

Andreas Graner

List of Publications by Year in descending order

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Version: 2024-02-01

155
papers

15,913
citations

17440

63
h-index

17592

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. | 9.3 | 1,543 |
| 2 | Genomics-assisted breeding for crop improvement. Trends in Plant Science, 2005, 10, 621-630. | 8.8 | 579 |
| 3 | Development and implementation of high-throughput SNP genotyping in barley. BMC Genomics, 2009, 10, 582. | 2.8 | 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. | 7.1 | 563 |
| 5 | Construction of an RFLP map of barley. Theoretical and Applied Genetics, 1991, 83, 250-256. | 3.6 | 542 |
| 6 | Unlocking the Barley Genome by Chromosomal and Comparative Genomics. Plant Cell, 2011, 23, 1249-1263. | 6.6 | 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. | 7.1 | 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. | 4.8 | 349 |
| 9 | Genome-wide association studies for agronomical traits in a world wide spring barley collection. BMC Plant Biology, 2012, 12, 16. | 3.6 | 341 |
| 10 | Genebank genomics highlights the diversity of a global barley collection. Nature Genetics, 2019, 51, 319-326. | 21.4 | 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. | 7.1 | 309 |
| 12 | A high density barley microsatellite consensus map with 775 SSR loci. Theoretical and Applied Genetics, 2007, 114, 1091-1103. | 3.6 | 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. | 3.6 | 294 |
| 14 | Interspecific transferability and comparative mapping of barley EST-SSR markers in wheat, rye and rice. Plant Science, 2005, 168, 195-202. | 3.6 | 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. | 7.0 | 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. | 4.8 | 250 |
| 17 | Designing Future Crops: Genomics-Assisted Breeding Comes of Age. Trends in Plant Science, 2021, 26, 631-649. | 8.8 | 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. | 3.6 | 239 |

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 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. | 5.7 | 229 |
| 20 | 454 sequencing put to the test using the complex genome of barley. <i>BMC Genomics</i> , 2006, 7, 275. | 2.8 | 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. | 4.8 | 195 |
| 22 | Genebank genomics bridges the gap between the conservation of crop diversity and plant breeding. <i>Nature Genetics</i> , 2019, 51, 1076-1081. | 21.4 | 176 |
| 23 | SNP2CAPS: a SNP and INDEL analysis tool for CAPS marker development. <i>Nucleic Acids Research</i> , 2004, 32, 5e-5. | 14.5 | 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. | 3.6 | 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. | 7.1 | 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. | 3.6 | 145 |
| 28 | QTLs for chlorophyll and chlorophyll fluorescence parameters in barley under post-flowering drought. <i>Euphytica</i> , 2008, 163, 203-214. | 1.2 | 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. | 1.6 | 140 |
| 30 | NGS technologies for analyzing germplasm diversity in genebanks*. <i>Briefings in Functional Genomics</i> , 2012, 11, 38-50. | 2.7 | 140 |
| 31 | An atlas of gene expression from seed to seed through barley development. <i>Functional and Integrative Genomics</i> , 2006, 6, 202-211. | 3.5 | 138 |
| 32 | Large-scale analysis of the barley transcriptome based on expressed sequence tags. <i>Plant Journal</i> , 2004, 40, 276-290. | 5.7 | 137 |
| 33 | Gene Content and Virtual Gene Order of Barley Chromosome 1H. <i>Plant Physiology</i> , 2009, 151, 496-505. | 4.8 | 135 |
| 34 | Mapping-by-sequencing accelerates forward genetics in barley. <i>Genome Biology</i> , 2014, 15, R78. | 9.6 | 131 |
| 35 | VRS2 regulates hormone-mediated inflorescence patterning in barley. <i>Nature Genetics</i> , 2017, 49, 157-161. | 21.4 | 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. | 5.7 | 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. | 3.6 | 124 |
| 38 | Relationships among European Barley Germplasm: II. Comparison of RFLP and Pedigree Data. <i>Crop Science</i> , 1994, 34, 1199-1205. | 1.8 | 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. | 3.6 | 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. | 3.6 | 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. | 1.8 | 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. | 2.5 | 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. | 3.9 | 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. | 3.6 | 96 |
| 45 | RFLP mapping of the ym4 virus resistance gene in barley. <i>Theoretical and Applied Genetics</i> , 1993, 86, 689-693. | 3.6 | 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. | 1.4 | 95 |
| 47 | Chloroplast development affects expression of phage-type RNA polymerases in barley leaves. <i>Plant Journal</i> , 2004, 38, 460-472. | 5.7 | 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. | 5.7 | 91 |
| 49 | Genome wide association analyses for drought tolerance related traits in barley (<i>Hordeum vulgare</i>) Tj ETQq1 1 0.784314 rgBT ₉₁ /Overlo | 5.1 | 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. | 3.5 | 87 |
| 52 | The Genetic Architecture of Barley Plant Stature. <i>Frontiers in Genetics</i> , 2016, 7, 117. | 2.3 | 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. | 3.6 | 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. | 3.5 | 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. | 4.8 | 77 |
| 56 | cDNA array analysis of stress-induced gene expression in barley androgenesis. <i>Physiologia Plantarum</i> , 2006, 127, 535-550. | 5.2 | 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. | 5.7 | 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. | 3.6 | 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. | 2.8 | 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. | 3.6 | 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. | 2.1 | 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. | 3.6 | 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. | 2.8 | 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. | 3.3 | 69 |
| 66 | Genetic basis of drought tolerance during seed germination in barley. <i>PLoS ONE</i> , 2018, 13, e0206682. | 2.5 | 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 rgBT /Overlock 10 Tf | 3.5 | 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. | 3.6 | 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. | 2.5 | 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. | 2.0 | 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. | 3.6 | 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. | 3.6 | 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. | 1.2 | 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. | 2.1 | 57 |
| 76 | EST analysis in barley defines a unigene set comprising 4,000 genes. <i>Theoretical and Applied Genetics</i> , 2002, 104, 97-103. | 3.6 | 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. | 3.5 | 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. | 3.6 | 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. | 3.3 | 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. | 3.6 | 51 |
| 82 | Predicting plant biomass accumulation from image-derived parameters. <i>GigaScience</i> , 2018, 7, . | 6.4 | 51 |
| 83 | Molecular characterization of two lipoxygenases from barley. <i>Plant Molecular Biology</i> , 1999, 39, 1283-1298. | 3.9 | 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. | 3.6 | 48 |
| 85 | Islands and streams: clusters and gene flow in wild barley populations from the Levant. <i>Molecular Ecology</i> , 2012, 21, 1115-1129. | 3.9 | 47 |
| 86 | BAC library resources for map-based cloning and physical map construction in barley (<i>Hordeum</i>) Tj ETQq0 0 0 rgBT JQverlock 10 Tf 50 2 | 2.8 | 46 |
| 87 | Introducing Beneficial Alleles from Plant Genetic Resources into the Wheat Germplasm. <i>Biology</i> , 2021, 10, 982. | 2.8 | 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. | 3.6 | 45 |
| 89 | Molecular mapping of the leaf rust resistance gene Rph7 in barley. <i>Plant Breeding</i> , 2000, 119, 389-392. | 1.9 | 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. | 2.0 | 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. | 3.5 | 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. | 2.9 | 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. | 2.0 | 43 |
| 94 | Molecular Plant Breeding: Methodology and Achievements. <i>Methods in Molecular Biology</i> , 2009, 513, 283-304. | 0.9 | 43 |
| 95 | Application of Genomics to Molecular Breeding of Wheat and Barley. <i>Advances in Genetics</i> , 2007, 58, 121-155. | 1.8 | 42 |
| 96 | Map construction of sequence-tagged sites (STs) in barley (<i>Hordeum vulgare</i> L.). <i>Theoretical and Applied Genetics</i> , 1999, 98, 937-946. | 3.6 | 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. | 3.6 | 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. | 3.6 | 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. | 5.7 | 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. | 5.7 | 36 |
| 102 | Features of SNP and SSR diversity in a set of ICARDA barley germplasm collection. <i>Molecular Breeding</i> , 2010, 26, 229-242. | 2.1 | 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. | 3.6 | 34 |
| 104 | Improved Culture System for Microspores of Barley to Become a Target for DNA Uptake. <i>Plant Breeding</i> , 1991, 107, 165-168. | 1.9 | 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. | 1.6 | 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. | 3.6 | 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. | 4.8 | 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. | 5.7 | 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. | 2.0 | 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. | 3.6 | 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. | 3.6 | 28 |
| 113 | Sequence analysis and gene identification in a set of mapped RFLP markers in barley (<i>Hordeum</i>) Tj ETQq1 1 0.784314 rgBTJ/Overlook | 2.0 | 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. | 3.5 | 26 |
| 115 | Molecular markers in breeding for virus resistance in barley. <i>Journal of Applied Genetics</i> , 2004, 45, 145-59. | 1.9 | 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. | 5.7 | 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. | 3.6 | 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. | 3.6 | 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. | 3.6 | 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. | 3.6 | 23 |
| 121 | Chromosomal Passports Provide New Insights into Diffusion of Emmer Wheat. <i>PLoS ONE</i> , 2015, 10, e0128556. | 2.5 | 23 |
| 122 | Development of RFLP Markers for Barley. <i>Plant Breeding</i> , 1991, 107, 73-76. | 1.9 | 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. | 3.6 | 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. | 2.1 | 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. | 3.6 | 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. | 3.5 | 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. | 0.8 | 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. | 0.8 | 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. | 3.6 | 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. | 3.6 | 16 |
| 131 | PCR-genotyping of barley seedlings using DNA samples from tissue prints. <i>Plant Breeding</i> , 2002, 121, 228-231. | 1.9 | 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. | 3.6 | 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. | 1.6 | 13 |
| 135 | Historical phenotypic data from seven decades of seed regeneration in a wheat ex situ collection. <i>Scientific Data</i> , 2019, 6, 137. | 5.3 | 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. | 2.9 | 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. | 1.8 | 12 |
| 138 | Unbalanced historical phenotypic data from seed regeneration of a barley ex situ collection. <i>Scientific Data</i> , 2018, 5, 180278. | 5.3 | 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. | 3.5 | 10 |
| 142 | SSR and SNP diversity in a barley germplasm collection. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2008, 6, 167-174. | 0.8 | 10 |
| 143 | Conserved synteny-based anchoring of the barley genome physical map. <i>Functional and Integrative Genomics</i> , 2013, 13, 339-350. | 3.5 | 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. | 3.6 | 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 |
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