

Andreas Graner

List of Publications by Year in descending order

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155
papers

15,913
citations

20036

63
h-index

20023

121
g-index

159
all docs

159
docs citations

159
times ranked

11973
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	The 3366 chickpea genomes for research and breeding. <i>Trends in Plant Science</i> , 2022, 27, 217-219.	4.3	2
3	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
4	Designing Future Crops: Genomics-Assisted Breeding Comes of Age. <i>Trends in Plant Science</i> , 2021, 26, 631-649.	4.3	244
5	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
6	Introducing Beneficial Alleles from Plant Genetic Resources into the Wheat Germplasm. <i>Biology</i> , 2021, 10, 982.	1.3	46
7	The INCREASE project: Intelligent Collections of foodâ€legume genetic resources for European agrofood systems. <i>Plant Journal</i> , 2021, 108, 646-660.	2.8	29
8	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
9	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
10	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
11	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
12	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
13	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
14	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
15	Genetic Dissection of Root System Architectural Traits in Spring Barley. <i>Frontiers in Plant Science</i> , 2019, 10, 400.	1.7	58
16	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
17	Transfer of stem rust resistance gene SrB 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
18	Genebank genomics highlights the diversity of a global barley collection. <i>Nature Genetics</i> , 2019, 51, 319-326.	9.4	322

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19	Predicting plant biomass accumulation from image-derived parameters. <i>GigaScience</i> , 2018, 7, .	3.3	51
20	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
21	Genetic basis of drought tolerance during seed germination in barley. <i>PLoS ONE</i> , 2018, 13, e0206682.	1.1	69
22	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
23	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
24	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
25	Unbalanced historical phenotypic data from seed regeneration of a barley ex situ collection. <i>Scientific Data</i> , 2018, 5, 180278.	2.4	12
26	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
27	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
28	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
29	VRS2 regulates hormone-mediated inflorescence patterning in barley. <i>Nature Genetics</i> , 2017, 49, 157-161.	9.4	127
30	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
31	The Genetic Architecture of Barley Plant Stature. <i>Frontiers in Genetics</i> , 2016, 7, 117.	1.1	86
32	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
33	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
34	Chromosomal Passports Provide New Insights into Diffusion of Emmer Wheat. <i>PLoS ONE</i> , 2015, 10, e0128556.	1.1	23
35	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
36	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

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37	Sequencing of 15,622 gene-bearing BACs clarifies the gene-dense regions of the barley genome. <i>Plant Journal</i> , 2015, 84, 216-227.	2.8	36
38	Molecular Breeding for Malting Quality. , 2014, , 293-309.		0
39	Mapping-by-sequencing accelerates forward genetics in barley. <i>Genome Biology</i> , 2014, 15, R78.	13.9	131
40	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
41	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
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	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
44	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
45	Conserved synteny-based anchoring of the barley genome physical map. <i>Functional and Integrative Genomics</i> , 2013, 13, 339-350.	1.4	10
46	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
47	Genome-wide association studies for agronomical traits in a world wide spring barley collection. <i>BMC Plant Biology</i> , 2012, 12, 16.	1.6	341
48	NGS technologies for analyzing germplasm diversity in genebanks*. <i>Briefings in Functional Genomics</i> , 2012, 11, 38-50.	1.3	140
49	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
50	Genome wide association analyses for drought tolerance related traits in barley (<i>Hordeum vulgare</i>)	2.3	91
51	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
52	Unlocking the Barley Genome by Chromosomal and Comparative Genomics. <i>Plant Cell</i> , 2011, 23, 1249-1263.	3.1	448
53	<i>Aegilops</i> . , 2011, , 1-76.		89
54	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

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55	QTL analysis of root-lesion nematode resistance in barley: 1. <i>Pratylenchus neglectus</i> . Theoretical and Applied Genetics, 2011, 122, 1321-1330.	1.8	31
56	BAC library resources for map-based cloning and physical map construction in barley (<i>Hordeum</i>) Tj ETQq0 0 0 rgBT JOverlock 10 Tf 50 70	1.2	46
57	Genomics of plant genetic resources: an introduction. Plant Genetic Resources: Characterisation and Utilisation, 2011, 9, 151-154.	0.4	18
58	Fine mapping and syntenic integration of the semi-dwarfing gene <i>sdw3</i> of barley. Functional and Integrative Genomics, 2010, 10, 509-521.	1.4	19
59	Features of SNP and SSR diversity in a set of ICARDA barley germplasm collection. Molecular Breeding, 2010, 26, 229-242.	1.0	34
60	DNA polymorphisms and haplotype patterns of transcription factors involved in barley endosperm development are associated with key agronomic traits. BMC Plant Biology, 2010, 10, 5.	1.6	34
61	Gene Content and Virtual Gene Order of Barley Chromosome 1H. Plant Physiology, 2009, 151, 496-505.	2.3	135
62	The International Barley Sequencing Consortium. At the Threshold of Efficient Access to the Barley Genome. Plant Physiology, 2009, 149, 142-147.	2.3	195
63	Evidence and evolutionary analysis of ancient whole-genome duplication in barley predating the divergence from rice. BMC Evolutionary Biology, 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. BMC Genomics, 2009, 10, 547.	1.2	69
65	Development and implementation of high-throughput SNP genotyping in barley. BMC Genomics, 2009, 10, 582.	1.2	570
66	Association mapping reveals gene action and interactions in the determination of flowering time in barley. Theoretical and Applied Genetics, 2009, 118, 259-273.	1.8	96
67	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. Plant Journal, 2009, 59, 712-722.	2.8	125
68	Strong correlation of wild barley (<i>Hordeum spontaneum</i>) population structure with temperature and precipitation variation. Molecular Ecology, 2009, 18, 1523-1536.	2.0	99
69	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
70	Wheat and Barley Genome Sequencing. , 2009, , 713-742.		11
71	Molecular Plant Breeding: Methodology and Achievements. Methods in Molecular Biology, 2009, 513, 283-304.	0.4	43
72	Identification and validation of a core set of informative genic SSR and SNP markers for assaying functional diversity in barley. Molecular Breeding, 2008, 22, 1-13.	1.0	57

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73	QTLs for chlorophyll and chlorophyll fluorescence parameters in barley under post-flowering drought. <i>Euphytica</i> , 2008, 163, 203-214.	0.6	140
74	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
75	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
76	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
77	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
78	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
79	SSR and SNP diversity in a barley germplasm collection. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2008, 6, 167-174.	0.4	10
80	Barley Grain Maturation and Germination: Metabolic Pathway and Regulatory Network Commonalities and Differences Highlighted by New MapMan/PageMan Profiling Tools. <i>Plant Physiology</i> , 2008, 146, 1738-1758.	2.3	250
81	Barley Genomics: An Overview. <i>International Journal of Plant Genomics</i> , 2008, 2008, 1-13.	2.2	64
82	Six-rowed barley originated from a mutation in a homeodomain-leucine zipper I-class homeobox gene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 1424-1429.	3.3	563
83	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
84	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. <i>Plant Science</i> , 2007, 173, 638-649.	1.7	294
85	Application of Genomics to Molecular Breeding of Wheat and Barley. <i>Advances in Genetics</i> , 2007, 58, 121-155.	0.8	42
86	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
87	A 1,000-loci transcript map of the barley genome: new anchoring points for integrative grass genomics. <i>Theoretical and Applied Genetics</i> , 2007, 114, 823-839.	1.8	239
88	A high density barley microsatellite consensus map with 775 SSR loci. <i>Theoretical and Applied Genetics</i> , 2007, 114, 1091-1103.	1.8	308
89	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
90	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

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91	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
92	New eSSR and gSSR markers added to Australian barley maps. <i>Australian Journal of Agricultural Research</i> , 2006, 57, 953.	1.5	14
93	cDNA array analysis of stress-induced gene expression in barley androgenesis. <i>Physiologia Plantarum</i> , 2006, 127, 535-550.	2.6	76
94	MappedDs/T-DNA launch pads for functional genomics in barley. <i>Plant Journal</i> , 2006, 47, 811-826.	2.8	36
95	Quest for seed immortality is mission impossible. <i>Nature</i> , 2006, 442, 353-353.	13.7	1
96	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
97	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
98	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
99	454 sequencing put to the test using the complex genome of barley. <i>BMC Genomics</i> , 2006, 7, 275.	1.2	200
100	Recent history of artificial outcrossing facilitates whole-genome association mapping in elite inbred crop varieties. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 18656-18661.	3.3	309
101	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
102	Genic microsatellite markers in plants: features and applications. <i>Trends in Biotechnology</i> , 2005, 23, 48-55.	4.9	1,543
103	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
104	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
105	Interspecific transferability and comparative mapping of barley EST-SSR markers in wheat, rye and rice. <i>Plant Science</i> , 2005, 168, 195-202.	1.7	266
106	Genomics-assisted breeding for crop improvement. <i>Trends in Plant Science</i> , 2005, 10, 621-630.	4.3	579
107	Large-scale analysis of the barley transcriptome based on expressed sequence tags. <i>Plant Journal</i> , 2004, 40, 276-290.	2.8	137
108	A detailed look at 7â€¦million years of genome evolution in a 439â€¦kb contiguous sequence at the barley Hv-eIF4E locus: recombination, rearrangements and repeats. <i>Plant Journal</i> , 2004, 41, 184-194.	2.8	91

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109	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
110	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
111	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
112	A simple hybridization-based strategy for the generation of non-redundant EST collections—a case study in barley (<i>Hordeum vulgare</i> L.). <i>Plant Science</i> , 2004, 167, 629-634.	1.7	8
113	SNP2CAPS: a SNP and INDEL analysis tool for CAPS marker development. <i>Nucleic Acids Research</i> , 2004, 32, 5e-5.	6.5	166
114	Chloroplast development affects expression of phage-type RNA polymerases in barley leaves. <i>Plant Journal</i> , 2004, 38, 460-472.	2.8	92
115	Map-Based Gene Isolation in Cereal Genomes. , 2004, , 331-360.		9
116	Molecular markers in breeding for virus resistance in barley. <i>Journal of Applied Genetics</i> , 2004, 45, 145-59.	1.0	26
117	Molecular diversity of the barley genome. <i>Developments in Plant Genetics and Breeding</i> , 2003, 7, 121-141.	0.6	9
118	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
119	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
120	PCR-genotyping of barley seedlings using DNA samples from tissue prints. <i>Plant Breeding</i> , 2002, 121, 228-231.	1.0	15
121	In silico analysis on frequency and distribution of microsatellites in ESTs of some cereal species. <i>Cellular and Molecular Biology Letters</i> , 2002, 7, 537-46.	2.7	264
122	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
123	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
124	An integrated map of the barley genome. <i>Advances in Cellular and Molecular Biology of Plants</i> , 2001, , 187-199.	0.2	55
125	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
126	Molecular mapping of the leaf rust resistance gene Rph7 in barley. <i>Plant Breeding</i> , 2000, 119, 389-392.	1.0	44

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127	Molecular characterization of two lipoxygenases from barley. <i>Plant Molecular Biology</i> , 1999, 39, 1283-1298.	2.0	50
128	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
129	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
130	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
131	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
132	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
133	Sequence analysis and gene identification in a set of mapped RFLP markers in barley (<i>Hordeum</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 0.9 27	0.9	27
134	Sequence analysis and gene identification in a set of mapped RFLP markers in barley (<i>Hordeum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 0.9 7	0.9	7
135	Molecular mapping of a new gene in wild barley conferring complete resistance to leaf rust (<i>Puccinia</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 1.8 83	1.8	83
136	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
137	Rapid reorganization of resistance gene homologues in cereal genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998, 95, 370-375.	3.3	365
138	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
139	Homology of AFLP products in three mapping populations of barley. <i>Molecular Genetics and Genomics</i> , 1997, 255, 311-321.	2.4	148
140	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
141	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
142	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
143	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
144	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

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145	Relationships among European Barley Germplasm: II. Comparison of RFLP and Pedigree Data. <i>Crop Science</i> , 1994, 34, 1199-1205.	0.8	111
146	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
147	RFLP mapping of the ym4 virus resistance gene in barley. <i>Theoretical and Applied Genetics</i> , 1993, 86, 689-693.	1.8	95
148	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
149	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
150	Screening by PCR for Defined DNA Sequences in Minimal Amounts of Barley Tissue. <i>Plant Breeding</i> , 1991, 107, 70-72.	1.0	4
151	Development of RFLP Markers for Barley. <i>Plant Breeding</i> , 1991, 107, 73-76.	1.0	22
152	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
153	Construction of an RFLP map of barley. <i>Theoretical and Applied Genetics</i> , 1991, 83, 250-256.	1.8	542
154	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
155	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