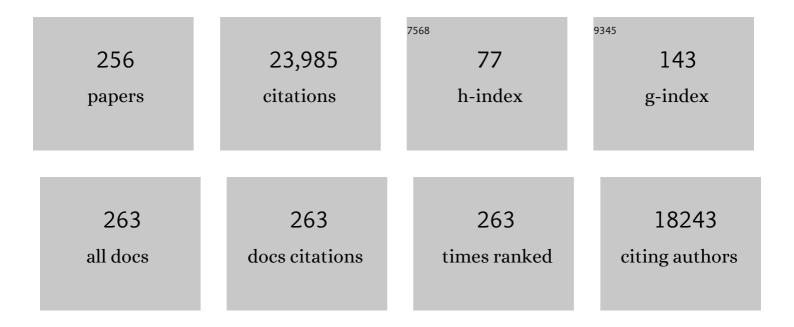
List of Publications by Year in descending order

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DETER LANCRIDGE

| # | Article | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Breeding Technologies to Increase Crop Production in a Changing World. Science, 2010, 327, 818-822. | 12.6 | 1,795 |
| 2 | A physical, genetic and functional sequence assembly of the barley genome. Nature, 2012, 491, 711-716. | 27.8 | 1,416 |
| 3 | A chromosome conformation capture ordered sequence of the barley genome. Nature, 2017, 544, 427-433. | 27.8 | 1,365 |
| 4 | Multiple wheat genomes reveal global variation in modern breeding. Nature, 2020, 588, 277-283. | 27.8 | 513 |
| 5 | Feeding the future. Nature, 2013, 499, 23-24. | 27.8 | 464 |
| 6 | Genetic and genomic tools to improve drought tolerance in wheat. Journal of Experimental Botany, 2010, 61, 3211-3222. | 4.8 | 461 |
| 7 | Boron-Toxicity Tolerance in Barley Arising from Efflux Transporter Amplification. Science, 2007, 318, 1446-1449. | 12.6 | 422 |
| 8 | Improvement of stress tolerance of wheat and barley by modulation of expression of DREB/CBF factors. Plant Biotechnology Journal, 2011, 9, 230-249. | 8.3 | 389 |
| 9 | Extraction of nucleic acids from agarose gels. Analytical Biochemistry, 1980, 103, 264-271. | 2.4 | 376 |
| 10 | Drought Responses of Leaf Tissues from Wheat Cultivars of Differing Drought Tolerance at the Metabolite Level. Molecular Plant, 2012, 5, 418-429. | 8.3 | 370 |
| 11 | Cereal breeding takes a walk on the wild side. Trends in Genetics, 2008, 24, 24-32. | 6.7 | 355 |
| 12 | The barley pan-genome reveals the hidden legacy of mutation breeding. Nature, 2020, 588, 284-289. | 27.8 | 314 |
| 13 | A high density barley microsatellite consensus map with 775 SSR loci. Theoretical and Applied Genetics, 2007, 114, 1091-1103. | 3.6 | 308 |
| 14 | Early Flowering as a Drought Escape Mechanism in Plants: How Can It Aid Wheat Production?. Frontiers in Plant Science, 2017, 8, 1950. | 3.6 | 302 |
| 15 | Different mechanisms of adaptation to cyclic water stress in two South Australian bread wheat cultivars. Journal of Experimental Botany, 2008, 59, 3327-3346. | 4.8 | 285 |
| 16 | Interspecific transferability and comparative mapping of barley EST-SSR markers in wheat, rye and rice. Plant Science, 2005, 168, 195-202. | 3.6 | 266 |
| 17 | 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 |
| 18 | Physiological breeding. Current Opinion in Plant Biology, 2016, 31, 162-171. | 7.1 | 249 |

| # | Article | IF | CITATIONS |
|----|---|------|-----------|
| 19 | Can genomics boost productivity of orphan crops?. Nature Biotechnology, 2012, 30, 1172-1176. | 17.5 | 248 |
| 20 | Marker-assisted wheat breeding: present status and future possibilities. Molecular Breeding, 2010, 26, 145-161. | 2.1 | 245 |
| 21 | Detection of two major grain yield QTL in bread wheat (Triticum aestivum L.) under heat, drought and high yield potential environments. Theoretical and Applied Genetics, 2012, 125, 1473-1485. | 3.6 | 243 |
| 22 | Hybrid breeding in wheat: technologies to improve hybrid wheat seed production. Journal of Experimental Botany, 2013, 64, 5411-5428. | 4.8 | 239 |
| 23 | Extreme Population-Dependent Linkage Disequilibrium Detected in an Inbreeding Plant Species, Hordeum vulgare. Genetics, 2006, 172, 557-567. | 2.9 | 229 |
| 24 | Phenotyping approaches for physiological breeding and gene discovery in wheat. Annals of Applied Biology, 2009, 155, 309-320. | 2.5 | 224 |
| 25 | Identification and mapping of polymorphisms in cereals based on the polymerase chain reaction. Theoretical and Applied Genetics, 1991, 82, 209-216. | 3.6 | 203 |
| 26 | Making the most of â€~omics' for crop breeding. Trends in Biotechnology, 2011, 29, 33-40. | 9.3 | 199 |
| 27 | The International Barley Sequencing Consortium—At the Threshold of Efficient Access to the Barley Genome Â. Plant Physiology, 2009, 149, 142-147. | 4.8 | 195 |
| 28 | Genetic dissection of grain yield in bread wheat. I. QTL analysis. Theoretical and Applied Genetics, 2007, 115, 1029-1041. | 3.6 | 191 |
| 29 | Zinc Deficiency Up-Regulates Expression of High-Affinity Phosphate Transporter Genes in Both Phosphate-Sufficient and -Deficient Barley Roots. Plant Physiology, 2000, 124, 415-422. | 4.8 | 174 |
| 30 | An Investigation of Boron Toxicity in Barley Using Metabolomics. Plant Physiology, 2006, 142, 1087-1101. | 4.8 | 174 |
| 31 | Regulation of hydrogen sulfide liberation in wine-producing Saccharomyces cerevisiae strains by assimilable nitrogen. Applied and Environmental Microbiology, 1995, 61, 461-467. | 3.1 | 171 |
| 32 | Metabolite Profiling Reveals Distinct Changes in Carbon and Nitrogen Metabolism in Phosphate-Deficient Barley Plants (Hordeum vulgare L.). Plant and Cell Physiology, 2008, 49, 691-703. | 3.1 | 169 |
| 33 | Boron Toxicity Tolerance in Barley through Reduced Expression of the Multifunctional Aquaporin HvNIP2;1 Â. Plant Physiology, 2010, 153, 1706-1715. | 4.8 | 159 |
| 34 | RFLP mapping of manganese efficiency in barley. Theoretical and Applied Genetics, 2000, 101, 1100-1108. | 3.6 | 157 |
| 35 | Isolation and characterization of wheat-rye recombinants involving chromosome arm 1DS of wheat. Theoretical and Applied Genetics, 1991, 82, 537-544. | 3.6 | 153 |
| 36 | Mapping loci associated with flour colour in wheat (Triticum aestivum L.). Theoretical and Applied Genetics, 1998, 97, 238-245. | 3.6 | 145 |

PETER LANGRIDGE

| # | Article | IF | CITATIONS |
|----|---|-----------------|-------------|
| 37 | Trends in genetic and genome analyses in wheat: a review. Australian Journal of Agricultural Research, 2001, 52, 1043. | 1.5 | 141 |
| 38 | The genetic control of milling yield, dough rheology and baking quality of wheat. Theoretical and Applied Genetics, 2006, 112, 1487-1495. | 3.6 | 141 |
| 39 | Modulation of plant growth by HDâ€Zip class I and II transcription factors in response to environmental stimuli. New Phytologist, 2011, 190, 823-837. | 7.3 | 139 |
| 40 | Cloning and characterisation of a new rye-specific repeated sequence. Genome, 1991, 34, 81-87. | 2.0 | 138 |
| 41 | An atlas of gene expression from seed to seed through barley development. Functional and Integrative Genomics, 2006, 6, 202-211. | 3.5 | 138 |
| 42 | Largeâ€scale analysis of the barley transcriptome based on expressed sequence tags. Plant Journal, 2004, 40, 276-290. | 5.7 | 137 |
| 43 | The transcript composition of egg cells changes significantly following fertilization in wheat (Triticum aestivum L.). Plant Journal, 2005, 41, 660-672. | 5.7 | 136 |
| 44 | Differential expression of micro <scp>RNA</scp> s and other small <scp>RNA</scp> s in barley between water and drought conditions. Plant Biotechnology Journal, 2015, 13, 2-13. | 8.3 | 134 |
| 45 | Decreasing acetic acid accumulation by a glycerol overproducing strain ofSaccharomyces cerevisiae by deleting theALD6 aldehyde dehydrogenase gene. Yeast, 2002, 19, 295-301. | 1.7 | 132 |
| 46 | HvNax3—a locus controlling shoot sodium exclusion derived from wild barley (Hordeum vulgare ssp.) Tj ETQq0 | О <u>Ş</u> ggBT | Overlock 10 |
| 47 | Genetic dissection of grain yield and physical grain quality in bread wheat (Triticum aestivum L.) under water-limited environments. Theoretical and Applied Genetics, 2012, 125, 255-271. | 3.6 | 132 |
| 48 | Construction of a map-based reference genome sequence for barley, Hordeum vulgare L Scientific Data, 2017, 4, 170044. | 5.3 | 130 |
| 49 | <scp>CRISPR</scp> /Cas9â€mediated knockout of <i>Ms1</i> enables the rapid generation of maleâ€sterile hexaploid wheat lines for use in hybrid seed production. Plant Biotechnology Journal, 2019, 17, 1905-1913. | 8.3 | 125 |
| 50 | Genomic tools to assist breeding for drought tolerance. Current Opinion in Biotechnology, 2015, 32, 130-135. | 6.6 | 124 |
| 51 | The impact of drought on wheat leaf cuticle properties. BMC Plant Biology, 2017, 17, 85. | 3.6 | 120 |
| 52 | Discovery of barley miRNAs through deep sequencing of short reads. BMC Genomics, 2011, 12, 129. | 2.8 | 118 |
| 53 | Thermostability variation in alleles of barley beta-amylase. Journal of Cereal Science, 1998, 28, 301-309. | 3.7 | 117 |

A zein gene of maize is transcribed from two widely separated promoter regions. Cell, 1983, 34, 28.9 116 1015-1022.

| # | Article | IF | CITATIONS |
|----|---|-----------|--------------|
| 55 | Whole-Genome Mapping of Agronomic and Metabolic Traits to Identify Novel Quantitative Trait Loci in Bread Wheat Grown in a Water-Limited Environment. Plant Physiology, 2013, 162, 1266-1281. | 4.8 | 115 |
| 56 | Construction of three linkage maps in bread wheat, Triticum aestivum. Australian Journal of Agricultural Research, 2001, 52, 1089. | 1.5 | 114 |
| 57 | Increased expression of six <i>ZIP</i> family genes by zinc (Zn) deficiency is associated with enhanced uptake and rootâ€toâ€shoot translocation of Zn in barley (<i>Hordeum vulgare</i>). New Phytologist, 2015, 207, 1097-1109. | 7.3 | 114 |
| 58 | Functional genomics of abiotic stress tolerance in cereals. Briefings in Functional Genomics & Proteomics, 2006, 4, 343-354. | 3.8 | 113 |
| 59 | <scp>H</scp> v <scp>ZIP</scp> 7 mediates zinc accumulation in barley (<i><scp>H</scp>ordeum) Tj ETQq1 1 0.</i> | 784314 rg | BT_/Overlock |
| 60 | A consensus linkage map of barley. Molecular Breeding, 1995, 1, 389-395. | 2.1 | 111 |
| 61 | Mapping of chromosome regions conferring boron toxicity tolerance in barley (Hordeum vulgare L.). Theoretical and Applied Genetics, 1999, 98, 1293-1303. | 3.6 | 107 |
| 62 | Genetic mapping and BAC assignment of EST-derived SSR markers shows non-uniform distribution of genes in the barley genome. Theoretical and Applied Genetics, 2006, 113, 239-250. | 3.6 | 107 |
| 63 | A Comprehensive Expression Profile of MicroRNAs and Other Classes of Non-Coding Small RNAs in Barley Under Phosphorous-Deficient and -Sufficient Conditions. DNA Research, 2013, 20, 109-125. | 3.4 | 106 |
| 64 | Molecular basis of adaptation to high soil boron in wheat landraces and elite cultivars. Nature, 2014, 514, 88-91. | 27.8 | 106 |
| 65 | Phosphate Utilization Efficiency Correlates with Expression of Low-Affinity Phosphate Transporters and Noncoding RNA, <i>IPS1</i> , in Barley Â. Plant Physiology, 2011, 156, 1217-1229. | 4.8 | 105 |
| 66 | TaASY1 promotes homologous chromosome interactions and is affected by deletion of <i>Ph1</i> . Plant Journal, 2009, 57, 487-497. | 5.7 | 104 |
| 67 | Nucleotide sequence of a circular single-stranded DNA associated with coconut foliar decay virus. Virology, 1990, 176, 648-651. | 2.4 | 103 |
| 68 | Genetic diversity in Australian wheat varieties and breeding material based on RFLP data. Theoretical and Applied Genetics, 1998, 96, 435-446. | 3.6 | 103 |
| 69 | Cloning plant genes differentially expressed during colonization of roots of Hordeum vulgare by the vesicular-arbuscular mycorrhizal fungus Clomus intraradices. New Phytologist, 1997, 135, 291-301. | 7.3 | 100 |
| 70 | AFLP fingerprinting for analysis of yeast genetic variation. International Journal of Systematic and Evolutionary Microbiology, 1999, 49, 915-924. | 1.7 | 100 |
| 71 | Mapping and validation of chromosome regions conferring boron toxicity tolerance in wheat (Triticum aestivum). Theoretical and Applied Genetics, 2000, 101, 767-777. | 3.6 | 100 |
| 72 | Characterization of phosphorus-regulated miR399 and miR827 and their isomirs in barley under phosphorus-sufficient and phosphorus-deficient conditions. BMC Plant Biology, 2013, 13, 214. | 3.6 | 94 |

| # | Article | IF | CITATIONS |
|----|--|------|-----------|
| 73 | Exploring genetic variation for salinity tolerance in chickpea using image-based phenotyping. Scientific Reports, 2017, 7, 1300. | 3.3 | 94 |
| 74 | A consensus map of barley integrating SSR, RFLP, and AFLP markers. Australian Journal of Agricultural Research, 2003, 54, 1173. | 1.5 | 89 |
| 75 | Differentiation and species identification of yeasts using PCR. International Journal of Systematic Bacteriology, 1998, 48, 279-286. | 2.8 | 87 |
| 76 | Abiotic stress miRNomes in the Triticeae. Functional and Integrative Genomics, 2017, 17, 145-170. | 3.5 | 86 |
| 77 | Genetic control of grain yield and grain physical characteristics in a bread wheat population grown under a range of environmental conditions. Theoretical and Applied Genetics, 2014, 127, 1607-1624. | 3.6 | 85 |
| 78 | Microarray expression analysis of meiosis and microsporogenesis in hexaploid bread wheat. BMC Genomics, 2006, 7, 267. | 2.8 | 82 |
| 79 | Molecular identification of the wheat male fertility gene Ms1 and its prospects for hybrid breeding. Nature Communications, 2017, 8, 869. | 12.8 | 82 |
| 80 | A study of the role of root morphological traits in growth of barley in zinc-deficient soil. Journal of Experimental Botany, 2007, 58, 2775-2784. | 4.8 | 80 |
| 81 | The <i>Ta<scp>DREB</scp>3</i> transgene transferred by conventional crossings to different genetic backgrounds of bread wheat improves drought tolerance. Plant Biotechnology Journal, 2016, 14, 313-322. | 8.3 | 80 |
| 82 | Multi-environment analysis and improved mapping of a yield-related QTL on chromosome 3B of wheat. Theoretical and Applied Genetics, 2013, 126, 747-761. | 3.6 | 77 |
| 83 | A Sequence-Ready Physical Map of Barley Anchored Genetically by Two Million Single-Nucleotide Polymorphisms Â. Plant Physiology, 2014, 164, 412-423. | 4.8 | 77 |
| 84 | Self-incompatibility in the Grasses. Annals of Botany, 2000, 85, 203-209. | 2.9 | 76 |
| 85 | Identification of novel quantitative trait loci for days to ear emergence and flag leaf glaucousness in a bread wheat (Triticum aestivum L.) population adapted to southern Australian conditions. Theoretical and Applied Genetics, 2012, 124, 697-711. | 3.6 | 76 |
| 86 | Optimization of <scp><i>TaDREB3</i></scp> gene expression in transgenic barley using coldâ€inducible promoters. Plant Biotechnology Journal, 2013, 11, 659-670. | 8.3 | 76 |
| 87 | Transformation of cereals via Agrobacterium and the pollen pathway: a critical assessment. Plant Journal, 1992, 2, 631-638. | 5.7 | 73 |
| 88 | The <i>Ph2</i> pairing homoeologous locus of wheat (<i>Triticum aestivum</i>): identification of candidate meiotic genes using a comparative genetics approach. Plant Journal, 2003, 36, 443-456. | 5.7 | 73 |
| 89 | Differential expression of microRNAs and potential targets under drought stress in barley. Plant, Cell and Environment, 2017, 40, 11-24. | 5.7 | 73 |
| 90 | STS-PCR markers appropriate for wheat-barley introgression. Theoretical and Applied Genetics, 1996, 93-93, 826-832. | 3.6 | 72 |

| # | Article | IF | CITATIONS |
|-----|--|-----|-----------|
| 91 | A barley activation tagging system. Plant Molecular Biology, 2007, 64, 329-347. | 3.9 | 72 |
| 92 | Detection of QTL for metabolic and agronomic traits in wheat with adjustments for variation at genetic loci that affect plant phenology. Plant Science, 2015, 233, 143-154. | 3.6 | 72 |
| 93 | Tetrapyrroleâ€based drought stress signalling. Plant Biotechnology Journal, 2015, 13, 447-459. | 8.3 | 71 |
| 94 | Breeding for drought and heat tolerance in wheat. Theoretical and Applied Genetics, 2021, 134, 1753-1769. | 3.6 | 70 |
| 95 | RFLP mapping of the Ha 2 cereal cyst nematode resistance gene in barley. Theoretical and Applied Genetics, 1997, 94, 1060-1064. | 3.6 | 69 |
| 96 | Genetic dissection of grain yield in bread wheat. II. QTL-by-environment interaction. Theoretical and Applied Genetics, 2007, 115, 1015-1027. | 3.6 | 69 |
| 97 | Marker-assisted backcross introgression of the Yd2 gene conferring resistance to barley yellow dwarf virus in barley. Plant Breeding, 2003, 122, 52-56. | 1.9 | 68 |
| 98 | Comparative Sequence Analysis of the Region Harboring the Hardness Locus in Barley and Its Colinear Region in Rice. Plant Physiology, 2004, 136, 3177-3190. | 4.8 | 68 |
| 99 | Combining field performance with controlled environment plant imaging to identify the genetic control of growth and transpiration underlying yield response to water-deficit stress in wheat. Journal of Experimental Botany, 2015, 66, 5481-5492. | 4.8 | 67 |
| 100 | Identification of Reference Genes for Quantitative Expression Analysis of MicroRNAs and mRNAs in Barley under Various Stress Conditions. PLoS ONE, 2015, 10, e0118503. | 2.5 | 67 |
| 101 | Identification of genetic loci associated with ear-emergence in bread wheat. Theoretical and Applied Genetics, 2006, 113, 1103-1112. | 3.6 | 66 |
| 102 | A Comparison of Mainstream Genotyping Platforms for the Evaluation and Use of Barley Genetic Resources. Frontiers in Plant Science, 2019, 10, 544. | 3.6 | 66 |
| 103 | RFLP markers associated with Sr22 and recombination between chromosome 7A of bread wheat and the diploid species Triticum boeoticum. Theoretical and Applied Genetics, 1994, 89-89, 1039-1045. | 3.6 | 62 |
| 104 | Comparative transcriptomics in the Triticeae. BMC Genomics, 2009, 10, 285. | 2.8 | 62 |
| 105 | Drought-inducible expression of Hv-miR827 enhances drought tolerance in transgenic barley. Functional and Integrative Genomics, 2017, 17, 279-292. | 3.5 | 62 |
| 106 | Identification and mapping of a gene conferring resistance to the spot form of net blotch (Pyrenophora teres f maculata) in barley. Theoretical and Applied Genetics, 1999, 99, 323-327. | 3.6 | 60 |
| 107 | TaMSH7: A cereal mismatch repair gene that affects fertility in transgenic barley (Hordeum vulgare L.). BMC Plant Biology, 2007, 7, 67. | 3.6 | 60 |
| 108 | QTL analysis and fine mapping of a QTL for yield-related traits in wheat grown in dry and hot environments. Theoretical and Applied Genetics, 2020, 133, 239-257. | 3.6 | 59 |

| # | Article | IF | CITATIONS |
|-----|---|------|-----------|
| 109 | Squashes of plant tissue as substrate for PCR. Nucleic Acids Research, 1991, 19, 6954-6954. | 14.5 | 57 |
| 110 | Fermentation properties of a wine yeast over-expressing the Saccharomyces cerevisiae glycerol 3-phosphate dehydrogenase gene (GPD2). Australian Journal of Grape and Wine Research, 2000, 6, 208-215. | 2.1 | 57 |
| 111 | Constitutive overexpression of the <i>TaNF-YB4</i> gene in transgenic wheat significantly improves grain yield. Journal of Experimental Botany, 2015, 66, 6635-6650. | 4.8 | 56 |
| 112 | gRNA validation for wheat genome editing with the CRISPR-Cas9 system. BMC Biotechnology, 2019, 19, 71. | 3.3 | 55 |
| 113 | Fine mapping and targeted SNP survey using rice-wheat gene colinearity in the region of the Bo1 boron toxicity tolerance locus of bread wheat. Theoretical and Applied Genetics, 2007, 115, 451-461. | 3.6 | 53 |
| 114 | Harnessing the potential of germplasm collections. Nature Genetics, 2019, 51, 200-201. | 21.4 | 53 |
| 115 | The incidence of killer activity of non-Saccharomycesyeasts towards indigenous yeast species of grape must: potential application in wine fermentation. Journal of Applied Microbiology, 2000, 89, 381-389. | 3.1 | 52 |
| 116 | Mutations of barley β-amylase that improve substrate-binding affinity and thermostability. Molecular Genetics and Genomics, 2001, 266, 345-352. | 2.1 | 52 |
| 117 | Identification of RFLP markers linked to the cereal cyst nematode resistance gene (Cre) in wheat. Theoretical and Applied Genetics, 1994, 89-89, 927-930. | 3.6 | 51 |
| 118 | Potential of SSR markers for plant breeding and variety identification in Australian barley germplasm. Australian Journal of Agricultural Research, 2003, 54, 1197. | 1.5 | 51 |
| 119 | Isolation of plant transcription factors using a modified yeast one-hybrid system. Plant Methods, 2006, 2, 3. | 4.3 | 51 |
| 120 | Transcriptome-scale homoeolog-specific transcript assemblies of bread wheat. BMC Genomics, 2012, 13, 492. | 2.8 | 51 |
| 121 | A DNA mismatch repair gene links to the <i>Ph2</i> locus in wheat. Genome, 2002, 45, 116-124. | 2.0 | 50 |
| 122 | Overexpression of the <i>TaSHN1</i> transcription factor in bread wheat leads to leaf surface modifications, improved drought tolerance, and no yield penalty under controlled growth conditions. Plant, Cell and Environment, 2018, 41, 2549-2566. | 5.7 | 50 |
| 123 | RFLP mapping of a new cereal cyst nematode resistance locus in barley. Plant Breeding, 1998, 117, 185-187. | 1.9 | 48 |
| 124 | A biolistic method for high-throughput production of transgenic wheat plants with single gene insertions. BMC Plant Biology, 2018, 18, 135. | 3.6 | 48 |
| 125 | Defensin promoters as potential tools for engineering disease resistance in cereal grains. Plant Biotechnology Journal, 2010, 8, 47-64. | 8.3 | 47 |
| 126 | Characterization of the wheat endosperm transfer cell-specific protein TaPR60. Plant Molecular Biology, 2009, 71, 81-98. | 3.9 | 46 |

| # | Article | IF | CITATIONS |
|-----|--|------------------|---------------|
| 127 | BAC library resources for map-based cloning and physical map construction in barley (Hordeum) Tj ETQq1 1 0.78 | 4314 rgB⁻ 2.8 | T/Qyerlock 10 |
| 128 | Analysis of rye B-chromosome structure using fluorescencein situ hybridization (FISH). Chromosome Research, 1995, 3, 466-472. | 2.2 | 45 |
| 129 | Bread matters: a national initiative to profile the genetic diversity of Australian wheat. Plant Biotechnology Journal, 2012, 10, 703-708. | 8.3 | 45 |
| 130 | Advantages of Amplifluor-like SNP markers over KASP in plant genotyping. BMC Plant Biology, 2017, 17, 254. | 3.6 | 45 |
| 131 | An early meiosis cDNA clone from wheat. Molecular Genetics and Genomics, 1994, 243, 17-23. | 2.4 | 44 |
| 132 | Expression and functional analysis of TaASY1 during meiosis of bread wheat (Triticum aestivum). BMC Molecular Biology, 2007, 8, 65. | 3.0 | 43 |
| 133 | Dynamic root responses to drought and rewatering in two wheat (Triticum aestivum) genotypes. Plant and Soil, 2015, 391, 139-152. | 3.7 | 43 |
| 134 | Salinity tolerance and sodium exclusion in genus Triticum. Breeding Science, 2009, 59, 671-678. | 1.9 | 43 |
| 135 | Mapping loci associated with milling yield in wheat (Triticum aestivum L.). Molecular Breeding, 1999, 5, 561-568. | 2.1 | 42 |
| 136 | Application of Genomics to Molecular Breeding of Wheat and Barley. Advances in Genetics, 2007, 58, 121-155. | 1.8 | 42 |
| 137 | Quantifying Wheat Sensitivities to Environmental Constraints to Dissect Genotype × Environment Interactions in the Field. Plant Physiology, 2017, 174, 1669-1682. | 4.8 | 42 |
| 138 | Synthesis of the large subunit of spinach ribulose bisphosphate carboxylase may involve a precursor polypeptide. FEBS Letters, 1981, 123, 85-89. | 2.8 | 41 |
| 139 | Thioredoxin activity in the C terminus of Phalaris S protein. Plant Journal, 1995, 8, 133-138. | 5.7 | 41 |
| 140 | Title is missing!. Molecular Breeding, 2000, 6, 169-174. | 2.1 | 41 |
| 141 | Isolation and characterization of wheat triticin cDNA revealing a unique lysine-rich repetitive domain. Plant Molecular Biology, 1993, 22, 227-237. | 3.9 | 40 |
| 142 | Zein precursor mRNAs from maize endosperm. Molecular Genetics and Genomics, 1982, 187, 432-438. | 2.4 | 39 |
| 143 | Structural heterogeneity in the R173 family of rye-specific repetitive DNA sequences. Plant Molecular Biology, 1992, 20, 95-102. | 3.9 | 39 |
| 144 | Capturing diversity in the cereals: many options but little promiscuity. Trends in Plant Science, 2007, 12, 71-79. | 8.8 | 39 |

| # | Article | IF | CITATIONS |
|-----|---|-----|-----------|
| 145 | Transcriptional effects of the opaque-2 mutation of Zea mays L Planta, 1982, 156, 166-170. | 3.2 | 38 |
| 146 | Spatial and temporal expression of endosperm transfer cellâ€specific promoters in transgenic rice and barley. Plant Biotechnology Journal, 2008, 6, 465-476. | 8.3 | 38 |
| 147 | Green revolution â€~stumbles' in a dry environment: Dwarf wheat with <i>Rht</i> genes fails to produce higher grain yield than taller plants under drought. Plant, Cell and Environment, 2020, 43, 2355-2364. | 5.7 | 38 |
| 148 | Self-incompatibility in the grasses: evolutionary relationship of the S gene from Phalaris coerulescens to homologous sequences in other grasses. Plant Molecular Biology, 1997, 34, 223-232. | 3.9 | 36 |
| 149 | MappedDs/T-DNA launch pads for functional genomics in barley. Plant Journal, 2006, 47, 811-826. | 5.7 | 36 |
| 150 | The R173 family of rye-specific repetitive DNA sequences: a structural analysis. Genome, 1991, 34, 88-95. | 2.0 | 34 |
| 151 | Complex Regulation by Apetala2 Domain-Containing Transcription Factors Revealed through Analysis of the Stress-Responsive TdCor410b Promoter from Durum Wheat. PLoS ONE, 2013, 8, e58713. | 2.5 | 34 |
| 152 | Making science more effective for agriculture. Advances in Agronomy, 2020, , 153-177. | 5.2 | 34 |
| 153 | Polymerase chain reaction based mapping of rye involving repeated DNA sequences. Genome, 1992, 35, 621-626. | 2.0 | 33 |
| 154 | Cloning and expression of a distinct subclass of plant thioredoxins. FEBS Journal, 2000, 267, 7109-7117. | 0.2 | 33 |
| 155 | Comparative Enzyme Kinetics of Two Allelic Forms of Barley (Hordeum vulgare L.) Beta -amylase. Journal of Cereal Science, 2000, 31, 335-344. | 3.7 | 33 |
| 156 | A Transgenic Transcription Factor (TaDREB3) in Barley Affects the Expression of MicroRNAs and Other Small Non-Coding RNAs. PLoS ONE, 2012, 7, e42030. | 2.5 | 33 |
| 157 | Isolation and characterization of a genomic sequence of maize coding for a zein gene. Molecular Genetics and Genomics, 1981, 182, 440-444. | 2.4 | 32 |
| 158 | Change of function of the wheat stressâ€responsive transcriptional repressor <i>Ta<scp>RAP</scp>2.1L</i> by repressor motif modification. Plant Biotechnology Journal, 2016, 14, 820-832. | 8.3 | 32 |
| 159 | Genetics of Na+ exclusion and salinity tolerance in Afghani durum wheat landraces. BMC Plant Biology, 2017, 17, 209. | 3.6 | 32 |
| 160 | Removal of the Four C-Terminal Glycine-Rich Repeats Enhances the Thermostability and Substrate Binding Affinity of Barley β-Amylase. Biochemistry, 2000, 39, 13350-13355. | 2.5 | 31 |
| 161 | Mapping of Barley (Hordeum vulgare L.) Beta -amylase Alleles in which an Amino Acid Substitution Determines Beta -amylase Isoenzyme Type and the Level of Free Beta -amylase. Journal of Cereal Science, 2002, 35, 39-50. | 3.7 | 31 |
| 162 | Genetic diversity within Australian wheat breeding programs based on molecular and pedigree data. Euphytica, 2002, 124, 293-306. | 1.2 | 31 |

| # | Article | IF | CITATIONS |
|-----|--|-----|-----------|
| 163 | Evaluation of Australian wheat genotypes for response to variable nitrogen application. Plant and Soil, 2016, 399, 247-255. | 3.7 | 31 |
| 164 | Molecular interactions of the γ-clade homeodomain-leucine zipper class I transcription factors during the wheat response to water deficit. Plant Molecular Biology, 2016, 90, 435-452. | 3.9 | 31 |
| 165 | Clusters of genes encoding fructan biosynthesizing enzymes in wheat and barley. Plant Molecular Biology, 2012, 80, 299-314. | 3.9 | 29 |
| 166 | A DNA-based method for studying root responses to drought in field-grown wheat genotypes. Scientific Reports, 2013, 3, 3194. | 3.3 | 29 |
| 167 | A molecular genetic map of the long arm of chromosome 6R of rye incorporating the cereal cyst nematode resistance gene, CreR. Theoretical and Applied Genetics, 1998, 97, 1000-1012. | 3.6 | 28 |
| 168 | Harnessing translational research in wheat for climate resilience. Journal of Experimental Botany, 2021, 72, 5134-5157. | 4.8 | 28 |
| 169 | Modes of reproduction in Australian populations of Hypericum perforatum L. (St. John's wort) revealed by DNA fingerprinting and cytological methods. Genome, 2003, 46, 573-579. | 2.0 | 27 |
| 170 | High-resolution mapping of the S and Z loci of Phalaris coerulescens. Genome, 2004, 47, 918-930. | 2.0 | 27 |
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