Peter Langridge

List of Publications by Year in descending order

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256	23,985	8755	10679
papers	citations	77 h-index	143 g-index

263	263	263	20240
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Micronutrient Toxicity and Deficiency. , 2022, , 433-449.		2
2	Developments and prospects for doubled haploid wheat. Biotechnology Advances, 2022, 60, 108007.	6.0	13
3	The wheat Seven in absentia gene is associated with increases in biomass and yield in hot climates. Journal of Experimental Botany, 2021, 72, 3774-3791.	2.4	11
4	Breeding for drought and heat tolerance in wheat. Theoretical and Applied Genetics, 2021, 134, 1753-1769.	1.8	70
5	Novel Salinity Tolerance Loci in Chickpea Identified in Glasshouse and Field Environments. Frontiers in Plant Science, 2021, 12, 667910.	1.7	20
6	Development of an Australian Bread Wheat Nested Association Mapping Population, a New Genetic Diversity Resource for Breeding under Dry and Hot Climates. International Journal of Molecular Sciences, 2021, 22, 4348.	1.8	9
7	Breeding crops for climate resilience. Theoretical and Applied Genetics, 2021, 134, 1607-1611.	1.8	26
8	Harnessing translational research in wheat for climate resilience. Journal of Experimental Botany, 2021, 72, 5134-5157.	2.4	28
9	Expression of Specific Alleles of Zinc-Finger Transcription Factors, HvSAP8 and HvSAP16, and Corresponding SNP Markers, Are Associated with Drought Tolerance in Barley Populations. International Journal of Molecular Sciences, 2021, 22, 12156.	1.8	9
10	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.	1.8	59
11	Altering Tetrapyrrole Biosynthesis by Overexpressing Ferrochelatases (Fc1 and Fc2) Improves Photosynthetic Efficiency in Transgenic Barley. Agronomy, 2020, 10, 1370.	1.3	0
12	The barley pan-genome reveals the hidden legacy of mutation breeding. Nature, 2020, 588, 284-289.	13.7	314
13	Multiple wheat genomes reveal global variation in modern breeding. Nature, 2020, 588, 277-283.	13.7	513
14	Identification, gene expression and genetic polymorphism of zinc finger A20/AN1 stress-associated genes, HvSAP, in salt stressed barley from Kazakhstan. BMC Plant Biology, 2020, 20, 156.	1.6	11
15	Barley Plants Overexpressing Ferrochelatases (HvFC1 and HvFC2) Show Improved Photosynthetic Rates and Have Reduced Photo-Oxidative Damage under Drought Stress than Non-Transgenic Controls. Agronomy, 2020, 10, 1351.	1.3	7
16	Salt-induced expression of intracellular vesicle trafficking genes, CaRab-GTP, and their association with Na+ accumulation in leaves of chickpea (Cicer arietinum L.). BMC Plant Biology, 2020, 20, 183.	1.6	13
17	Strengths and Weaknesses of National Variety Trial Data for Multi-Environment Analysis: A Case Study on Grain Yield and Protein Content. Agronomy, 2020, 10, 753.	1.3	10
18	Green revolution â€˜stumblesâ€™ in a dry environment: Dwarf wheat with Rht genes fails to produce higher grain yield than taller plants under drought. Plant, Cell and Environment, 2020, 43, 2355-2364.	2.8	38

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19	Making science more effective for agriculture. Advances in Agronomy, 2020, , 153-177.	2.4	34
20	Understanding the Interactions between Biomass, Grain Production and Grain Protein Content in High and Low Protein Wheat Genotypes under Controlled Environments. Agronomy, 2019, 9, 706.	1.3	10
21	gRNA validation for wheat genome editing with the CRISPR-Cas9 system. BMC Biotechnology, 2019, 19, 71.	1.7	55
22	Harnessing the potential of germplasm collections. Nature Genetics, 2019, 51, 200-201.	9.4	53
23	A Comparison of Mainstream Genotyping Platforms for the Evaluation and Use of Barley Genetic Resources. Frontiers in Plant Science, 2019, 10, 544.	1.7	66
24	Wheat wounding-responsive HD-Zip IV transcription factor GL7 is predominantly expressed in grain and activates genes encoding defensins. Plant Molecular Biology, 2019, 101, 41-61.	2.0	6
25	Reduced response diversity does not negatively impact wheat climate resilience. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 10623-10624.	3.3	11
26	Modelâ€Driven Multidisciplinary Global Research to Meet Future Needs: The Case for â€œImproving Radiation Use Efficiency to Increase Yieldâ€• Crop Science, 2019, 59, 843-849.	0.8	9
27	<scp>CRISPR</scp>/Cas9â€mediated knockout of Ms1 enables the rapid generation of maleâ€sterile hexaploid wheat lines for use in hybrid seed production. Plant Biotechnology Journal, 2019, 17, 1905-1913.	4.1	125
28	Intracellular Vesicle Trafficking Genes, RabC-GTP, Are Highly Expressed Under Salinity and Rapid Dehydration but Down-Regulated by Drought in Leaves of Chickpea (Cicer arietinum L.). Frontiers in Genetics, 2019, 10, 40.	1.1	14
29	The General Transcription Repressor TaDr1 Is Co-expressed With TaVrn1 and TaFT1 in Bread Wheat Under Drought. Frontiers in Genetics, 2019, 10, 63.	1.1	14
30	Genes Encoding Transcription Factors TaDREB5 and TaNFYC-A7 Are Differentially Expressed in Leaves of Bread Wheat in Response to Drought, Dehydration and ABA. Frontiers in Plant Science, 2018, 9, 1441.	1.7	21
31	Overexpression of the TaSHN1 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.	2.8	50
32	A biolistic method for high-throughput production of transgenic wheat plants with single gene insertions. BMC Plant Biology, 2018, 18, 135.	1.6	48
33	Economic and Academic Importance of Barley. Compendium of Plant Genomes, 2018, , 1-10.	0.3	20
34	The pseudogenes of barley. Plant Journal, 2018, 93, 502-514.	2.8	14
35	Differential expression of microRNAs and potential targets under drought stress in barley. Plant, Cell and Environment, 2017, 40, 11-24.	2.8	73
36	Exploring genetic variation for salinity tolerance in chickpea using image-based phenotyping. Scientific Reports, 2017, 7, 1300.	1.6	94

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37	A chromosome conformation capture ordered sequence of the barley genome. Nature, 2017, 544, 427-433.	13.7	1,365
38	Construction of a map-based reference genome sequence for barley, Hordeum vulgare L.. Scientific Data, 2017, 4, 170044.	2.4	130
39	Quantifying Wheat Sensitivities to Environmental Constraints to Dissect Genotype Ã— Environment Interactions in the Field. Plant Physiology, 2017, 174, 1669-1682.	2.3	42
40	Molecular identification of the wheat male fertility gene Ms1 and its prospects for hybrid breeding. Nature Communications, 2017, 8, 869.	5.8	82
41	The impact of drought on wheat leaf cuticle properties. BMC Plant Biology, 2017, 17, 85.	1.6	120
42	Abiotic stress miRNomes in the Triticeae. Functional and Integrative Genomics, 2017, 17, 145-170.	1.4	86
43	Drought-inducible expression of Hv-miR827 enhances drought tolerance in transgenic barley. Functional and Integrative Genomics, 2017, 17, 279-292.	1.4	62
44	Early Flowering as a Drought Escape Mechanism in Plants: How Can It Aid Wheat Production?. Frontiers in Plant Science, 2017, 8, 1950.	1.7	302
45	Genetics of Na+ exclusion and salinity tolerance in Afghani durum wheat landraces. BMC Plant Biology, 2017, 17, 209.	1.6	32
46	Advantages of Amplifluor-like SNP markers over KASP in plant genotyping. BMC Plant Biology, 2017, 17, 254.	1.6	45
47	Endopolyploidy levels in barley vary in different root types and significantly decrease under phosphorus deficiency. Plant Physiology and Biochemistry, 2017, 118, 11-21.	2.8	5
48	Quantitative trait loci for yield and grain plumpness relative to maturity in three populations of barley (Hordeum vulgare L.) grown in a low rain-fall environment. PLoS ONE, 2017, 12, e0178111.	1.1	10
49	Expression Level of the DREB2-Type Gene, Identified with Amplifluor SNP Markers, Correlates with Performance, and Tolerance to Dehydration in Bread Wheat Cultivars from Northern Kazakhstan. Frontiers in Plant Science, 2016, 7, 1736.	1.7	24
50	The homeodomain transcription factor Ta HDZ ipIâ€2 from wheat regulates frost tolerance, flowering time and spike development in transgenic barley. New Phytologist, 2016, 211, 671-687.	3.5	26
51	The Ta<scp>DREB</scp>3 transgene transferred by conventional crossings to different genetic backgrounds of bread wheat improves drought tolerance. Plant Biotechnology Journal, 2016, 14, 313-322.	4.1	80
52	Change of function of the wheat stressâ€responsive transcriptional repressor Ta<scp>RAP</scp>2.1L by repressor motif modification. Plant Biotechnology Journal, 2016, 14, 820-832.	4.1	32
53	Physiological breeding. Current Opinion in Plant Biology, 2016, 31, 162-171.	3.5	249
54	Generation of different sizes and classes of small RNAs in barley is locus, chromosome and/or cultivar-dependent. BMC Genomics, 2016, 17, 735.	1.2	7

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55	Evaluation of Australian wheat genotypes for response to variable nitrogen application. Plant and Soil, 2016, 399, 247-255.	1.8	31
56	Molecular interactions of the Î³-clade homeodomain-leucine zipper class I transcription factors during the wheat response to water deficit. Plant Molecular Biology, 2016, 90, 435-452.	2.0	31
57	Genetic analysis of developmental and adaptive traits in three doubled haploid populations of barley (Hordeum vulgare L.). Theoretical and Applied Genetics, 2016, 129, 1139-1151.	1.8	26
58	The Genetic Control of Grain Protein Content under Variable Nitrogen Supply in an Australian Wheat Mapping Population. PLoS ONE, 2016, 11, e0159371.	1.1	25
59	Genetic Basis for Variation in Wheat Grain Yield in Response to Varying Nitrogen Application. PLoS ONE, 2016, 11, e0159374.	1.1	25
60	Increased expression of six ZIP family genes by zinc (Zn) deficiency is associated with enhanced uptake and rootâ€toâ€shoot translocation of Zn in barley (Hordeum vulgare). New Phytologist, 2015, 207, 1097-1109.	3.5	114
61	Constitutive overexpression of theTaNF-YB4gene in transgenic wheat significantly improves grain yield. Journal of Experimental Botany, 2015, 66, 6635-6650.	2.4	56
62	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.	1.7	72
63	Dynamic root responses to drought and rewatering in two wheat (Triticum aestivum) genotypes. Plant and Soil, 2015, 391, 139-152.	1.8	43
64	Genetic control of grain protein, dough rheology traits and loaf traits in a bread wheat population grown in three environments. Journal of Cereal Science, 2015, 64, 147-152.	1.8	20
65	Tetrapyrroleâ€based drought stress signalling. Plant Biotechnology Journal, 2015, 13, 447-459.	4.1	71
66	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.	2.4	67
67	Genomic tools to assist breeding for drought tolerance. Current Opinion in Biotechnology, 2015, 32, 130-135.	3.3	124
68	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.	4.1	134
69	Identification of Reference Genes for Quantitative Expression Analysis of MicroRNAs and mRNAs in Barley under Various Stress Conditions. PLoS ONE, 2015, 10, e0118503.	1.1	67
70	Application of next-generation sequencing technology to study genetic diversity and identify unique SNP markers in bread wheat from Kazakhstan. BMC Plant Biology, 2014, 14, 258.	1.6	25
71	Endosperm transfer cell-specific genes and proteins: structure, function and applications in biotechnology. Frontiers in Plant Science, 2014, 5, 64.	1.7	19
72	Firefighter feedback during active cooling: A useful tool for heat stress management?. Journal of Thermal Biology, 2014, 46, 65-71.	1.1	18

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73	<scp>H</scp>v<scp>ZIP</scp>7 mediates zinc accumulation in barley (<scp>H</scp>ordeum) Tj ETQq1 1 0.784314 rgBT /Overlock	3.5	112
74	Expression patterns and protein structure of a lipid transfer protein END1 from Arabidopsis. Planta, 2014, 240, 1319-1334.	1.6	6
75	Coronary Heart Disease Risk in Volunteer Firefighters in Victoria, Australia. Archives of Environmental and Occupational Health, 2014, 69, 112-120.	0.7	15
76	Reinventing the Green Revolution by Harnessing Crop Mutant Resources. Plant Physiology, 2014, 166, 1682-1683.	2.3	20
77	Molecular basis of adaptation to high soil boron in wheat landraces and elite cultivars. Nature, 2014, 514, 88-91.	13.7	106
78	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.	1.8	85
79	A Sequence-Ready Physical Map of Barley Anchored Genetically by Two Million Single-Nucleotide Polymorphisms Â Â. Plant Physiology, 2014, 164, 412-423.	2.3	77
80	Genetic control of processing quality in a bread wheat mapping population grown in water-limited environments. Journal of Cereal Science, 2013, 57, 304-311.	1.8	21
81	Hybrid breeding in wheat: technologies to improve hybrid wheat seed production. Journal of Experimental Botany, 2013, 64, 5411-5428.	2.4	239
82	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.	1.6	94
83	Wheat genomics and the ambitious targets for future wheat production. Genome, 2013, 56, 545-547.	0.9	27
84	Multi-environment analysis and improved mapping of a yield-related QTL on chromosome 3B of wheat. Theoretical and Applied Genetics, 2013, 126, 747-761.	1.8	77
85	Letter to the editor. Food and Chemical Toxicology, 2013, 53, 441.	1.8	3
86	Optimization of <scp>TaDREB3</scp> gene expression in transgenic barley using coldâ€inducible promoters. Plant Biotechnology Journal, 2013, 11, 659-670.	4.1	76
87	Functional Genomics of Seed Development in Cereals. , 2013, , 215-245.		5
88	Feeding the future. Nature, 2013, 499, 23-24.	13.7	464
89	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.	1.5	106
90	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.	2.3	115

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91	A DNA-based method for studying root responses to drought in field-grown wheat genotypes. Scientific Reports, 2013, 3, 3194.	1.6	29
92	Germanium as a tool to dissect boron toxicity effects in barley and wheat. Functional Plant Biology, 2013, 40, 618.	1.1	26
93	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.	1.1	34
94	Decoding our daily bread. Nature, 2012, 491, 678-680.	13.7	11
95	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.	1.8	243
96	Clusters of genes encoding fructan biosynthesizing enzymes in wheat and barley. Plant Molecular Biology, 2012, 80, 299-314.	2.0	29
97	Biotechnology for enhancing plant production and food quality: IBS 2010 part III. Journal of Biotechnology, 2012, 159, 249-250.	1.9	0
98	Boron toxicity and deficiency in Triticeae: Update on tolerance mechanisms and transporters. New Biotechnology, 2012, 29, S137.	2.4	0
99	Can genomics boost productivity of orphan crops?. Nature Biotechnology, 2012, 30, 1172-1176.	9.4	248
100	A physical, genetic and functional sequence assembly of the barley genome. Nature, 2012, 491, 711-716.	13.7	1,416
101	Drought Responses of Leaf Tissues from Wheat Cultivars of Differing Drought Tolerance at the Metabolite Level. Molecular Plant, 2012, 5, 418-429.	3.9	370
102	Characterization of the wheat gene encoding a grain-specific lipid transfer protein TdPR61, and promoter activity in wheat, barley and rice. Journal of Experimental Botany, 2012, 63, 2025-2040.	2.4	17
103	Transcriptome-scale homoeolog-specific transcript assemblies of bread wheat. BMC Genomics, 2012, 13, 492.	1.2	51
104	Plant genome sequencing. , 2012, , 83-97.		3
105	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.	1.8	132
106	The scutellar vascular bundleâ€“specific promoter of the wheat HDâ€Zip IV transcription factor shows similar spatial and temporal activity in transgenic wheat, barley and rice. Plant Biotechnology Journal, 2012, 10, 43-53.	4.1	15
107	Bread matters: a national initiative to profile the genetic diversity of Australian wheat. Plant Biotechnology Journal, 2012, 10, 703-708.	4.1	45
108	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.	1.8	76

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109	A Transgenic Transcription Factor (TaDREB3) in Barley Affects the Expression of MicroRNAs and Other Small Non-Coding RNAs. PLoS ONE, 2012, 7, e42030.	1.1	33
110	Salinity tolerance and Na⁺ exclusion in wheat: variability, genetics, mapping populations and QTL analysis. Czech Journal of Genetics and Plant Breeding, 2011, 47, S85-S93.	0.4	18
111	Agronomyâ€"A Multidisciplinary and Open Access Journal. Agronomy, 2011, 1, 1-2.	1.3	0
112	Improvement of stress tolerance of wheat and barley by modulation of expression of DREB/CBF factors. Plant Biotechnology Journal, 2011, 9, 230-249.	4.1	389
113	Modulation of plant growth by HDâ€Zip class I and II transcription factors in response to environmental stimuli. New Phytologist, 2011, 190, 823-837.	3.5	139
114	Making the most of â€˜omicsâ€™ for crop breeding. Trends in Biotechnology, 2011, 29, 33-40.	4.9	199
115	Discovery of barley miRNAs through deep sequencing of short reads. BMC Genomics, 2011, 12, 129.	1.2	118
116	BAC library resources for map-based cloning and physical map construction in barley (Hordeum) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 46	1.2	46
117	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.	2.3	105
118	HvNax3â€"a locus controlling shoot sodium exclusion derived from wild barley (Hordeum vulgare ssp.) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.4	132
119	Marker-assisted wheat breeding: present status and future possibilities. Molecular Breeding, 2010, 26, 145-161.	1.0	245
120	Physical mapping of a large plant genome using global high-information-content-fingerprinting: the distal region of the wheat ancestor Aegilops tauschii chromosome 3DS. BMC Genomics, 2010, 11, 382.	1.2	12
121	Genes mapping to boron tolerance QTL in barley identified by suppression subtractive hybridization. Plant, Cell and Environment, 2010, 33, 188-198.	2.8	11
122	Defensin promoters as potential tools for engineering disease resistance in cereal grains. Plant Biotechnology Journal, 2010, 8, 47-64.	4.1	47
123	Construction of a barley bacterial artificial chromosome library suitable for cloning genes for boron tolerance, sodium exclusion and high grain zinc content. Plant Breeding, 2010, 129, 291-296.	1.0	14
124	Boron Toxicity Tolerance in Barley through Reduced Expression of the Multifunctional Aquaporin HvNIP2;1 Â. Plant Physiology, 2010, 153, 1706-1715.	2.3	159
125	Wide genetic diversity of salinity tolerance, sodium exclusion and growth in wild emmer wheat, Triticum dicoccoides. Breeding Science, 2010, 60, 426-435.	0.9	26
126	Genetic and genomic tools to improve drought tolerance in wheat. Journal of Experimental Botany, 2010, 61, 3211-3222.	2.4	461

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127	Breeding Technologies to Increase Crop Production in a Changing World. Science, 2010, 327, 818-822.	6.0	1,795
128	The International Barley Sequencing Consortiumâ€"At the Threshold of Efficient Access to the Barley Genome Â. Plant Physiology, 2009, 149, 142-147.	2.3	195
129	Comparative transcriptomics in the Triticeae. BMC Genomics, 2009, 10, 285.	1.2	62
130	Characterization of the wheat endosperm transfer cell-specific protein TaPR60. Plant Molecular Biology, 2009, 71, 81-98.	2.0	46
131	Physical analysis of the complex rye (Secale cereale L.) Alt4 aluminium (aluminum) tolerance locus using a whole-genome BAC library of rye cv. Blanco. Theoretical and Applied Genetics, 2009, 119, 695-704.	1.8	13
132	TaASY1 promotes homologous chromosome interactions and is affected by deletion of Ph1. Plant Journal, 2009, 57, 487-497.	2.8	104
133	Phenotyping approaches for physiological breeding and gene discovery in wheat. Annals of Applied Biology, 2009, 155, 309-320.	1.3	224
134	Genetic Mapping in the Triticeae. , 2009, , 201-235.		8
135	A Simple TAE-Based Method to Generate Large Insert BAC Libraries from Plant Species. Methods in Molecular Biology, 2009, 513, 57-80.	0.4	1
136	Salinity tolerance and sodium exclusion in genus Triticum. Breeding Science, 2009, 59, 671-678.	0.9	43
137	Spatial and temporal expression of endosperm transfer cellâ€specific promoters in transgenic rice and barley. Plant Biotechnology Journal, 2008, 6, 465-476.	4.1	38
138	Cereal breeding takes a walk on the wild side. Trends in Genetics, 2008, 24, 24-32.	2.9	355
139	Crops aren't invasive. New Scientist, 2008, 197, 24.	0.0	0
140	Different mechanisms of adaptation to cyclic water stress in two South Australian bread wheat cultivars. Journal of Experimental Botany, 2008, 59, 3327-3346.	2.4	285
141	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.	1.5	169
142	The Bo1-specific PCR marker AWW5L7 is predictive of boron tolerance status in a range of exotic durum and bread wheats. Genome, 2008, 51, 963-971.	0.9	26
143	Genomics of Wheat, the Basis of Our Daily Bread. , 2008, , 515-548.		1
144	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.	2.4	80

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145	A study of the role of root morphological traits in growth of barley in zinc-deficient soil. Journal of Experimental Botany, 2007, 58, 4017-4017.	2.4	1
146	Capturing diversity in the cereals: many options but little promiscuity. Trends in Plant Science, 2007, 12, 71-79.	4.3	39
147	Genetic dissection of grain yield in bread wheat. I. QTL analysis. Theoretical and Applied Genetics, 2007, 115, 1029-1041.	1.8	191
148	Application of Genomics to Molecular Breeding of Wheat and Barley. Advances in Genetics, 2007, 58, 121-155.	0.8	42
149	Meeting Report The Aaronsohn-ITMI International Conference. Israel Journal of Plant Sciences, 2007, 55, 315-319.	0.3	1
150	Boron-Toxicity Tolerance in Barley Arising from Efflux Transporter Amplification. Science, 2007, 318, 1446-1449.	6.0	422
151	Expression and functional analysis of TaASY1 during meiosis of bread wheat (Triticum aestivum). BMC Molecular Biology, 2007, 8, 65.	3.0	43
152	TaMSH7: A cereal mismatch repair gene that affects fertility in transgenic barley (Hordeum vulgare L.). BMC Plant Biology, 2007, 7, 67.	1.6	60
153	A high density barley microsatellite consensus map with 775 SSR loci. Theoretical and Applied Genetics, 2007, 114, 1091-1103.	1.8	308
154	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.	1.8	53
155	Genetic dissection of grain yield in bread wheat. II. QTL-by-environment interaction. Theoretical and Applied Genetics, 2007, 115, 1015-1027.	1.8	69
156	A barley activation tagging system. Plant Molecular Biology, 2007, 64, 329-347.	2.0	72
157	Isolation of plant transcription factors using a modified yeast one-hybrid system. Plant Methods, 2006, 2, 3.	1.9	51
158	Wheat. , 2006, , 79-134.		6
159	Wild sex in the grasses. Trends in Plant Science, 2006, 11, 261-263.	4.3	21
160	New eSSR and gSSR markers added to Australian barley maps. Australian Journal of Agricultural Research, 2006, 57, 953.	1.5	14
161	MappedDs/T-DNA launch pads for functional genomics in barley. Plant Journal, 2006, 47, 811-826.	2.8	36
162	Systematic identification of factors involved in post-transcriptional processes in wheat grain. Plant Molecular Biology, 2006, 62, 637-653.	2.0	17

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163	An atlas of gene expression from seed to seed through barley development. Functional and Integrative Genomics, 2006, 6, 202-211.	1.4	138
164	Identification of transposons, retroelements, and a gene family predominantly expressed in floral tissues in chromosome 3DS of the hexaploid wheat progenitor Aegilops tauschii. Functional and Integrative Genomics, 2006, 7, 37-52.	1.4	9
165	The genetic control of milling yield, dough rheology and baking quality of wheat. Theoretical and Applied Genetics, 2006, 112, 1487-1495.	1.8	141
166	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.	1.8	107
167	Identification of genetic loci associated with ear-emergence in bread wheat. Theoretical and Applied Genetics, 2006, 113, 1103-1112.	1.8	66
168	Microarray expression analysis of meiosis and microsporogenesis in hexaploid bread wheat. BMC Genomics, 2006, 7, 267.	1.2	82
169	An Investigation of Boron Toxicity in Barley Using Metabolomics. Plant Physiology, 2006, 142, 1087-1101.	2.3	174
170	Functional genomics of abiotic stress tolerance in cereals. Briefings in Functional Genomics & Proteomics, 2006, 4, 343-354.	3.8	113
171	Extreme Population-Dependent Linkage Disequilibrium Detected in an Inbreeding Plant Species, Hordeum vulgare. Genetics, 2006, 172, 557-567.	1.2	229
172	WM5: Isolation and characterisation of a gene expressed during early meiosis and shoot meristem development in wheat. Functional Plant Biology, 2005, 32, 249.	1.1	9
173	The transcript composition of egg cells changes significantly following fertilization in wheat (Triticum aestivum L.). Plant Journal, 2005, 41, 660-672.	2.8	136
174	Interspecific transferability and comparative mapping of barley EST-SSR markers in wheat, rye and rice. Plant Science, 2005, 168, 195-202.	1.7	266
175	Comparative Sequence Analysis of the Region Harboring the Hardness Locus in Barley and Its Colinear Region in Rice. Plant Physiology, 2004, 136, 3177-3190.	2.3	68
176	Large-scale analysis of the barley transcriptome based on expressed sequence tags. Plant Journal, 2004, 40, 276-290.	2.8	137
177	Physical Localization of rRNA Genes by Two-Colour Fluorescent In-Situ Hybridization and Sequence Analysis of the 5s rRNA Gene in Phalaris Coerulescens. Hereditas, 2004, 126, 289-294.	0.5	8
178	High-resolution mapping of the S and Z loci of Phalaris coerulescens. Genome, 2004, 47, 918-930.	0.9	27
179	Unfashionable crop species flourish in the 21st century. Genome Biology, 2004, 5, 233.	13.9	11
180	A simple hybridization-based strategy for the generation of non-redundant EST collectionsâ€"a case study in barley (Hordeum vulgare L.). Plant Science, 2004, 167, 629-634.	1.7	8

#	Article	IF	Citations
181	The Principle: Identification and Application of Molecular Markers. , 2004, , 3-22.		17
182	Functional Genomics of Seed Development in Cereals. , 2004, , 447-481.		0
183	ThePh2pairing homoeologous locus of wheat (Triticum aestivum): identification of candidate meiotic genes using a comparative genetics approach. Plant Journal, 2003, 36, 443-456.	2.8	73
184	Marker-assisted backcross introgression of the Yd2 gene conferring resistance to barley yellow dwarf virus in barley. Plant Breeding, 2003, 122, 52-56.	1.0	68
185	A consensus map of barley integrating SSR, RFLP, and AFLP markers. Australian Journal of Agricultural Research, 2003, 54, 1173.	1.5	89
186	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
187	Subunit and cofactor binding of Saccharomyces cerevisiae sulfite reductase - towards developing wine yeast with lowered ability to produce hydrogen sulfide. Australian Journal of Grape and Wine Research, 2003, 9, 186-193.	1.0	22
188	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.	0.9	27
189	A DNA mismatch repair gene links to thePh2locus in wheat. Genome, 2002, 45, 116-124.	0.9	50
190	Decreasing acetic acid accumulation by a glycerol overproducing strain ofSaccharomyces cerevisiae by deleting theALD6 aldehyde dehydrogenase gene. Yeast, 2002, 19, 295-301.	0.8	132
191	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.	1.8	31
192	A Single Amino Acid Substitution that Determines IEF Band Pattern of Barley Beta -amylase. Journal of Cereal Science, 2002, 35, 79-84.	1.8	11
193	Genetic diversity within Australian wheat breeding programs based on molecular and pedigree data. Euphytica, 2002, 124, 293-306.	0.6	31
194	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
195	Trends in genetic and genome analyses in wheat: a review. Australian Journal of Agricultural Research, 2001, 52, 1043.	1.5	141
196	Construction of three linkage maps in bread wheat, Triticum aestivum. Australian Journal of Agricultural Research, 2001, 52, 1089.	1.5	114
197	Mutations of barley Î²-amylase that improve substrate-binding affinity and thermostability. Molecular Genetics and Genomics, 2001, 266, 345-352.	1.0	52
198	Genetic drift and host-mediated selection cause genetic differentiation among Gaeumannomyces graminis populations infecting cereals in southern Australia. Mycological Research, 2001, 105, 927-935.	2.5	18

#	Article	IF	Citations
199	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.	2.3	174
200	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.	1.4	52
201	Cloning and expression of a distinct subclass of plant thioredoxins. FEBS Journal, 2000, 267, 7109-7117.	0.2	33
202	Title is missing!. Molecular Breeding, 2000, 6, 169-174.	1.0	41
203	Comparative Enzyme Kinetics of Two Allelic Forms of Barley (Hordeum vulgare L.) Beta -amylase. Journal of Cereal Science, 2000, 31, 335-344.	1.8	33
204	Mapping and validation of chromosome regions conferring boron toxicity tolerance in wheat (Triticum aestivum). Theoretical and Applied Genetics, 2000, 101, 767-777.	1.8	100
205	RFLP mapping of manganese efficiency in barley. Theoretical and Applied Genetics, 2000, 101, 1100-1108.	1.8	157
206	Self-incompatibility in the Grasses. Annals of Botany, 2000, 85, 203-209.	1.4	76
207	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.	1.0	57
208	Removal of the Four C-Terminal Glycine-Rich Repeats Enhances the Thermostability and Substrate Binding Affinity of Barley Î²-Amylase. Biochemistry, 2000, 39, 13350-13355.	1.2	31
209	From Genome Structure to Pragmatic Breeding of Wheat and Barley. Stadler Genetics Symposia Series, 2000, , 197-209.	0.0	0
210	AFLP fingerprinting for analysis of yeast genetic variation. International Journal of Systematic and Evolutionary Microbiology, 1999, 49, 915-924.	0.8	100
211	Mapping loci associated with milling yield in wheat (Triticum aestivum L.). Molecular Breeding, 1999, 5, 561-568.	1.0	42
212	Mapping of chromosome regions conferring boron toxicity tolerance in barley (Hordeum vulgare L.). Theoretical and Applied Genetics, 1999, 98, 1293-1303.	1.8	107
213	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.	1.8	60
214	Revisiting and Revising the Self-Incompatibility Genetics of Phalaris coerulescens. Plant Cell, 1999, 11, 1826-1826.	3.1	16
215	RFLP mapping of a new cereal cyst nematode resistance locus in barley. Plant Breeding, 1998, 117, 185-187.	1.0	48
216	Isolation of lambda and YAC clones from defined regions of the rye genome. Molecular Genetics and Genomics, 1998, 257, 568-575.	2.4	8

#	Article	IF	Citations
217	Genetic diversity in Australian wheat varieties and breeding material based on RFLP data. Theoretical and Applied Genetics, 1998, 96, 435-446.	1.8	103
218	Mapping loci associated with flour colour in wheat (Triticum aestivum L.). Theoretical and Applied Genetics, 1998, 97, 238-245.	1.8	145
219	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.	1.8	28
220	Thermostability variation in alleles of barley beta-amylase. Journal of Cereal Science, 1998, 28, 301-309.	1.8	117
221	Differentiation and species identification of yeasts using PCR. International Journal of Systematic Bacteriology, 1998, 48, 279-286.	2.8	87
222	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.	2.0	36
223	RFLP mapping of the Ha 2 cereal cyst nematode resistance gene in barley. Theoretical and Applied Genetics, 1997, 94, 1060-1064.	1.8	69
224	Cloning plant genes differentially expressed during colonization of roots of Hordeum vulgare by the vesicular-arbuscular mycorrhizal fungus Glomus intraradices. New Phytologist, 1997, 135, 291-301.	3.5	100
225	Development of a PCR-based allele-specific assay from an RFLP probe linked to resistance to cereal cyst nematode in wheat. Genome, 1996, 39, 798-801.	0.9	17
226	A self-fertile mutant of Phalaris produces an S protein with reduced thioredoxin activity. Plant Journal, 1996, 10, 505-513.	2.8	26
227	STS-PCR markers appropriate for wheat-barley introgression. Theoretical and Applied Genetics, 1996, 93-93, 826-832.	1.8	72
228	A consensus linkage map of barley. Molecular Breeding, 1995, 1, 389-395.	1.0	111
229	Analysis of rye B-chromosome structure using fluorescencein situ hybridization (FISH). Chromosome Research, 1995, 3, 466-472.	1.0	45
230	Thioredoxin activity in the C terminus of Phalaris S protein. Plant Journal, 1995, 8, 133-138.	2.8	41
231	Regulation of hydrogen sulfide liberation in wine-producing Saccharomyces cerevisiae strains by assimilable nitrogen. Applied and Environmental Microbiology, 1995, 61, 461-467.	1.4	171
232	Cloning a Putative Self-Incompatibility Gene from the Pollen of the Grass Phalaris coerulescens. Plant Cell, 1994, 6, 1923.	3.1	9
233	Identification of RFLP markers linked to the cereal cyst nematode resistance gene (Cre) in wheat. Theoretical and Applied Genetics, 1994, 89-89, 927-930.	1.8	51
234	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.	1.8	62

#	Article	IF	Citations
235	An early meiosis cDNA clone from wheat. Molecular Genetics and Genomics, 1994, 243, 17-23.	2.4	44
236	Isolation and characterization of wheat triticin cDNA revealing a unique lysine-rich repetitive domain. Plant Molecular Biology, 1993, 22, 227-237.	2.0	40
237	[1] Megabase DNA preparation from plant tissue. Methods in Enzymology, 1992, 216, 3-12.	0.4	12
238	Polymerase chain reaction based mapping of rye involving repeated DNA sequences. Genome, 1992, 35, 621-626.	0.9	33
239	Structural heterogeneity in the R173 family of rye-specific repetitive DNA sequences. Plant Molecular Biology, 1992, 20, 95-102.	2.0	39
240	Transformation of cereals via Agrobacterium and the pollen pathway: a critical assessment. Plant Journal, 1992, 2, 631-638.	2.8	73
241	The R173 family of rye-specific repetitive DNA sequences: a structural analysis. Genome, 1991, 34, 88-95.	0.9	34
242	Cloning and characterisation of a new rye-specific repeated sequence. Genome, 1991, 34, 81-87.	0.9	138
243	Identification and mapping of polymorphisms in cereals based on the polymerase chain reaction. Theoretical and Applied Genetics, 1991, 82, 209-216.	1.8	203
244	Isolation and characterization of wheat-rye recombinants involving chromosome arm 1DS of wheat. Theoretical and Applied Genetics, 1991, 82, 537-544.	1.8	153
245	A segment of rye chromosome 1 enhances growth and embryogenesis of calli derived from immature embryos of wheat. Plant Cell Reports, 1991, 10, 148-51.	2.8	17
246	Squashes of plant tissue as substrate for PCR. Nucleic Acids Research, 1991, 19, 6954-6954.	6.5	57
247	Nucleotide sequence of a circular single-stranded DNA associated with coconut foliar decay virus. Virology, 1990, 176, 648-651.	1.1	103
248	A rapid method of preparing megabase plant DNA. Nucleic Acids Research, 1990, 18, 4955-4955.	6.5	21
249	Identification of legumin-like proteins in wheat. Plant Molecular Biology, 1988, 11, 633-639.	2.0	24
250	A zein gene of maize is transcribed from two widely separated promoter regions. Cell, 1983, 34, 1015-1022.	13.5	116
251	Isolation and characterization of maize genes coding for zein proteins of the 21000 dalton size class. Nucleic Acids Research, 1982, 10, 3845-3860.	6.5	20
252	Transcriptional effects of the opaque-2 mutation of Zea mays L.. Planta, 1982, 156, 166-170.	1.6	38

#	Article	IF	Citations
253	Zein precursor mRNAs from maize endosperm. Molecular Genetics and Genomics, 1982, 187, 432-438.	2.4	39
254	Synthesis of the large subunit of spinach ribulose bisphosphate carboxylase may involve a precursor polypeptide. FEBS Letters, 1981, 123, 85-89.	1.3	41
255	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
256	Extraction of nucleic acids from agarose gels. Analytical Biochemistry, 1980, 103, 264-271.	1.1	376