

Peter Langridge

List of Publications by Year in descending order

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256
papers

23,985
citations

8755

77
h-index

10679

143
g-index

263
all docs

263
docs citations

263
times ranked

20240
citing authors

#	ARTICLE	IF	CITATIONS
1	Breeding Technologies to Increase Crop Production in a Changing World. <i>Science</i> , 2010, 327, 818-822.	6.0	1,795
2	A physical, genetic and functional sequence assembly of the barley genome. <i>Nature</i> , 2012, 491, 711-716.	13.7	1,416
3	A chromosome conformation capture ordered sequence of the barley genome. <i>Nature</i> , 2017, 544, 427-433.	13.7	1,365
4	Multiple wheat genomes reveal global variation in modern breeding. <i>Nature</i> , 2020, 588, 277-283.	13.7	513
5	Feeding the future. <i>Nature</i> , 2013, 499, 23-24.	13.7	464
6	Genetic and genomic tools to improve drought tolerance in wheat. <i>Journal of Experimental Botany</i> , 2010, 61, 3211-3222.	2.4	461
7	Boron-Toxicity Tolerance in Barley Arising from Efflux Transporter Amplification. <i>Science</i> , 2007, 318, 1446-1449.	6.0	422
8	Improvement of stress tolerance of wheat and barley by modulation of expression of DREB/CBF factors. <i>Plant Biotechnology Journal</i> , 2011, 9, 230-249.	4.1	389
9	Extraction of nucleic acids from agarose gels. <i>Analytical Biochemistry</i> , 1980, 103, 264-271.	1.1	376
10	Drought Responses of Leaf Tissues from Wheat Cultivars of Differing Drought Tolerance at the Metabolite Level. <i>Molecular Plant</i> , 2012, 5, 418-429.	3.9	370
11	Cereal breeding takes a walk on the wild side. <i>Trends in Genetics</i> , 2008, 24, 24-32.	2.9	355
12	The barley pan-genome reveals the hidden legacy of mutation breeding. <i>Nature</i> , 2020, 588, 284-289.	13.7	314
13	A high density barley microsatellite consensus map with 775 SSR loci. <i>Theoretical and Applied Genetics</i> , 2007, 114, 1091-1103.	1.8	308
14	Early Flowering as a Drought Escape Mechanism in Plants: How Can It Aid Wheat Production?. <i>Frontiers in Plant Science</i> , 2017, 8, 1950.	1.7	302
15	Different mechanisms of adaptation to cyclic water stress in two South Australian bread wheat cultivars. <i>Journal of Experimental Botany</i> , 2008, 59, 3327-3346.	2.4	285
16	Interspecific transferability and comparative mapping of barley EST-SSR markers in wheat, rye and rice. <i>Plant Science</i> , 2005, 168, 195-202.	1.7	266
17	In silico analysis on frequency and distribution of microsatellites in ESTs of some cereal species. <i>Cellular and Molecular Biology Letters</i> , 2002, 7, 537-46.	2.7	264
18	Physiological breeding. <i>Current Opinion in Plant Biology</i> , 2016, 31, 162-171.	3.5	249

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19	Can genomics boost productivity of orphan crops?. <i>Nature Biotechnology</i> , 2012, 30, 1172-1176.	9.4	248
20	Marker-assisted wheat breeding: present status and future possibilities. <i>Molecular Breeding</i> , 2010, 26, 145-161.	1.0	245
21	Detection of two major grain yield QTL in bread wheat (<i>Triticum aestivum</i> L.) under heat, drought and high yield potential environments. <i>Theoretical and Applied Genetics</i> , 2012, 125, 1473-1485.	1.8	243
22	Hybrid breeding in wheat: technologies to improve hybrid wheat seed production. <i>Journal of Experimental Botany</i> , 2013, 64, 5411-5428.	2.4	239
23	Extreme Population-Dependent Linkage Disequilibrium Detected in an Inbreeding Plant Species, <i>Hordeum vulgare</i> . <i>Genetics</i> , 2006, 172, 557-567.	1.2	229
24	Phenotyping approaches for physiological breeding and gene discovery in wheat. <i>Annals of Applied Biology</i> , 2009, 155, 309-320.	1.3	224
25	Identification and mapping of polymorphisms in cereals based on the polymerase chain reaction. <i>Theoretical and Applied Genetics</i> , 1991, 82, 209-216.	1.8	203
26	Making the most of "omics"™ for crop breeding. <i>Trends in Biotechnology</i> , 2011, 29, 33-40.	4.9	199
27	The International Barley Sequencing Consortium "At the Threshold of Efficient Access to the Barley Genome". <i>Plant Physiology</i> , 2009, 149, 142-147.	2.3	195
28	Genetic dissection of grain yield in bread wheat. I. QTL analysis. <i>Theoretical and Applied Genetics</i> , 2007, 115, 1029-1041.	1.8	191
29	Zinc Deficiency Up-Regulates Expression of High-Affinity Phosphate Transporter Genes in Both Phosphate-Sufficient and -Deficient Barley Roots. <i>Plant Physiology</i> , 2000, 124, 415-422.	2.3	174
30	An Investigation of Boron Toxicity in Barley Using Metabolomics. <i>Plant Physiology</i> , 2006, 142, 1087-1101.	2.3	174
31	Regulation of hydrogen sulfide liberation in wine-producing <i>Saccharomyces cerevisiae</i> strains by assimilable nitrogen. <i>Applied and Environmental Microbiology</i> , 1995, 61, 461-467.	1.4	171
32	Metabolite Profiling Reveals Distinct Changes in Carbon and Nitrogen Metabolism in Phosphate-Deficient Barley Plants (<i>Hordeum vulgare</i> L.). <i>Plant and Cell Physiology</i> , 2008, 49, 691-703.	1.5	169
33	Boron Toxicity Tolerance in Barley through Reduced Expression of the Multifunctional Aquaporin HvNIP2;1. <i>Plant Physiology</i> , 2010, 153, 1706-1715.	2.3	159
34	RFLP mapping of manganese efficiency in barley. <i>Theoretical and Applied Genetics</i> , 2000, 101, 1100-1108.	1.8	157
35	Isolation and characterization of wheat-rye recombinants involving chromosome arm 1DS of wheat. <i>Theoretical and Applied Genetics</i> , 1991, 82, 537-544.	1.8	153
36	Mapping loci associated with flour colour in wheat (<i>Triticum aestivum</i> L.). <i>Theoretical and Applied Genetics</i> , 1998, 97, 238-245.	1.8	145

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37	Trends in genetic and genome analyses in wheat: a review. <i>Australian Journal of Agricultural Research</i> , 2001, 52, 1043.	1.5	141
38	The genetic control of milling yield, dough rheology and baking quality of wheat. <i>Theoretical and Applied Genetics</i> , 2006, 112, 1487-1495.	1.8	141
39	Modulation of plant growth by HD-Zip class I and II transcription factors in response to environmental stimuli. <i>New Phytologist</i> , 2011, 190, 823-837.	3.5	139
40	Cloning and characterisation of a new rye-specific repeated sequence. <i>Genome</i> , 1991, 34, 81-87.	0.9	138
41	An atlas of gene expression from seed to seed through barley development. <i>Functional and Integrative Genomics</i> , 2006, 6, 202-211.	1.4	138
42	Large-scale analysis of the barley transcriptome based on expressed sequence tags. <i>Plant Journal</i> , 2004, 40, 276-290.	2.8	137
43	The transcript composition of egg cells changes significantly following fertilization in wheat (<i>Triticum aestivum</i> L.). <i>Plant Journal</i> , 2005, 41, 660-672.	2.8	136
44	Differential expression of microRNA and other small RNA in barley between water and drought conditions. <i>Plant Biotechnology Journal</i> , 2015, 13, 2-13.	4.1	134
45	Decreasing acetic acid accumulation by a glycerol overproducing strain of <i>Saccharomyces cerevisiae</i> by deleting the <i>ALD6</i> aldehyde dehydrogenase gene. <i>Yeast</i> , 2002, 19, 295-301.	0.8	132
46	HvNax3a locus controlling shoot sodium exclusion derived from wild barley (<i>Hordeum vulgare</i> ssp.) <i>Trends in Plant Science</i> , 2010, 15, 145-152.	1.45	132
47	Genetic dissection of grain yield and physical grain quality in bread wheat (<i>Triticum aestivum</i> L.) under water-limited environments. <i>Theoretical and Applied Genetics</i> , 2012, 125, 255-271.	1.8	132
48	Construction of a map-based reference genome sequence for barley, <i>Hordeum vulgare</i> L.. <i>Scientific Data</i> , 2017, 4, 170044.	2.4	130
49	CRISPR/Cas9-mediated knockout of <i>Ms1</i> enables the rapid generation of male-sterile hexaploid wheat lines for use in hybrid seed production. <i>Plant Biotechnology Journal</i> , 2019, 17, 1905-1913.	4.1	125
50	Genomic tools to assist breeding for drought tolerance. <i>Current Opinion in Biotechnology</i> , 2015, 32, 130-135.	3.3	124
51	The impact of drought on wheat leaf cuticle properties. <i>BMC Plant Biology</i> , 2017, 17, 85.	1.6	120
52	Discovery of barley miRNAs through deep sequencing of short reads. <i>BMC Genomics</i> , 2011, 12, 129.	1.2	118
53	Thermostability variation in alleles of barley beta-amylase. <i>Journal of Cereal Science</i> , 1998, 28, 301-309.	1.8	117
54	A zein gene of maize is transcribed from two widely separated promoter regions. <i>Cell</i> , 1983, 34, 1015-1022.	13.5	116

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55	Whole-Genome Mapping of Agronomic and Metabolic Traits to Identify Novel Quantitative Trait Loci in Bread Wheat Grown in a Water-Limited Environment. <i>Plant Physiology</i> , 2013, 162, 1266-1281.	2.3	115
56	Construction of three linkage maps in bread wheat, <i>Triticum aestivum</i> . <i>Australian Journal of Agricultural Research</i> , 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 root-to-shoot translocation of Zn in barley (<i>Hordeum vulgare</i>). <i>New Phytologist</i> , 2015, 207, 1097-1109.	3.5	114
58	Functional genomics of abiotic stress tolerance in cereals. <i>Briefings in Functional Genomics & Proteomics</i> , 2006, 4, 343-354.	3.8	113
59	<i>HvZIP7</i> mediates zinc accumulation in barley (<i>Hordeum vulgare</i>) Tj ETQq1 1 0.784314 rgBT/Overlook	3.5	112
60	A consensus linkage map of barley. <i>Molecular Breeding</i> , 1995, 1, 389-395.	1.0	111
61	Mapping of chromosome regions conferring boron toxicity tolerance in barley (<i>Hordeum vulgare</i> L.). <i>Theoretical and Applied Genetics</i> , 1999, 98, 1293-1303.	1.8	107
62	Genetic mapping and BAC assignment of EST-derived SSR markers shows non-uniform distribution of genes in the barley genome. <i>Theoretical and Applied Genetics</i> , 2006, 113, 239-250.	1.8	107
63	A Comprehensive Expression Profile of MicroRNAs and Other Classes of Non-Coding Small RNAs in Barley Under Phosphorous-Deficient and -Sufficient Conditions. <i>DNA Research</i> , 2013, 20, 109-125.	1.5	106
64	Molecular basis of adaptation to high soil boron in wheat landraces and elite cultivars. <i>Nature</i> , 2014, 514, 88-91.	13.7	106
65	Phosphate Utilization Efficiency Correlates with Expression of Low-Affinity Phosphate Transporters and Noncoding RNA, <i>IPS1</i> , in Barley Å. <i>Plant Physiology</i> , 2011, 156, 1217-1229.	2.3	105
66	TaASY1 promotes homologous chromosome interactions and is affected by deletion of <i>Ph1</i> . <i>Plant Journal</i> , 2009, 57, 487-497.	2.8	104
67	Nucleotide sequence of a circular single-stranded DNA associated with coconut foliar decay virus. <i>Virology</i> , 1990, 176, 648-651.	1.1	103
68	Genetic diversity in Australian wheat varieties and breeding material based on RFLP data. <i>Theoretical and Applied Genetics</i> , 1998, 96, 435-446.	1.8	103
69	Cloning plant genes differentially expressed during colonization of roots of <i>Hordeum vulgare</i> by the vesicular-arbuscular mycorrhizal fungus <i>Glomus intraradices</i> . <i>New Phytologist</i> , 1997, 135, 291-301.	3.5	100
70	AFLP fingerprinting for analysis of yeast genetic variation. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 1999, 49, 915-924.	0.8	100
71	Mapping and validation of chromosome regions conferring boron toxicity tolerance in wheat (<i>Triticum aestivum</i>). <i>Theoretical and Applied Genetics</i> , 2000, 101, 767-777.	1.8	100
72	Characterization of phosphorus-regulated miR399 and miR827 and their isomirs in barley under phosphorus-sufficient and phosphorus-deficient conditions. <i>BMC Plant Biology</i> , 2013, 13, 214.	1.6	94

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73	Exploring genetic variation for salinity tolerance in chickpea using image-based phenotyping. <i>Scientific Reports</i> , 2017, 7, 1300.	1.6	94
74	A consensus map of barley integrating SSR, RFLP, and AFLP markers. <i>Australian Journal of Agricultural Research</i> , 2003, 54, 1173.	1.5	89
75	Differentiation and species identification of yeasts using PCR. <i>International Journal of Systematic Bacteriology</i> , 1998, 48, 279-286.	2.8	87
76	Abiotic stress miRNomes in the Triticeae. <i>Functional and Integrative Genomics</i> , 2017, 17, 145-170.	1.4	86
77	Genetic control of grain yield and grain physical characteristics in a bread wheat population grown under a range of environmental conditions. <i>Theoretical and Applied Genetics</i> , 2014, 127, 1607-1624.	1.8	85
78	Microarray expression analysis of meiosis and microsporogenesis in hexaploid bread wheat. <i>BMC Genomics</i> , 2006, 7, 267.	1.2	82
79	Molecular identification of the wheat male fertility gene <i>Ms1</i> and its prospects for hybrid breeding. <i>Nature Communications</i> , 2017, 8, 869.	5.8	82
80	A study of the role of root morphological traits in growth of barley in zinc-deficient soil. <i>Journal of Experimental Botany</i> , 2007, 58, 2775-2784.	2.4	80
81	The <i>TaDREB3</i> transgene transferred by conventional crossings to different genetic backgrounds of bread wheat improves drought tolerance. <i>Plant Biotechnology Journal</i> , 2016, 14, 313-322.	4.1	80
82	Multi-environment analysis and improved mapping of a yield-related QTL on chromosome 3B of wheat. <i>Theoretical and Applied Genetics</i> , 2013, 126, 747-761.	1.8	77
83	A Sequence-Ready Physical Map of Barley Anchored Genetically by Two Million Single-Nucleotide Polymorphisms. <i>Plant Physiology</i> , 2014, 164, 412-423.	2.3	77
84	Self-incompatibility in the Grasses. <i>Annals of Botany</i> , 2000, 85, 203-209.	1.4	76
85	Identification of novel quantitative trait loci for days to ear emergence and flag leaf glaucousness in a bread wheat (<i>Triticum aestivum</i> L.) population adapted to southern Australian conditions. <i>Theoretical and Applied Genetics</i> , 2012, 124, 697-711.	1.8	76
86	Optimization of <i>TaDREB3</i> gene expression in transgenic barley using cold-inducible promoters. <i>Plant Biotechnology Journal</i> , 2013, 11, 659-670.	4.1	76
87	Transformation of cereals via <i>Agrobacterium</i> and the pollen pathway: a critical assessment. <i>Plant Journal</i> , 1992, 2, 631-638.	2.8	73
88	ThePh2pairing homoeologous locus of wheat (<i>Triticum aestivum</i>): identification of candidate meiotic genes using a comparative genetics approach. <i>Plant Journal</i> , 2003, 36, 443-456.	2.8	73
89	Differential expression of microRNAs and potential targets under drought stress in barley. <i>Plant, Cell and Environment</i> , 2017, 40, 11-24.	2.8	73
90	STS-PCR markers appropriate for wheat-barley introgression. <i>Theoretical and Applied Genetics</i> , 1996, 93-93, 826-832.	1.8	72

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91	A barley activation tagging system. <i>Plant Molecular Biology</i> , 2007, 64, 329-347.	2.0	72
92	Detection of QTL for metabolic and agronomic traits in wheat with adjustments for variation at genetic loci that affect plant phenology. <i>Plant Science</i> , 2015, 233, 143-154.	1.7	72
93	Tetrapyrrole-based drought stress signalling. <i>Plant Biotechnology Journal</i> , 2015, 13, 447-459.	4.1	71
94	Breeding for drought and heat tolerance in wheat. <i>Theoretical and Applied Genetics</i> , 2021, 134, 1753-1769.	1.8	70
95	RFLP mapping of the Ha 2 cereal cyst nematode resistance gene in barley. <i>Theoretical and Applied Genetics</i> , 1997, 94, 1060-1064.	1.8	69
96	Genetic dissection of grain yield in bread wheat. II. QTL-by-environment interaction. <i>Theoretical and Applied Genetics</i> , 2007, 115, 1015-1027.	1.8	69
97	Marker-assisted backcross introgression of the Yd2 gene conferring resistance to barley yellow dwarf virus in barley. <i>Plant Breeding</i> , 2003, 122, 52-56.	1.0	68
98	Comparative Sequence Analysis of the Region Harboring the Hardness Locus in Barley and Its Colinear Region in Rice. <i>Plant Physiology</i> , 2004, 136, 3177-3190.	2.3	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. <i>Journal of Experimental Botany</i> , 2015, 66, 5481-5492.	2.4	67
100	Identification of Reference Genes for Quantitative Expression Analysis of MicroRNAs and mRNAs in Barley under Various Stress Conditions. <i>PLoS ONE</i> , 2015, 10, e0118503.	1.1	67
101	Identification of genetic loci associated with ear-emergence in bread wheat. <i>Theoretical and Applied Genetics</i> , 2006, 113, 1103-1112.	1.8	66
102	A Comparison of Mainstream Genotyping Platforms for the Evaluation and Use of Barley Genetic Resources. <i>Frontiers in Plant Science</i> , 2019, 10, 544.	1.7	66
103	RFLP markers associated with Sr22 and recombination between chromosome 7A of bread wheat and the diploid species <i>Triticum boeoticum</i> . <i>Theoretical and Applied Genetics</i> , 1994, 89-89, 1039-1045.	1.8	62
104	Comparative transcriptomics in the Triticeae. <i>BMC Genomics</i> , 2009, 10, 285.	1.2	62
105	Drought-inducible expression of Hv-miR827 enhances drought tolerance in transgenic barley. <i>Functional and Integrative Genomics</i> , 2017, 17, 279-292.	1.4	62
106	Identification and mapping of a gene conferring resistance to the spot form of net blotch (<i>Pyrenophora teres f maculata</i>) in barley. <i>Theoretical and Applied Genetics</i> , 1999, 99, 323-327.	1.8	60
107	TaMSH7: A cereal mismatch repair gene that affects fertility in transgenic barley (<i>Hordeum vulgare</i> L.). <i>BMC Plant Biology</i> , 2007, 7, 67.	1.6	60
108	QTL analysis and fine mapping of a QTL for yield-related traits in wheat grown in dry and hot environments. <i>Theoretical and Applied Genetics</i> , 2020, 133, 239-257.	1.8	59

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109	Squashes of plant tissue as substrate for PCR. <i>Nucleic Acids Research</i> , 1991, 19, 6954-6954.	6.5	57
110	Fermentation properties of a wine yeast over-expressing the <i>Saccharomyces cerevisiae</i> glycerol 3-phosphate dehydrogenase gene (GPD2). <i>Australian Journal of Grape and Wine Research</i> , 2000, 6, 208-215.	1.0	57
111	Constitutive overexpression of the <i>TaNF-YB4</i> gene in transgenic wheat significantly improves grain yield. <i>Journal of Experimental Botany</i> , 2015, 66, 6635-6650.	2.4	56
112	gRNA validation for wheat genome editing with the CRISPR-Cas9 system. <i>BMC Biotechnology</i> , 2019, 19, 71.	1.7	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. <i>Theoretical and Applied Genetics</i> , 2007, 115, 451-461.	1.8	53
114	Harnessing the potential of germplasm collections. <i>Nature Genetics</i> , 2019, 51, 200-201.	9.4	53
115	The incidence of killer activity of non- <i>Saccharomyces</i> yeasts towards indigenous yeast species of grape must: potential application in wine fermentation. <i>Journal of Applied Microbiology</i> , 2000, 89, 381-389.	1.4	52
116	Mutations of barley β -amylase that improve substrate-binding affinity and thermostability. <i>Molecular Genetics and Genomics</i> , 2001, 266, 345-352.	1.0	52
117	Identification of RFLP markers linked to the cereal cyst nematode resistance gene (Cre) in wheat. <i>Theoretical and Applied Genetics</i> , 1994, 89-89, 927-930.	1.8	51
118	Potential of SSR markers for plant breeding and variety identification in Australian barley germplasm. <i>Australian Journal of Agricultural Research</i> , 2003, 54, 1197.	1.5	51
119	Isolation of plant transcription factors using a modified yeast one-hybrid system. <i>Plant Methods</i> , 2006, 2, 3.	1.9	51
120	Transcriptome-scale homoeolog-specific transcript assemblies of bread wheat. <i>BMC Genomics</i> , 2012, 13, 492.	1.2	51
121	A DNA mismatch repair gene links to the Ph2 locus in wheat. <i>Genome</i> , 2002, 45, 116-124.	0.9	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. <i>Plant, Cell and Environment</i> , 2018, 41, 2549-2566.	2.8	50
123	RFLP mapping of a new cereal cyst nematode resistance locus in barley. <i>Plant Breeding</i> , 1998, 117, 185-187.	1.0	48
124	A biolistic method for high-throughput production of transgenic wheat plants with single gene insertions. <i>BMC Plant Biology</i> , 2018, 18, 135.	1.6	48
125	Defensin promoters as potential tools for engineering disease resistance in cereal grains. <i>Plant Biotechnology Journal</i> , 2010, 8, 47-64.	4.1	47
126	Characterization of the wheat endosperm transfer cell-specific protein TaPR60. <i>Plant Molecular Biology</i> , 2009, 71, 81-98.	2.0	46

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127	BAC library resources for map-based cloning and physical map construction in barley (<i>Hordeum</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 1.2 46		
128	Analysis of rye B-chromosome structure using fluorescence in situ hybridization (FISH). <i>Chromosome Research</i> , 1995, 3, 466-472.	1.0	45
129	Bread matters: a national initiative to profile the genetic diversity of Australian wheat. <i>Plant Biotechnology Journal</i> , 2012, 10, 703-708.	4.1	45
130	Advantages of Amplifluor-like SNP markers over KASP in plant genotyping. <i>BMC Plant Biology</i> , 2017, 17, 254.	1.6	45
131	An early meiosis cDNA clone from wheat. <i>Molecular Genetics and Genomics</i> , 1994, 243, 17-23.	2.4	44
132	Expression and functional analysis of TaASY1 during meiosis of bread wheat (<i>Triticum aestivum</i>). <i>BMC Molecular Biology</i> , 2007, 8, 65.	3.0	43
133	Dynamic root responses to drought and rewatering in two wheat (<i>Triticum aestivum</i>) genotypes. <i>Plant and Soil</i> , 2015, 391, 139-152.	1.8	43
134	Salinity tolerance and sodium exclusion in genus <i>Triticum</i> . <i>Breeding Science</i> , 2009, 59, 671-678.	0.9	43
135	Mapping loci associated with milling yield in wheat (<i>Triticum aestivum</i> L.). <i>Molecular Breeding</i> , 1999, 5, 561-568.	1.0	42
136	Application of Genomics to Molecular Breeding of Wheat and Barley. <i>Advances in Genetics</i> , 2007, 58, 121-155.	0.8	42
137	Quantifying Wheat Sensitivities to Environmental Constraints to Dissect Genotype × Environment Interactions in the Field. <i>Plant Physiology</i> , 2017, 174, 1669-1682.	2.3	42
138	Synthesis of the large subunit of spinach ribulose biphosphate carboxylase may involve a precursor polypeptide. <i>FEBS Letters</i> , 1981, 123, 85-89.	1.3	41
139	Thioredoxin activity in the C terminus of Phalaris S protein. <i>Plant Journal</i> , 1995, 8, 133-138.	2.8	41
140	Title is missing!. <i>Molecular Breeding</i> , 2000, 6, 169-174.	1.0	41
141	Isolation and characterization of wheat tritacin cDNA revealing a unique lysine-rich repetitive domain. <i>Plant Molecular Biology</i> , 1993, 22, 227-237.	2.0	40
142	Zein precursor mRNAs from maize endosperm. <i>Molecular Genetics and Genomics</i> , 1982, 187, 432-438.	2.4	39
143	Structural heterogeneity in the R173 family of rye-specific repetitive DNA sequences. <i>Plant Molecular Biology</i> , 1992, 20, 95-102.	2.0	39
144	Capturing diversity in the cereals: many options but little promiscuity. <i>Trends in Plant Science</i> , 2007, 12, 71-79.	4.3	39

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145	Transcriptional effects of the opaque-2 mutation of <i>Zea mays</i> L.. <i>Planta</i> , 1982, 156, 166-170.	1.6	38
146	Spatial and temporal expression of endosperm transfer cell-specific promoters in transgenic rice and barley. <i>Plant Biotechnology Journal</i> , 2008, 6, 465-476.	4.1	38
147	Green revolution "stumbles"™ in a dry environment: Dwarf wheat with <i>Rht</i> genes fails to produce higher grain yield than taller plants under drought. <i>Plant, Cell and Environment</i> , 2020, 43, 2355-2364.	2.8	38
148	Self-incompatibility in the grasses: evolutionary relationship of the S gene from <i>Phalaris coerulescens</i> to homologous sequences in other grasses. <i>Plant Molecular Biology</i> , 1997, 34, 223-232.	2.0	36
149	MappedDs/T-DNA launch pads for functional genomics in barley. <i>Plant Journal</i> , 2006, 47, 811-826.	2.8	36
150	The R173 family of rye-specific repetitive DNA sequences: a structural analysis. <i>Genome</i> , 1991, 34, 88-95.	0.9	34
151	Complex Regulation by Apetala2 Domain-Containing Transcription Factors Revealed through Analysis of the Stress-Responsive TdCor410b Promoter from Durum Wheat. <i>PLoS ONE</i> , 2013, 8, e58713.	1.1	34
152	Making science more effective for agriculture. <i>Advances in Agronomy</i> , 2020, , 153-177.	2.4	34
153	Polymerase chain reaction based mapping of rye involving repeated DNA sequences. <i>Genome</i> , 1992, 35, 621-626.	0.9	33
154	Cloning and expression of a distinct subclass of plant thioredoxins. <i>FEBS Journal</i> , 2000, 267, 7109-7117.	0.2	33
155	Comparative Enzyme Kinetics of Two Allelic Forms of Barley (<i>Hordeum vulgare</i> L.) Beta -amylase. <i>Journal of Cereal Science</i> , 2000, 31, 335-344.	1.8	33
156	A Transgenic Transcription Factor (TaDREB3) in Barley Affects the Expression of MicroRNAs and Other Small Non-Coding RNAs. <i>PLoS ONE</i> , 2012, 7, e42030.	1.1	33
157	Isolation and characterization of a genomic sequence of maize coding for a zein gene. <i>Molecular Genetics and Genomics</i> , 1981, 182, 440-444.	2.4	32
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