, .	4.7	33
26	Genome-wide identification of loci modifying spike-branching in tetraploid wheat. <i>Theoretical and Applied Genetics</i> , 2021, 134, 1925-1943.	1.8	9
27	Optical maps refine the bread wheat <i>Triticum aestivum</i> cv. Chinese Spring genome assembly. <i>Plant Journal</i> , 2021, 107, 303-314.	2.8	237
28	Chromosome-scale genome assembly of the transformation-amenable common wheat cultivar 'Fielder'. <i>DNA Research</i> , 2021, 28, .	1.5	74
29	Chromosome-scale assembly of wild barley accession 'OUH602'. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	14
30	<i>ENHANCED GRAVITROPISM 2</i> encodes a STERILE ALPHA MOTIF-containing protein that controls root growth angle in barley and wheat. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	32
31	A simple model explains the cell cycle-dependent assembly of centromeric nucleosomes in holocentric species. <i>Nucleic Acids Research</i> , 2021, 49, 9053-9065.	6.5	8
32	Multiple Wheat Genomes Reveal Novel Gli-2 Sublocus Location and Variation of Celiac Disease Epitopes in Duplicated \pm -Gliadin Genes. <i>Frontiers in Plant Science</i> , 2021, 12, 715985.	1.7	7
33	Building pan-genome infrastructures for crop plants and their use in association genetics. <i>DNA Research</i> , 2021, 28, .	1.5	57
34	Evolution and Domestication of Rye. <i>Compendium of Plant Genomes</i> , 2021, , 85-100.	0.3	4
35	High molecular weight glutenin gene diversity in <i>Aegilops tauschii</i> demonstrates unique origin of superior wheat quality. <i>Communications Biology</i> , 2021, 4, 1242.	2.0	14
36	Quantitative monitoring of nucleotide sequence data from genetic resources in context of their citation in the scientific literature. <i>GigaScience</i> , 2021, 10, .	3.3	3

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37	The barley pan-genome reveals the hidden legacy of mutation breeding. <i>Nature</i> , 2020, 588, 284-289.	13.7	314
38	Multiple wheat genomes reveal global variation in modern breeding. <i>Nature</i> , 2020, 588, 277-283.	13.7	513
39	Dissecting the Genetic Basis of Lateral and Central Spikelet Development and Grain Traits in Intermedium-Spike Barley (<i>Hordeum vulgare</i> Convar. <i>Intermedium</i>). <i>Plants</i> , 2020, 9, 1655.	1.6	7
40	BRIDGE – A Visual Analytics Web Tool for Barley Genebank Genomics. <i>Frontiers in Plant Science</i> , 2020, 11, 701.	1.7	31
41	The contribution of cis- and trans-acting variants to gene regulation in wild and domesticated barley under cold stress and control conditions. <i>Journal of Experimental Botany</i> , 2020, 71, 2573-2584.	2.4	15
42	A Genome Assembly of the Barley –Transformation Reference™ Cultivar Golden Promise. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1823-1827.	0.8	61
43	Genebank genomics bridges the gap between the conservation of crop diversity and plant breeding. <i>Nature Genetics</i> , 2019, 51, 1076-1081.	9.4	176
44	Sweet genes in melon and watermelon. <i>Nature Genetics</i> , 2019, 51, 1572-1573.	9.4	7
45	Exome sequences and multi-environment field trials elucidate the genetic basis of adaptation in barley. <i>Plant Journal</i> , 2019, 99, 1172-1191.	2.8	50
46	A Comparison of Mainstream Genotyping Platforms for the Evaluation and Use of Barley Genetic Resources. <i>Frontiers in Plant Science</i> , 2019, 10, 544.	1.7	66
47	Variation in Recombination Rate Is Shaped by Domestication and Environmental Conditions in Barley. <i>Molecular Biology and Evolution</i> , 2019, 36, 2029-2039.	3.5	39
48	Combining next-generation sequencing and progeny testing for rapid identification of induced recessive and dominant mutations in maize M2 individuals. <i>Plant Journal</i> , 2019, 100, 851-862.	2.8	7
49	Leaf Variegation and Impaired Chloroplast Development Caused by a Truncated CCT Domain Gene in <i>Hordeum vulgare</i> Barley. <i>Plant Cell</i> , 2019, 31, 1430-1445.	3.1	52
50	The highly divergent <i>Jekyll</i> genes, required for sexual reproduction, are lineage specific for the related grass tribes <i>Triticeae</i> and <i>Bromeae</i> . <i>Plant Journal</i> , 2019, 98, 961-974.	2.8	7
51	High Resolution Genetic and Physical Mapping of a Major Powdery Mildew Resistance Locus in Barley. <i>Frontiers in Plant Science</i> , 2019, 10, 146.	1.7	27
52	Durum wheat genome highlights past domestication signatures and future improvement targets. <i>Nature Genetics</i> , 2019, 51, 885-895.	9.4	576
53	In Situ Hi-C for Plants: An Improved Method to Detect Long-Range Chromatin Interactions. <i>Methods in Molecular Biology</i> , 2019, 1933, 441-472.	0.4	26
54	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.	1.6	28

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55	Unleashing floret fertility in wheat through the mutation of a homeobox gene. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 5182-5187.	3.3	158
56	Genetic insights into morphometric inflorescence traits of wheat. Theoretical and Applied Genetics, 2019, 132, 1661-1676.	1.8	37
57	TRITEX: chromosome-scale sequence assembly of Triticeae genomes with open-source tools. Genome Biology, 2019, 20, 284.	3.8	179
58	Genetic modification of spikelet arrangement in wheat increases grain number without significantly affecting grain weight. Molecular Genetics and Genomics, 2019, 294, 457-468.	1.0	38
59	Domestication and crop evolution of wheat and barley: Genes, genomics, and future directions. Journal of Integrative Plant Biology, 2019, 61, 204-225.	4.1	89
60	Genebank genomics highlights the diversity of a global barley collection. Nature Genetics, 2019, 51, 319-326.	9.4	322
61	Prospects of pan-genomics in barley. Theoretical and Applied Genetics, 2019, 132, 785-796.	1.8	38
62	The Wheat <i>Lr67</i> Gene from the Sugar Transport Protein 13 Family Confers Multipathogen Resistance in Barley. Plant Physiology, 2019, 179, 1285-1297.	2.3	53
63	Genetic diversity and relationship between domesticated rye and its wild relatives as revealed through genotyping-by-sequencing. Evolutionary Applications, 2019, 12, 66-77.	1.5	50
64	Laser Capture Microdissection-Based RNA-Seq of Barley Grain Tissues. Methods in Molecular Biology, 2018, 1723, 397-409.	0.4	9
65	Origin and evolution of qingke barley in Tibet. Nature Communications, 2018, 9, 5433.	5.8	141
66	Discovery of multi-megabase polymorphic inversions by chromosome conformation capture sequencing in large-genome plant species. Plant Journal, 2018, 96, 1309-1316.	2.8	26
67	Genomic approaches for studying crop evolution. Genome Biology, 2018, 19, 140.	3.8	54
68	The transcriptional landscape of polyploid wheat. Science, 2018, 361, .	6.0	768
69	Barley Genome Sequencing and Assembly—A First Version Reference Sequence. Compendium of Plant Genomes, 2018, , 57-71.	0.3	3
70	Tethered Chromosome Conformation Capture Sequencing in Triticeae: A Valuable Tool for Genome Assembly. Bio-protocol, 2018, 8, e2955.	0.2	6
71	Natural diversity of inflorescence architecture traces cryptic domestication genes in barley (<i>Hordeum vulgare</i> L.). Genetic Resources and Crop Evolution, 2017, 64, 843-853.	0.8	11
72	MISA-web: a web server for microsatellite prediction. Bioinformatics, 2017, 33, 2583-2585.	1.8	1,248

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73	CRISPR-Cas9 Targeted Mutagenesis Leads to Simultaneous Modification of Different Homoeologous Gene Copies in Polyploid Oilseed Rape (<i>Brassica napus</i>). <i>Plant Physiology</i> , 2017, 174, 935-942.	2.3	257
74	A chromosome conformation capture ordered sequence of the barley genome. <i>Nature</i> , 2017, 544, 427-433.	13.7	1,365
75	Construction of a map-based reference genome sequence for barley, <i>Hordeum vulgare</i> L.. <i>Scientific Data</i> , 2017, 4, 170044.	2.4	130
76	Wild emmer genome architecture and diversity elucidate wheat evolution and domestication. <i>Science</i> , 2017, 357, 93-97.	6.0	781
77	Towards a whole-genome sequence for rye (<i>Secale cereale</i> L.). <i>Plant Journal</i> , 2017, 89, 853-869.	2.8	238
78	A High-Density, Sequence-Enriched Genetic Map of <i>Hordeum bulbosum</i> and Its Collinearity to <i>H. vulgare</i> . <i>Plant Genome</i> , 2017, 10, plantgenome2017.06.0049.	1.6	17
79	transPLANT Resources for Triticeae Genomic Data. <i>Plant Genome</i> , 2016, 9, plantgenome2015.06.0038.	1.6	8
80	Aadh2p: an <i>Arxula adenivorans</i> alcohol dehydrogenase involved in the first step of the 1-butanol degradation pathway. <i>Microbial Cell Factories</i> , 2016, 15, 175.	1.9	6
81	Barley Seed Aging: Genetics behind the Dry Elevated Pressure of Oxygen Aging and Moist Controlled Deterioration. <i>Frontiers in Plant Science</i> , 2016, 7, 388.	1.7	40
82	A homolog of Blade-On-Petiole 1 and 2 (BOP1/2) controls internode length and homeotic changes of the barley inflorescence. <i>Plant Physiology</i> , 2016, 171, pp.00124.2016.	2.3	41
83	Multiplex sequencing of bacterial artificial chromosomes for assembling complex plant genomes. <i>Plant Biotechnology Journal</i> , 2016, 14, 1511-1522.	4.1	20
84	Exome sequencing of geographically diverse barley landraces and wild relatives gives insights into environmental adaptation. <i>Nature Genetics</i> , 2016, 48, 1024-1030.	9.4	259
85	Genomic analysis of 6,000-year-old cultivated grain illuminates the domestication history of barley. <i>Nature Genetics</i> , 2016, 48, 1089-1093.	9.4	122
86	Diversity analysis and genomic prediction of <i>Sclerotinia</i> resistance in sunflower using a new 25K SNP genotyping array. <i>Theoretical and Applied Genetics</i> , 2016, 129, 317-329.	1.8	22
87	Centromeric chromatin and its dynamics in plants. <i>Plant Journal</i> , 2015, 83, 4-17.	2.8	46
88	Evolution of the Grain Dispersal System in Barley. <i>Cell</i> , 2015, 162, 527-539.	13.5	265
89	Behavior of a modified Dissociation element in barley: a tool for genetic studies and for breeding transgenic barley. <i>Molecular Breeding</i> , 2015, 35, 1.	1.0	4
90	A whole-genome shotgun approach for assembling and anchoring the hexaploid bread wheat genome. <i>Genome Biology</i> , 2015, 16, 26.	3.8	256

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91	Genetic linkage facilitates cloning of Ert-m regulating plant architecture in barley and identified a strong candidate of Ant1 involved in anthocyanin biosynthesis. <i>Plant Molecular Biology</i> , 2015, 88, 609-626.	2.0	14
92	BARLEX – the Barley Draft Genome Explorer. <i>Molecular Plant</i> , 2015, 8, 964-966.	3.9	114
93	Bulbosum to Go: A Toolbox to Utilize <i>Hordeum vulgare</i> /bulbosum Introgressions for Breeding and Beyond. <i>Molecular Plant</i> , 2015, 8, 1507-1519.	3.9	58
94	Sequence and Ionomic Analysis of Divergent Strains of Maize Inbred Line B73 with an Altered Growth Phenotype. <i>PLoS ONE</i> , 2014, 9, e96782.	1.1	13
95	Genetic anchoring of whole-genome shotgun assemblies. <i>Frontiers in Genetics</i> , 2014, 5, 208.	1.1	48
96	Unlocking the secondary gene pool of barley with next-generation sequencing. <i>Plant Biotechnology Journal</i> , 2014, 12, 1122-1131.	4.1	111
97	DNA methylation maintenance consolidates RNA-directed DNA methylation and transcriptional gene silencing over generations in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2014, 80, 269-281.	2.8	15
98	Mapping-by-sequencing accelerates forward genetics in barley. <i>Genome Biology</i> , 2014, 15, R78.	13.9	131
99	A chromosome-based draft sequence of the hexaploid bread wheat (<i>Triticum aestivum</i>) genome. <i>Science</i> , 2014, 345, 1251788.	6.0	1,479
100	Ancient hybridizations among the ancestral genomes of bread wheat. <i>Science</i> , 2014, 345, 1250092.	6.0	629
101	The complete genome of <i>Blastobotrys (Arxula) adenivorans</i> LS3 - a yeast of biotechnological interest. <i>Biotechnology for Biofuels</i> , 2014, 7, 66.	6.2	57
102	A Sequence-Ready Physical Map of Barley Anchored Genetically by Two Million Single-Nucleotide Polymorphisms. <i>Plant Physiology</i> , 2014, 164, 412-423.	2.3	77
103	Distribution, functional impact, and origin mechanisms of copy number variation in the barley genome. <i>Genome Biology</i> , 2013, 14, R58.	3.8	125
104	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.	2.8	260
105	Anchoring and ordering NGS contig assemblies by population sequencing (POPSEQ). <i>Plant Journal</i> , 2013, 76, 718-727.	2.8	264
106	Patterns of nucleotide asymmetries in plant and animal genomes. <i>BioSystems</i> , 2013, 111, 181-189.	0.9	17
107	Application of Genotyping-by-Sequencing on Semiconductor Sequencing Platforms: A Comparison of Genetic and Reference-Based Marker Ordering in Barley. <i>PLoS ONE</i> , 2013, 8, e76925.	1.1	186
108	Maize Source Leaf Adaptation to Nitrogen Deficiency Affects Not Only Nitrogen and Carbon Metabolism But Also Control of Phosphate Homeostasis. <i>Plant Physiology</i> , 2012, 160, 1384-1406.	2.3	170

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109	OPTIMAS-DW: A comprehensive transcriptomics, metabolomics, ionomics, proteomics and phenomics data resource for maize. BMC Plant Biology, 2012, 12, 245.	1.6	47
110	From RNA-seq to large-scale genotyping - genomics resources for rye (<i>Secale cereale</i> L.). BMC Plant Biology, 2011, 11, 131.	1.6	109