

# Andreas Graner

## List of Publications by Year in descending order

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155  
papers

15,913  
citations

17429

63  
h-index

17580

121  
g-index

159  
all docs

159  
docs citations

159  
times ranked

10783  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genic microsatellite markers in plants: features and applications. Trends in Biotechnology, 2005, 23, 48-55.	4.9	1,543
2	Genomics-assisted breeding for crop improvement. Trends in Plant Science, 2005, 10, 621-630.	4.3	579
3	Development and implementation of high-throughput SNP genotyping in barley. BMC Genomics, 2009, 10, 582.	1.2	570
4	Six-rowed barley originated from a mutation in a homeodomain-leucine zipper I-class homeobox gene. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 1424-1429.	3.3	563
5	Construction of an RFLP map of barley. Theoretical and Applied Genetics, 1991, 83, 250-256.	1.8	542
6	Unlocking the Barley Genome by Chromosomal and Comparative Genomics. Plant Cell, 2011, 23, 1249-1263.	3.1	448
7	Rapid reorganization of resistance gene homologues in cereal genomes. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 370-375.	3.3	365
8	Differentially expressed genes between drought-tolerant and drought-sensitive barley genotypes in response to drought stress during the reproductive stage. Journal of Experimental Botany, 2009, 60, 3531-3544.	2.4	349
9	Genome-wide association studies for agronomical traits in a world wide spring barley collection. BMC Plant Biology, 2012, 12, 16.	1.6	341
10	Genebank genomics highlights the diversity of a global barley collection. Nature Genetics, 2019, 51, 319-326.	9.4	322
11	Recent history of artificial outcrossing facilitates whole-genome association mapping in elite inbred crop varieties. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 18656-18661.	3.3	309
12	A high density barley microsatellite consensus map with 775 SSR loci. Theoretical and Applied Genetics, 2007, 114, 1091-1103.	1.8	308
13	Comparative assessment of EST-SSR, EST-SNP and AFLP markers for evaluation of genetic diversity and conservation of genetic resources using wild, cultivated and elite barleys. Plant Science, 2007, 173, 638-649.	1.7	294
14	Interspecific transferability and comparative mapping of barley EST-SSR markers in wheat, rye and rice. Plant Science, 2005, 168, 195-202.	1.7	266
15	In silico analysis on frequency and distribution of microsatellites in ESTs of some cereal species. Cellular and Molecular Biology Letters, 2002, 7, 537-46.	2.7	264
16	Barley Grain Maturation and Germination: Metabolic Pathway and Regulatory Network Commonalities and Differences Highlighted by New MapMan/PageMan Profiling Tools. Plant Physiology, 2008, 146, 1738-1758.	2.3	250
17	Designing Future Crops: Genomics-Assisted Breeding Comes of Age. Trends in Plant Science, 2021, 26, 631-649.	4.3	244
18	A 1,000-loci transcript map of the barley genome: new anchoring points for integrative grass genomics. Theoretical and Applied Genetics, 2007, 114, 823-839.	1.8	239

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19	The eukaryotic translation initiation factor 4E confers multiallelic recessive Bymovirus resistance in <i>Hordeum vulgare</i> (L.). <i>Plant Journal</i> , 2005, 42, 912-922.	2.8	229
20	454 sequencing put to the test using the complex genome of barley. <i>BMC Genomics</i> , 2006, 7, 275.	1.2	200
21	The International Barley Sequencing Consortium "At the Threshold of Efficient Access to the Barley Genome". <i>Plant Physiology</i> , 2009, 149, 142-147.	2.3	195
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	SNP2CAPS: a SNP and INDEL analysis tool for CAPS marker development. <i>Nucleic Acids Research</i> , 2004, 32, 5e-5.	6.5	166
24	Localization of quantitative trait loci (QTL) for agronomic important characters by the use of a RFLP map in barley ( <i>Hordeum vulgare</i> L.). <i>Theoretical and Applied Genetics</i> , 1995, 90, 294-302.	1.8	165
25	Induced mutations in circadian clock regulator <i>Mat-a</i> facilitated short-season adaptation and range extension in cultivated barley. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 4326-4331.	3.3	163
26	Homology of AFLP products in three mapping populations of barley. <i>Molecular Genetics and Genomics</i> , 1997, 255, 311-321.	2.4	148
27	A high-density consensus map of barley to compare the distribution of QTLs for partial resistance to <i>Puccinia hordei</i> and of defence gene homologues. <i>Theoretical and Applied Genetics</i> , 2007, 114, 487-500.	1.8	145
28	QTLs for chlorophyll and chlorophyll fluorescence parameters in barley under post-flowering drought. <i>Euphytica</i> , 2008, 163, 203-214.	0.6	140
29	Geographic distribution and domestication of wild emmer wheat ( <i>Triticum dicoccoides</i> ). <i>Genetic Resources and Crop Evolution</i> , 2011, 58, 11-53.	0.8	140
30	NGS technologies for analyzing germplasm diversity in genebanks*. <i>Briefings in Functional Genomics</i> , 2012, 11, 38-50.	1.3	140
31	An atlas of gene expression from seed to seed through barley development. <i>Functional and Integrative Genomics</i> , 2006, 6, 202-211.	1.4	138
32	Large-scale analysis of the barley transcriptome based on expressed sequence tags. <i>Plant Journal</i> , 2004, 40, 276-290.	2.8	137
33	Gene Content and Virtual Gene Order of Barley Chromosome 1H. <i>Plant Physiology</i> , 2009, 151, 496-505.	2.3	135
34	Mapping-by-sequencing accelerates forward genetics in barley. <i>Genome Biology</i> , 2014, 15, R78.	13.9	131
35	VRS2 regulates hormone-mediated inflorescence patterning in barley. <i>Nature Genetics</i> , 2017, 49, 157-161.	9.4	127
36	A whole-genome snapshot of 454 sequences exposes the composition of the barley genome and provides evidence for parallel evolution of genome size in wheat and barley. <i>Plant Journal</i> , 2009, 59, 712-722.	2.8	125

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37	Association mapping of salt tolerance in barley ( <i>Hordeum vulgare</i> L.). <i>Theoretical and Applied Genetics</i> , 2013, 126, 2335-2351.	1.8	124
38	Relationships among European Barley Germplasm: II. Comparison of RFLP and Pedigree Data. <i>Crop Science</i> , 1994, 34, 1199-1205.	0.8	111
39	Assessment of the degree and the type of restriction fragment length polymorphism in barley ( <i>Hordeum vulgare</i> ). <i>Theoretical and Applied Genetics</i> , 1990, 80, 826-832.	1.8	109
40	Genetic mapping and BAC assignment of EST-derived SSR markers shows non-uniform distribution of genes in the barley genome. <i>Theoretical and Applied Genetics</i> , 2006, 113, 239-250.	1.8	107
41	Relationships among European Barley Germplasm: I. Genetic Diversity among Winter and Spring Cultivars Revealed by RFLPs. <i>Crop Science</i> , 1994, 34, 1191-1199.	0.8	106
42	Genetic Dissection of Photoperiod Response Based on GWAS of Pre-Anthesis Phase Duration in Spring Barley. <i>PLoS ONE</i> , 2014, 9, e113120.	1.1	105
43	Strong correlation of wild barley ( <i>Hordeum spontaneum</i> ) population structure with temperature and precipitation variation. <i>Molecular Ecology</i> , 2009, 18, 1523-1536.	2.0	99
44	Association mapping reveals gene action and interactions in the determination of flowering time in barley. <i>Theoretical and Applied Genetics</i> , 2009, 118, 259-273.	1.8	96
45	RFLP mapping of the ym4 virus resistance gene in barley. <i>Theoretical and Applied Genetics</i> , 1993, 86, 689-693.	1.8	95
46	Generation and Comparison of EST-Derived SSRs and SNPs in Barley ( <i>Hordeum Vulgare</i> L.). <i>Hereditas</i> , 2004, 135, 145-151.	0.5	95
47	Chloroplast development affects expression of phage-type RNA polymerases in barley leaves. <i>Plant Journal</i> , 2004, 38, 460-472.	2.8	92
48	A detailed look at 7 million years of genome evolution in a 439 kb contiguous sequence at the barley Hv-eIF4E locus: recombination, rearrangements and repeats. <i>Plant Journal</i> , 2004, 41, 184-194.	2.8	91
49	Genome wide association analyses for drought tolerance related traits in barley ( <i>Hordeum vulgare</i> ) Tj ETQq1 1 0.784314 rgBT/Overlo 2.3 91		
50	<i>Aegilops</i> . , 2011, , 1-76.		89
51	EST-derived single nucleotide polymorphism markers for assembling genetic and physical maps of the barley genome. <i>Functional and Integrative Genomics</i> , 2008, 8, 223-233.	1.4	87
52	The Genetic Architecture of Barley Plant Stature. <i>Frontiers in Genetics</i> , 2016, 7, 117.	1.1	86
53	Molecular mapping and genetic fine-structure of the rym5 locus encoding resistance to different strains of the Barley Yellow Mosaic Virus Complex. <i>Theoretical and Applied Genetics</i> , 1999, 98, 285-290.	1.8	81
54	Differential gene expression during seed germination in barley ( <i>Hordeum vulgare</i> L.). <i>Functional and Integrative Genomics</i> , 2002, 2, 28-39.	1.4	81

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55	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
56	cDNA array analysis of stress-induced gene expression in barley androgenesis. <i>Physiologia Plantarum</i> , 2006, 127, 535-550.	2.6	76
57	Dissecting spatiotemporal biomass accumulation in barley under different water regimes using high-throughput image analysis. <i>Plant, Cell and Environment</i> , 2015, 38, 1980-1996.	2.8	76
58	Comparison of wheat physical maps with barley linkage maps for group 7 chromosomes. <i>Theoretical and Applied Genetics</i> , 1995, 91, 618-626.	1.8	75
59	Low-pass shotgun sequencing of the barley genome facilitates rapid identification of genes, conserved non-coding sequences and novel repeats. <i>BMC Genomics</i> , 2008, 9, 518.	1.2	75
60	Microdissection and microcloning of the barley ( <i>Hordeum vulgare</i> L.) chromosome 1HS. <i>Theoretical and Applied Genetics</i> , 1993, 86, 629-636.	1.8	73
61	Functional association between malting quality trait components and cDNA array based expression patterns in barley ( <i>Hordeum vulgare</i> L.). <i>Molecular Breeding</i> , 2004, 14, 153-170.	1.0	72
62	Transferability and polymorphism of barley EST-SSR markers used for phylogenetic analysis in <i>Hordeum chilense</i> . <i>BMC Plant Biology</i> , 2008, 8, 97.	1.6	72
63	Evidence and evolutionary analysis of ancient whole-genome duplication in barley predating the divergence from rice. <i>BMC Evolutionary Biology</i> , 2009, 9, 209.	3.2	70
64	De novo 454 sequencing of barcoded BAC pools for comprehensive gene survey and genome analysis in the complex genome of barley. <i>BMC Genomics</i> , 2009, 10, 547.	1.2	69
65	Whole genome sequencing-based association study to unravel genetic architecture of cooked grain width and length traits in rice. <i>Scientific Reports</i> , 2017, 7, 12478.	1.6	69
66	Genetic basis of drought tolerance during seed germination in barley. <i>PLoS ONE</i> , 2018, 13, e0206682.	1.1	69
67	Barley Genomics: An Overview. <i>International Journal of Plant Genomics</i> , 2008, 2008, 1-13.	2.2	64
68	Molecular mapping of a new gene in wild barley conferring complete resistance to leaf rust ( <i>Puccinia</i> ) Tj ETQq0 0 0 r gBT /Overlock 10 Tf	1.8	63
69	RFLP- and physical mapping of resistance gene homologues in rice ( <i>O. sativa</i> ) and Barley ( <i>H. vulgare</i> ). <i>Theoretical and Applied Genetics</i> , 1999, 98, 509-520.	1.8	63
70	Genetic Diversity and Population Structure in a Legacy Collection of Spring Barley Landraces Adapted to a Wide Range of Climates. <i>PLoS ONE</i> , 2014, 9, e116164.	1.1	61
71	Comparative mapping of the two wheat leaf rust resistance loci Lr1 and Lr10 in rice and barley. <i>Genome</i> , 1998, 41, 328-336.	0.9	58
72	Single nucleotide polymorphisms in rye ( <i>Secale cereale</i> L.): discovery, frequency, and applications for genome mapping and diversity studies. <i>Theoretical and Applied Genetics</i> , 2007, 114, 1105-1116.	1.8	58

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73	Genetic Dissection of Root System Architectural Traits in Spring Barley. <i>Frontiers in Plant Science</i> , 2019, 10, 400.	1.7	58
74	RFLP mapping of a gene in barley conferring resistance to net blotch ( <i>Pyrenophora teres</i> ). <i>Euphytica</i> , 1996, 91, 229-234.	0.6	57
75	Identification and validation of a core set of informative genic SSR and SNP markers for assaying functional diversity in barley. <i>Molecular Breeding</i> , 2008, 22, 1-13.	1.0	57
76	EST analysis in barley defines a unigene set comprising 4,000 genes. <i>Theoretical and Applied Genetics</i> , 2002, 104, 97-103.	1.8	56
77	An integrated approach for comparative mapping in rice and barley with special reference to the Rph16 resistance locus. <i>Functional and Integrative Genomics</i> , 2004, 4, 74-83.	1.4	55
78	An integrated map of the barley genome. <i>Advances in Cellular and Molecular Biology of Plants</i> , 2001, , 187-199.	0.2	55
79	Molecular mapping of novel resistance genes against Barley Mild Mosaic Virus (BaMMV). <i>Theoretical and Applied Genetics</i> , 1997, 95, 1263-1269.	1.8	54
80	Separating the wheat from the chaff – a strategy to utilize plant genetic resources from ex situ genebanks. <i>Scientific Reports</i> , 2014, 4, 5231.	1.6	51
81	Prediction of malting quality traits in barley based on genome-wide marker data to assess the potential of genomic selection. <i>Theoretical and Applied Genetics</i> , 2016, 129, 203-213.	1.8	51
82	Predicting plant biomass accumulation from image-derived parameters. <i>GigaScience</i> , 2018, 7, .	3.3	51
83	Molecular characterization of two lipoxygenases from barley. <i>Plant Molecular Biology</i> , 1999, 39, 1283-1298.	2.0	50
84	High-resolution mapping of the Rym4/Rym5 locus conferring resistance to the barley yellow mosaic virus complex (BaMMV, BaYMV, BaYMV-2) in barley ( <i>Hordeum vulgare</i> ssp. <i>vulgare</i> L.). <i>Theoretical and Applied Genetics</i> , 2005, 110, 283-293.	1.8	48
85	Islands and streams: clusters and gene flow in wild barley populations from the Levant. <i>Molecular Ecology</i> , 2012, 21, 1115-1129.	2.0	47
86	BAC library resources for map-based cloning and physical map construction in barley ( <i>Hordeum</i> ) Tj ETQq0 0 0 rgBT /Qverlock 10 Tf 50 2	1.2	46
87	Introducing Beneficial Alleles from Plant Genetic Resources into the Wheat Germplasm. <i>Biology</i> , 2021, 10, 982.	1.3	46
88	Genetic architecture and temporal patterns of biomass accumulation in spring barley revealed by image analysis. <i>BMC Plant Biology</i> , 2017, 17, 137.	1.6	45
89	Molecular mapping of the leaf rust resistance gene Rph7 in barley. <i>Plant Breeding</i> , 2000, 119, 389-392.	1.0	44
90	New evidence for the synteny of rice chromosome 1 and barley chromosome 3H from rice expressed sequence tags. <i>Genome</i> , 2001, 44, 361-367.	0.9	44

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91	Expression genetics and haplotype analysis reveal cis regulation of serine carboxypeptidase I (Cxp1), a candidate gene for malting quality in barley ( <i>Hordeum vulgare</i> L.). <i>Functional and Integrative Genomics</i> , 2006, 6, 25-35.	1.4	44
92	Effects of Introgression and Recombination on Haplotype Structure and Linkage Disequilibrium Surrounding a Locus Encoding Bymovirus Resistance in Barley. <i>Genetics</i> , 2007, 175, 805-817.	1.2	44
93	Application of denaturing high-performance liquid chromatography for mapping of single nucleotide polymorphisms in barley ( <i>Hordeum vulgare</i> L.). <i>Genome</i> , 2001, 44, 523-528.	0.9	43
94	Molecular Plant Breeding: Methodology and Achievements. <i>Methods in Molecular Biology</i> , 2009, 513, 283-304.	0.4	43
95	Application of Genomics to Molecular Breeding of Wheat and Barley. <i>Advances in Genetics</i> , 2007, 58, 121-155.	0.8	42
96	Map construction of sequence-tagged sites (STSs) in barley ( <i>Hordeum vulgare</i> L.). <i>Theoretical and Applied Genetics</i> , 1999, 98, 937-946.	1.8	41
97	Genome-wide association mapping in a diverse spring barley collection reveals the presence of QTL hotspots and candidate genes for root and shoot architecture traits at seedling stage. <i>BMC Plant Biology</i> , 2019, 19, 216.	1.6	40
98	Natural variation and genetic make-up of leaf blade area in spring barley. <i>Theoretical and Applied Genetics</i> , 2018, 131, 873-886.	1.8	39
99	Construction of a barley ( <i>Hordeum vulgare</i> L.) YAC library and isolation of a Hor1-specific clone. <i>Molecular Genetics and Genomics</i> , 1993, 240, 265-272.	2.4	37
100	MappedDs/T-DNA launch pads for functional genomics in barley. <i>Plant Journal</i> , 2006, 47, 811-826.	2.8	36
101	Sequencing of 15,622 gene-bearing BACs clarifies the dense regions of the barley genome. <i>Plant Journal</i> , 2015, 84, 216-227.	2.8	36
102	Features of SNP and SSR diversity in a set of ICARDA barley germplasm collection. <i>Molecular Breeding</i> , 2010, 26, 229-242.	1.0	34
103	DNA polymorphisms and haplotype patterns of transcription factors involved in barley endosperm development are associated with key agronomic traits. <i>BMC Plant Biology</i> , 2010, 10, 5.	1.6	34
104	Improved Culture System for Microspores of Barley to Become a Target for DNA Uptake. <i>Plant Breeding</i> , 1991, 107, 165-168.	1.0	33
105	Construction of physical maps of the Hor1 locus of two barley cultivars by pulsed field gel electrophoresis. <i>Molecular Genetics and Genomics</i> , 1991, 226-226, 177-181.	2.4	32
106	Diversity of germination and seedling traits in a spring barley ( <i>Hordeum vulgare</i> L.) collection under drought simulated conditions. <i>Genetic Resources and Crop Evolution</i> , 2015, 62, 275-292.	0.8	32
107	QTL analysis of root-lesion nematode resistance in barley: 1. <i>Pratylenchus neglectus</i> . <i>Theoretical and Applied Genetics</i> , 2011, 122, 1321-1330.	1.8	31
108	Dissecting the genome-wide genetic variants of milling and appearance quality traits in rice. <i>Journal of Experimental Botany</i> , 2019, 70, 5115-5130.	2.4	30

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109	The INCREASE project: Intelligent Collections of food legume genetic resources for European agrofood systems. <i>Plant Journal</i> , 2021, 108, 646-660.	2.8	29
110	Application of denaturing high-performance liquid chromatography for mapping of single nucleotide polymorphisms in barley ( <i>Hordeum vulgare</i> L.). <i>Genome</i> , 2001, 44, 523-528.	0.9	29
111	Molecular mapping of two dwarfing genes differing in their GA response on chromosome 2H of barley. <i>Theoretical and Applied Genetics</i> , 1999, 99, 670-675.	1.8	28
112	High level of conservation between genes coding for the GAMYB transcription factor in barley ( <i>Hordeum vulgare</i> L.) and bread wheat ( <i>Triticum aestivum</i> L.) collections. <i>Theoretical and Applied Genetics</i> , 2008, 117, 321-331.	1.8	28
113	Sequence analysis and gene identification in a set of mapped RFLP markers in barley ( <i>Hordeum</i> ) Tj ETQq1 1 0.784314 rgBT <sub>1</sub> Overlook	0.9	27
114	Shoot sodium exclusion in salt stressed barley ( <i>Hordeum vulgare</i> L.) is determined by allele specific increased expression of HKT1;5. <i>Journal of Plant Physiology</i> , 2019, 241, 153029.	1.6	26
115	Molecular markers in breeding for virus resistance in barley. <i>Journal of Applied Genetics</i> , 2004, 45, 145-59.	1.0	26
116	Leaf primordium size specifies leaf width and vein number among row type classes in barley. <i>Plant Journal</i> , 2017, 91, 601-612.	2.8	25
117	Identification of QTL hot spots for malting quality in two elite breeding lines with distinct tolerance to abiotic stress. <i>BMC Plant Biology</i> , 2018, 18, 106.	1.6	25
118	Comparative mapping of a gibberellic acid-insensitive dwarfing gene ( <i>Dwf2</i> ) on chromosome 4HS in barley. <i>Theoretical and Applied Genetics</i> , 1999, 98, 728-731.	1.8	24
119	Transfer of stem rust resistance gene <i>SrB</i> from <i>Thinopyrum ponticum</i> into wheat and development of a closely linked PCR-based marker. <i>Theoretical and Applied Genetics</i> , 2019, 132, 371-382.	1.8	24
120	Fine-mapping of the BaMMV, BaYMV-1 and BaYMV-2 resistance of barley ( <i>Hordeum vulgare</i> ) accession PI1963. <i>Theoretical and Applied Genetics</i> , 2005, 110, 212-218.	1.8	23
121	Chromosomal Passports Provide New Insights into Diffusion of Emmer Wheat. <i>PLoS ONE</i> , 2015, 10, e0128556.	1.1	23
122	Development of RFLP Markers for Barley. <i>Plant Breeding</i> , 1991, 107, 73-76.	1.0	22
123	Sequence diversification in recessive alleles of two host factor genes suggests adaptive selection for bymovirus resistance in cultivated barley from East Asia. <i>Theoretical and Applied Genetics</i> , 2017, 130, 331-344.	1.8	21
124	Gene-based high-density mapping of the gene <i>rym7</i> conferring resistance to Barley mild mosaic virus (BaMMV). <i>Molecular Breeding</i> , 2013, 32, 27-37.	1.0	20
125	Genetic diversity, distribution and domestication history of the neglected GGAtAt gene pool of wheat. <i>Theoretical and Applied Genetics</i> , 2022, 135, 755-776.	1.8	20
126	Fine mapping and syntenic integration of the semi-dwarfing gene <i>sdw3</i> of barley. <i>Functional and Integrative Genomics</i> , 2010, 10, 509-521.	1.4	19



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127	Genomics of plant genetic resources: an introduction. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2011, 9, 151-154.	0.4	18
128	A comparative assessment of genetic diversity in cultivated barley collected in different decades of the last century in Austria, Albania and India by using genomic and genic simple sequence repeat (SSR) markers. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2006, 4, 125-133.	0.4	17
129	Unlocking historical phenotypic data from an ex situ collection to enhance the informed utilization of genetic resources of barley ( <i>Hordeum</i> sp.). <i>Theoretical and Applied Genetics</i> , 2018, 131, 2009-2019.	1.8	16
130	Non-Invasive Phenotyping Reveals Genomic Regions Involved in Pre-Anthesis Drought Tolerance and Recovery in Spring Barley. <i>Frontiers in Plant Science</i> , 2019, 10, 1307.	1.7	16
131	PCR-genotyping of barley seedlings using DNA samples from tissue prints. <i>Plant Breeding</i> , 2002, 121, 228-231.	1.0	15
132	Leveraging the Use of Historical Data Gathered During Seed Regeneration of an ex Situ Genebank Collection of Wheat. <i>Frontiers in Plant Science</i> , 2018, 9, 609.	1.7	15
133	New eSSR and gSSR markers added to Australian barley maps. <i>Australian Journal of Agricultural Research</i> , 2006, 57, 953.	1.5	14
134	Generation and exploitation of EST-derived SSR markers for assaying molecular diversity in durum wheat populations. <i>Genetic Resources and Crop Evolution</i> , 2008, 55, 869-881.	0.8	13
135	Historical phenotypic data from seven decades of seed regeneration in a wheat ex situ collection. <i>Scientific Data</i> , 2019, 6, 137.	2.4	13
136	Towards the Development, Maintenance, and Standardized Phenotypic Characterization of Singleâ€Seedâ€Descent Genetic Resources for Common Bean. <i>Current Protocols</i> , 2021, 1, e133.	1.3	13
137	Chromosome Engineering and Physical Mapping of the <i>Thinopyrum ponticum</i> Translocation in Wheat Carrying the Rust Resistance Gene <i>Sr26</i> . <i>Crop Science</i> , 2015, 55, 648-657.	0.8	12
138	Unbalanced historical phenotypic data from seed regeneration of a barley ex situ collection. <i>Scientific Data</i> , 2018, 5, 180278.	2.4	12
139	Wheat and Barley Genome Sequencing. , 2009, , 713-742.		11
140	Genomic Sequence and Mapping of a Methyljasmonate-Induced O-Methyltransferase from Barley ( <i>Hordeum vulgare</i> L.). <i>DNA Sequence</i> , 1997, 7, 357-363.	0.7	10
141	An integrated approach for the comparative analysis of a multigene family: The nicotianamine synthase genes of barley. <i>Functional and Integrative Genomics</i> , 2007, 7, 169-179.	1.4	10
142	SSR and SNP diversity in a barley germplasm collection. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2008, 6, 167-174.	0.4	10
143	Conserved synteny-based anchoring of the barley genome physical map. <i>Functional and Integrative Genomics</i> , 2013, 13, 339-350.	1.4	10
144	A tiered approach to genome-wide association analysis for the adherence of hulls to the caryopsis of barley seeds reveals footprints of selection. <i>BMC Plant Biology</i> , 2019, 19, 95.	1.6	10

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145	Molecular diversity of the barley genome. <i>Developments in Plant Genetics and Breeding</i> , 2003, 7, 121-141.	0.6	9
146	Map-Based Gene Isolation in Cereal Genomes. , 2004, , 331-360.		9
147	Towards Development, Maintenance, and Standardized Phenotypic Characterization of Singleâ€Seedâ€Descent Genetic Resources for Lupins. <i>Current Protocols</i> , 2021, 1, e191.	1.3	9
148	A simple hybridization-based strategy for the generation of non-redundant EST collectionsâ€™a case study in barley ( <i>Hordeum vulgare</i> L.). <i>Plant Science</i> , 2004, 167, 629-634.	1.7	8
149	Using Genome-Wide Predictions to Assess the Phenotypic Variation of a Barley ( <i>Hordeum</i> sp.) Gene Bank Collection for Important Agronomic Traits and Passport Information. <i>Frontiers in Plant Science</i> , 2020, 11, 604781.	1.7	7
150	Sequence analysis and gene identification in a set of mapped RFLP markers in barley (<i>Hordeum) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	0.9	7
151	RFLP-mapping the haploid genome of barley ( <i>Hordeum vulgare</i> L.). <i>Current Plant Science and Biotechnology in Agriculture</i> , 1996, , 127-150.	0.0	6
152	Screening by PCR for Defined DNA Sequences in Minimal Amounts of Barley Tissue. <i>Plant Breeding</i> , 1991, 107, 70-72.	1.0	4
153	The 3366 chickpea genomes for research and breeding. <i>Trends in Plant Science</i> , 2022, 27, 217-219.	4.3	2
154	Quest for seed immortality is mission impossible. <i>Nature</i> , 2006, 442, 353-353.	18.7	1
155	Molecular Breeding for Malting Quality. , 2014, , 293-309.		0