

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	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
2	A chromosome conformation capture ordered sequence of the barley genome. <i>Nature</i> , 2017, 544, 427-433.	13.7	1,365
3	MISA-web: a web server for microsatellite prediction. <i>Bioinformatics</i> , 2017, 33, 2583-2585.	1.8	1,248
4	Wild emmer genome architecture and diversity elucidate wheat evolution and domestication. <i>Science</i> , 2017, 357, 93-97.	6.0	781
5	The transcriptional landscape of polyploid wheat. <i>Science</i> , 2018, 361, .	6.0	768
6	Ancient hybridizations among the ancestral genomes of bread wheat. <i>Science</i> , 2014, 345, 1250092.	6.0	629
7	Durum wheat genome highlights past domestication signatures and future improvement targets. <i>Nature Genetics</i> , 2019, 51, 885-895.	9.4	576
8	Multiple wheat genomes reveal global variation in modern breeding. <i>Nature</i> , 2020, 588, 277-283.	13.7	513
9	Genebank genomics highlights the diversity of a global barley collection. <i>Nature Genetics</i> , 2019, 51, 319-326.	9.4	322
10	The barley pan-genome reveals the hidden legacy of mutation breeding. <i>Nature</i> , 2020, 588, 284-289.	13.7	314
11	Evolution of the Grain Dispersal System in Barley. <i>Cell</i> , 2015, 162, 527-539.	13.5	265
12	Anchoring and ordering <i>NGS</i> contig assemblies by population sequencing (<i>POPSEQ</i>). <i>Plant Journal</i> , 2013, 76, 718-727.	2.8	264
13	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
14	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
15	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
16	A whole-genome shotgun approach for assembling and anchoring the hexaploid bread wheat genome. <i>Genome Biology</i> , 2015, 16, 26.	3.8	256
17	Towards a whole-genome sequence for rye (<i>Secale cereale</i> L.). <i>Plant Journal</i> , 2017, 89, 853-869.	2.8	238
18	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

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19	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
20	Long-read sequence assembly: a technical evaluation in barley. <i>Plant Cell</i> , 2021, 33, 1888-1906.	3.1	180
21	TRITEX: chromosome-scale sequence assembly of Triticeae genomes with open-source tools. <i>Genome Biology</i> , 2019, 20, 284.	3.8	179
22	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
23	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
24	Unleashing floret fertility in wheat through the mutation of a homeobox gene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 5182-5187.	3.3	158
25	Origin and evolution of qingke barley in Tibet. <i>Nature Communications</i> , 2018, 9, 5433.	5.8	141
26	Chromosome-scale genome assembly provides insights into rye biology, evolution and agronomic potential. <i>Nature Genetics</i> , 2021, 53, 564-573.	9.4	138
27	Mapping-by-sequencing accelerates forward genetics in barley. <i>Genome Biology</i> , 2014, 15, R78.	13.9	131
28	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
29	Distribution, functional impact, and origin mechanisms of copy number variation in the barley genome. <i>Genome Biology</i> , 2013, 14, R58.	3.8	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.	9.4	122
31	BARLEX – the Barley Draft Genome Explorer. <i>Molecular Plant</i> , 2015, 8, 964-966.	3.9	114
32	Unlocking the secondary gene pool of barley with next-generation sequencing. <i>Plant Biotechnology Journal</i> , 2014, 12, 1122-1131.	4.1	111
33	From RNA-seq to large-scale genotyping - genomics resources for rye (<i>Secale cereale</i> L.). <i>BMC Plant Biology</i> , 2011, 11, 131.	1.6	109
34	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
35	Domestication and crop evolution of wheat and barley: Genes, genomics, and future directions. <i>Journal of Integrative Plant Biology</i> , 2019, 61, 204-225.	4.1	89
36	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

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37	Chromosome-scale genome assembly of the transformation-amenable common wheat cultivar 'Fielder'. DNA Research, 2021, 28, .	1.5	74
38	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> . New Phytologist, 2021, 229, 2812-2826.	3.5	72
39	The mosaic oat genome gives insights into a uniquely healthy cereal crop. Nature, 2022, 606, 113-119.	13.7	70
40	A Comparison of Mainstream Genotyping Platforms for the Evaluation and Use of Barley Genetic Resources. Frontiers in Plant Science, 2019, 10, 544.	1.7	66
41	A Genome Assembly of the Barley 'Transformation Reference' Cultivar Golden Promise. G3: Genes, Genomes, Genetics, 2020, 10, 1823-1827.	0.8	61
42	Bulbosum to Go: A Toolbox to Utilize <i>Hordeum vulgare</i> /bulbosum Introgressions for Breeding and Beyond. Molecular Plant, 2015, 8, 1507-1519.	3.9	58
43	The complete genome of <i>Blastobotrys (Arxula) adenivorans</i> LS3 - a yeast of biotechnological interest. Biotechnology for Biofuels, 2014, 7, 66.	6.2	57
44	Building pan-genome infrastructures for crop plants and their use in association genetics. DNA Research, 2021, 28, .	1.5	57
45	Genomic approaches for studying crop evolution. Genome Biology, 2018, 19, 140.	3.8	54
46	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
47	Leaf Variegation and Impaired Chloroplast Development Caused by a Truncated CCT Domain Gene in <i>albostrians</i> Barley. Plant Cell, 2019, 31, 1430-1445.	3.1	52
48	Exome sequences and multi-environment field trials elucidate the genetic basis of adaptation in barley. Plant Journal, 2019, 99, 1172-1191.	2.8	50
49	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
50	Genetic anchoring of whole-genome shotgun assemblies. Frontiers in Genetics, 2014, 5, 208.	1.1	48
51	The <i>Aegilops ventricosa</i> 2NvS segment in bread wheat: cytology, genomics and breeding. Theoretical and Applied Genetics, 2021, 134, 529-542.	1.8	48
52	<i>Aegilops sharonensis</i> genome-assisted identification of stem rust resistance gene Sr62. Nature Communications, 2022, 13, 1607.	5.8	48
53	OPTIMAS-DW: A comprehensive transcriptomics, metabolomics, ionomics, proteomics and phenomics data resource for maize. BMC Plant Biology, 2012, 12, 245.	1.6	47
54	Centromeric chromatin and its dynamics in plants. Plant Journal, 2015, 83, 4-17.	2.8	46

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55	Genome sequences of three <i>Aegilops</i> species of the section Sitopsis reveal phylogenetic relationships and provide resources for wheat improvement. <i>Plant Journal</i> , 2022, 110, 179-192.	2.8	46
56	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
57	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
58	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
59	Genetic modification of spikelet arrangement in wheat increases grain number without significantly affecting grain weight. <i>Molecular Genetics and Genomics</i> , 2019, 294, 457-468.	1.0	38
60	Prospects of pan-genomics in barley. <i>Theoretical and Applied Genetics</i> , 2019, 132, 785-796.	1.8	38
61	Genetic insights into morphometric inflorescence traits of wheat. <i>Theoretical and Applied Genetics</i> , 2019, 132, 1661-1676.	1.8	37
62	Transcriptional landscapes of floral meristems in barley. <i>Science Advances</i> , 2021, 7, .	4.7	33
63	<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
64	BRIDGE – A Visual Analytics Web Tool for Barley Genebank Genomics. <i>Frontiers in Plant Science</i> , 2020, 11, 701.	1.7	31
65	Dense genotyping-by-sequencing linkage maps of two Synthetic W7984–Opatá reference populations provide insights into wheat structural diversity. <i>Scientific Reports</i> , 2019, 9, 1793.	1.6	28
66	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
67	Discovery of multi-megabase polymorphic inversions by chromosome conformation capture sequencing in large-genome plant species. <i>Plant Journal</i> , 2018, 96, 1309-1316.	2.8	26
68	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
69	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
70	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
71	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
72	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

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73	Multiplex sequencing of bacterial artificial chromosomes for assembling complex plant genomes. <i>Plant Biotechnology Journal</i> , 2016, 14, 1511-1522.	4.1	20
74	Patterns of nucleotide asymmetries in plant and animal genomes. <i>BioSystems</i> , 2013, 111, 181-189.	0.9	17
75	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
76	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
77	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
78	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
79	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
80	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
81	Chromosome-scale assembly of wild barley accession ‘OUH602’: G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	14
82	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
83	Sequence and Iomic Analysis of Divergent Strains of Maize Inbred Line B73 with an Altered Growth Phenotype. <i>PLoS ONE</i> , 2014, 9, e96782.	1.1	13
84	The barley leaf rust resistance gene Rph3 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
85	Natural diversity of inflorescence architecture traces cryptic domestication genes in barley (<i>Hordeum vulgare</i> L.). <i>Genetic Resources and Crop Evolution</i> , 2017, 64, 843-853.	0.8	11
86	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
87	Laser Capture Microdissection-Based RNA-Seq of Barley Grain Tissues. <i>Methods in Molecular Biology</i> , 2018, 1723, 397-409.	0.4	9
88	Genome-wide identification of loci modifying spike-branching in tetraploid wheat. <i>Theoretical and Applied Genetics</i> , 2021, 134, 1925-1943.	1.8	9
89	transPLANT Resources for Triticeae Genomic Data. <i>Plant Genome</i> , 2016, 9, plantgenome2015.06.0038.	1.6	8
90	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

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91	Sweet genes in melon and watermelon. <i>Nature Genetics</i> , 2019, 51, 1572-1573.	9.4	7
92	Combining next-generation sequencing and progeny testing for rapid identification of induced recessive and dominant mutations in maize M 2 individuals. <i>Plant Journal</i> , 2019, 100, 851-862.	2.8	7
93	The highly divergent Jekyll genes, required for sexual reproduction, are lineage specific for the related grass tribes Triticeae and Bromeae. <i>Plant Journal</i> , 2019, 98, 961-974.	2.8	7
94	Dissecting the Genetic Basis of Lateral and Central Spikelet Development and Grain Traits in Intermedium-Spike Barley (<i>Hordeum vulgare</i> Convar. Intermedium). <i>Plants</i> , 2020, 9, 1655.	1.6	7
95	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
96	The barley mutant multiflorus2.b reveals quantitative genetic variation for new spikelet architecture. <i>Theoretical and Applied Genetics</i> , 2022, 135, 571-590.	1.8	7
97	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
98	Genome Assembly of the Canadian two-row Malting Barley cultivar AAC Synergy. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	6
99	Tethered Chromosome Conformation Capture Sequencing in Triticeae: A Valuable Tool for Genome Assembly. <i>Bio-protocol</i> , 2018, 8, e2955.	0.2	6
100	Chromosome-scale assembly of barley cv. "Haruna Nijo"™ as a resource for barley genetics. <i>DNA Research</i> , 2022, 29, .	1.5	6
101	Advancing Grain Legumes Domestication and Evolution Studies with Genomics. <i>Plant and Cell Physiology</i> , 2022, 63, 1540-1553.	1.5	6
102	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
103	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
104	Evolution and Domestication of Rye. <i>Compendium of Plant Genomes</i> , 2021, , 85-100.	0.3	4
105	Barley Genome Sequencing and Assembly" A First Version Reference Sequence. <i>Compendium of Plant Genomes</i> , 2018, , 57-71.	0.3	3
106	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
107	The Barley and Wheat Pan-Genomes. <i>Methods in Molecular Biology</i> , 2022, 2443, 147-159.	0.4	2
108	Cherish your weeds. <i>Molecular Plant</i> , 2022, 15, 396-397.	3.9	1

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109	High-Resolution Mapping of Barley mild mosaic virus Resistance Gene rym15. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	1
110	Six-rowed wild-growing barleys are hybrids of diverse origins. <i>Plant Journal</i> , 2022, 111, 849-858.	2.8	1