

# Andreas Maurer

## List of Publications by Year in descending order

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Version: 2024-02-01

29  
papers

1,048  
citations

643344

15  
h-index

563245

28  
g-index

33  
all docs

33  
docs citations

33  
times ranked

1262  
citing authors

#	ARTICLE	IF	CITATIONS
1	Dynamics and genetic regulation of leaf nutrient concentration in barley based on hyperspectral imaging and machine learning. <i>Plant Science</i> , 2022, 315, 111123.	1.7	15
2	Identifying plant genes shaping microbiota composition in the barley rhizosphere. <i>Nature Communications</i> , 2022, 13, .	5.8	44
3	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
4	Genome-wide association study on metabolite accumulation in a wild barley NAM population reveals natural variation in sugar metabolism. <i>PLoS ONE</i> , 2021, 16, e0246510.	1.1	5
5	Evaluation of RGB and Multispectral Unmanned Aerial Vehicle (UAV) Imagery for High-Throughput Phenotyping and Yield Prediction in Barley Breeding. <i>Remote Sensing</i> , 2021, 13, 2670.	1.8	17
6	Footprints of Selection Derived From Temporal Heterozygosity Patterns in a Barley Nested Association Mapping Population. <i>Frontiers in Plant Science</i> , 2021, 12, 764537.	1.7	0
7	Genomic Dissection of Peduncle Morphology in Barley through Nested Association Mapping. <i>Plants</i> , 2021, 10, 10.	1.6	5
8	Natural variation in meiotic recombination rate shapes introgression patterns in intraspecific hybrids between wild and domesticated barley. <i>New Phytologist</i> , 2020, 228, 1852-1863.	3.5	26
9	Identification of wild barley derived alleles associated with plant development in an Australian environment. <i>Euphytica</i> , 2020, 216, 1.	0.6	8
10	Identification of QTLs conferring resistance to scald ( <i>Rhynchosporium commune</i> ) in the barley nested association mapping population HEB-25. <i>BMC Genomics</i> , 2020, 21, 837.	1.2	10
11	Can metabolic prediction be an alternative to genomic prediction in barley?. <i>PLoS ONE</i> , 2020, 15, e0234052.	1.1	17
12	Evaluation of wild barley introgression lines for agronomic traits related to nitrogen fertilization. <i>Euphytica</i> , 2020, 216, 1.	0.6	8
13	Optimizing the procedure of grain nutrient predictions in barley via hyperspectral imaging. <i>PLoS ONE</i> , 2019, 14, e0224491.	1.1	15
14	Genetic dissection of grain elements predicted by hyperspectral imaging associated with yield-related traits in a wild barley NAM population. <i>Plant Science</i> , 2019, 285, 151-164.	1.7	24
15	Barley yield formation under abiotic stress depends on the interplay between flowering time genes and environmental cues. <i>Scientific Reports</i> , 2019, 9, 6397.	1.6	71
16	Genome-wide association of barley plant growth under drought stress using a nested association mapping population. <i>BMC Plant Biology</i> , 2019, 19, 134.	1.6	73
17	“Wild barley serves as a source for biofortification of barley grains”. <i>Plant Science</i> , 2019, 283, 83-94.	1.7	33
18	Contrasting genetic regulation of plant development in wild barley grown in two European environments revealed by nested association mapping. <i>Journal of Experimental Botany</i> , 2018, 69, 1517-1531.	2.4	33

#	ARTICLE	IF	CITATIONS
19	Genome scan identifies flowering-independent effects of barley HsDry2.2 locus on yield traits under water deficit. <i>Journal of Experimental Botany</i> , 2018, 69, 1765-1779.	2.4	18
20	Adaptive selection of founder segments and epistatic control of plant height in the MAGIC winter wheat population WM-800. <i>BMC Genomics</i> , 2018, 19, 559.	1.2	43
21	Genome-wide association of yield traits in a nested association mapping population of barley reveals new gene diversity for future breeding. <i>Journal of Experimental Botany</i> , 2018, 69, 3811-3822.	2.4	66
22	Identification of QTL conferring resistance to stripe rust ( <i>Puccinia striiformis</i> f. sp. <i>hordei</i> ) and leaf rust ( <i>Puccinia hordei</i> ) in barley using nested association mapping (NAM). <i>PLoS ONE</i> , 2018, 13, e0191666.	1.1	12
23	A nested association mapping population identifies multiple small effect QTL conferring resistance against net blotch ( <i>Pyrenophora teres</i> f. <i>teres</i> ) in wild barley. <i>PLoS ONE</i> , 2017, 12, e0186803.	1.1	42
24	A donor-specific QTL, exhibiting allelic variation for leaf sheath hairiness in a nested association mapping population, is located on barley chromosome 4H. <i>PLoS ONE</i> , 2017, 12, e0189446.	1.1	9
25	Exotic QTL improve grain quality in the tri-parental wheat population SW84. <i>PLoS ONE</i> , 2017, 12, e0179851.	1.1	11
26	Yield-related salinity tolerance traits identified in a nested association mapping (NAM) population of wild barley. <i>Scientific Reports</i> , 2016, 6, 32586.	1.6	118
27	Genomic dissection of plant development and its impact on thousand grain weight in barley through nested association mapping. <i>Journal of Experimental Botany</i> , 2016, 67, 2507-2518.	2.4	82
28	Modelling the genetic architecture of flowering time control in barley through nested association mapping. <i>BMC Genomics</i> , 2015, 16, 290.	1.2	192
29	Detection of nitrogen deficiency QTL in juvenile wild barley introgression lines growing in a hydroponic system. <i>BMC Genetics</i> , 2012, 13, 88.	2.7	41