

Robbie Waugh

List of Publications by Year in descending order

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Version: 2024-02-01

180
papers

19,990
citations

18482

62
h-index

11939

134
g-index

197
all docs

197
docs citations

197
times ranked

14385
citing authors

#	ARTICLE	IF	CITATIONS
1	The proteome of developing barley anthers during meiotic prophase I. <i>Journal of Experimental Botany</i> , 2022, 73, 1464-1482.	4.8	3
2	Grain dispersal mechanism in cereals arose from a genome duplication followed by changes in spatial expression of genes involved in pollen development. <i>Theoretical and Applied Genetics</i> , 2022, 135, 1263-1277.	3.6	1
3	Genome-Wide Association Study for Resistance to <i>Rhynchosporium</i> in a Diverse Collection of Spring Barley Germplasm. <i>Agronomy</i> , 2022, 12, 782.	3.0	2
4	Barley (<i>Hordeum Vulgare</i>) Anther and Meicyte RNA Sequencing: Mapping Sequencing Reads and Downstream Data Analyses. <i>Methods in Molecular Biology</i> , 2022, 2484, 291-311.	0.9	2
5	The value of genotype-specific reference for transcriptome analyses in barley. <i>Life Science Alliance</i> , 2022, 5, e202101255.	2.8	2
6	The genome and gene editing system of sea barleygrass provide a novel platform for cereal domestication and stress tolerance studies. <i>Plant Communications</i> , 2022, 3, 100333.	7.7	8
7	<scp>BaRTv2</scp>: a highly resolved barley reference transcriptome for accurate transcript-specific <scp>RNA</scp>seq quantification. <i>Plant Journal</i> , 2022, 111, 1183-1202.	5.7	17
8	Identifying plant genes shaping microbiota composition in the barley rhizosphere. <i>Nature Communications</i> , 2022, 13, .	12.8	44
9	3D RNA-seq: a powerful and flexible tool for rapid and accurate differential expression and alternative splicing analysis of RNA-seq data for biologists. <i>RNA Biology</i> , 2021, 18, 1574-1587.	3.1	58
10	The effect of heat stress on sugar beet recombination. <i>Theoretical and Applied Genetics</i> , 2021, 134, 81-93.	3.6	5
11	EORNA, a barley gene and transcript abundance database. <i>Scientific Data</i> , 2021, 8, 90.	5.3	20
12	Ubiquitination in Plant Meiosis: Recent Advances and High Throughput Methods. <i>Frontiers in Plant Science</i> , 2021, 12, 667314.	3.6	6
13	MADS1 maintains barley spike morphology at high ambient temperatures. <i>Nature Plants</i> , 2021, 7, 1093-1107.	9.3	35
14	Downregulation of Barley Regulator of Telomere Elongation Helicase 1 Alters the Distribution of Meiotic Crossovers. <i>Frontiers in Plant Science</i> , 2021, 12, 745070.	3.6	2
15	A single residue deletion in the barley HKT1;5 P189 variant restores plasma membrane localisation but not Na ⁺ conductance. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2021, 1863, 183669.	2.6	5
16	Genome-wide association study reveals the genetic complexity of fructan accumulation patterns in barley grain. <i>Journal of Experimental Botany</i> , 2021, 72, 2383-2402.	4.8	17
17	The barley immune receptor Mla recognizes multiple pathogens and contributes to host range dynamics. <i>Nature Communications</i> , 2021, 12, 6915.	12.8	29
18	An Induced Mutation in HvRECQL4 Increases the Overall Recombination and Restores Fertility in a Barley HvMLH3 Mutant Background. <i>Frontiers in Plant Science</i> , 2021, 12, 706560.	3.6	8

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19	The barley pan-genome reveals the hidden legacy of mutation breeding. <i>Nature</i> , 2020, 588, 284-289.	27.8	314
20	Dissecting new genetic components of salinity tolerance in two-row spring barley at the vegetative and reproductive stages. <i>PLoS ONE</i> , 2020, 15, e0236037.	2.5	25
21	Association mapping identifies quantitative trait loci (QTL) for digestibility in rice straw. <i>Biotechnology for Biofuels</i> , 2020, 13, 165.	6.2	7
22	Mobilizing Crop Biodiversity. <i>Molecular Plant</i> , 2020, 13, 1341-1344.	8.3	50
23	Targeted mutation of barley (1,3;1,4)- α -glucan synthases reveals complex relationships between the storage and cell wall polysaccharide content. <i>Plant Journal</i> , 2020, 104, 1009-1022.	5.7	35
24	Association mapping of malting quality traits in UK spring and winter barley cultivar collections. <i>Theoretical and Applied Genetics</i> , 2020, 133, 2567-2582.	3.6	23
25	Development of barley introgression lines carrying the leaf rust resistance genes <i>Rph1</i> to <i>Rph15</i> . <i>Crop Science</i> , 2020, 60, 282-302.	1.8	11
26	Segmental duplications are hot spots of copy number variants affecting barley gene content. <i>Plant Journal</i> , 2020, 103, 1073-1088.	5.7	6
27	A Genome Assembly of the Barley Transformation Reference™ Cultivar Golden Promise. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1823-1827.	1.8	61
28	Barley Anther and Meiocyte Transcriptome Dynamics in Meiotic Prophase I. <i>Frontiers in Plant Science</i> , 2020, 11, 619404.	3.6	19
29	Following the Formation of Synaptonemal Complex Formation in Wheat and Barley by High-Resolution Microscopy. <i>Methods in Molecular Biology</i> , 2020, 2061, 207-215.	0.9	5
30	A Modular Tray Growth System for Barley. <i>Methods in Molecular Biology</i> , 2020, 2061, 367-379.	0.9	6
31	Barley sodium content is regulated by natural variants of the Na ⁺ transporter HvHKT1;5. <i>Communications Biology</i> , 2020, 3, 258.	4.4	21
32	Title is missing!. , 2020, 15, e0236037.		0
33	Title is missing!. , 2020, 15, e0236037.		0
34	Title is missing!. , 2020, 15, e0236037.		0
35	Title is missing!. , 2020, 15, e0236037.		0
36	RNAi suppression of barley caffeic acid O-methyltransferase modifies lignin despite redundancy in the gene family. <i>Plant Biotechnology Journal</i> , 2019, 17, 594-607.	8.3	37

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37	A highly mutagenised barley (cv. Golden Promise) TILLING population coupled with strategies for screening-by-sequencing. <i>Plant Methods</i> , 2019, 15, 99.	4.3	39
38	Harnessing the potential of germplasm collections. <i>Nature Genetics</i> , 2019, 51, 200-201.	21.4	53
39	Exome sequences and multi-environment field trials elucidate the genetic basis of adaptation in barley. <i>Plant Journal</i> , 2019, 99, 1172-1191.	5.7	50
40	A Comparison of Mainstream Genotyping Platforms for the Evaluation and Use of Barley Genetic Resources. <i>Frontiers in Plant Science</i> , 2019, 10, 544.	3.6	66
41	APETALA2 control of barley internode elongation. <i>Development (Cambridge)</i> , 2019, 146, .	2.5	36
42	Application of a Sensitive and Reproducible Label-Free Proteomic Approach to Explore the Proteome of Individual Meiotic-Phase Barley Anthers. <i>Frontiers in Plant Science</i> , 2019, 10, 393.	3.6	12
43	desynaptic5 carries a spontaneous semi-dominant mutation affecting Disrupted Meiotic cDNA 1 in barley. <i>Journal of Experimental Botany</i> , 2019, 70, 2683-2698.	4.8	24
44	Tracing the ancestry of modern bread wheats. <i>Nature Genetics</i> , 2019, 51, 905-911.	21.4	230
45	Barley grain (1,3;1,4)- β -glucan content: effects of transcript and sequence variation in genes encoding the corresponding synthase and endohydrolase enzymes. <i>Scientific Reports</i> , 2019, 9, 17250.	3.3	24
46	BaRTv1.0: an improved barley reference transcript dataset to determine accurate changes in the barley transcriptome using RNA-seq. <i>BMC Genomics</i> , 2019, 20, 968.	2.8	50
47	TRITEX: chromosome-scale sequence assembly of Triticeae genomes with open-source tools. <i>Genome Biology</i> , 2019, 20, 284.	8.8	179
48	Characterisation of barley resistance to rhynchosporium on chromosome 6HS. <i>Theoretical and Applied Genetics</i> , 2019, 132, 1089-1107.	3.6	13
49	Exome Capture for Variant Discovery and Analysis in Barley. <i>Methods in Molecular Biology</i> , 2019, 1900, 283-310.	0.9	5
50	Preparation of Barley Pollen Mother Cells for Confocal and Super Resolution Microscopy. <i>Methods in Molecular Biology</i> , 2019, 1900, 167-179.	0.9	8
51	Interaction between row-type genes in barley controls meristem determinacy and reveals novel routes to improved grain. <i>New Phytologist</i> , 2019, 221, 1950-1965.	7.3	39
52	<i>ELIGULUM-A</i> Regulates Lateral Branch and Leaf Development in Barley. <i>Plant Physiology</i> , 2018, 176, 2750-2760.	4.8	22
53	Genetic dissection of quantitative and qualitative traits using a minimum set of barley Recombinant Chromosome Substitution Lines. <i>BMC Plant Biology</i> , 2018, 18, 340.	3.6	7
54	The Expressed Portion of the Barley Genome. <i>Compendium of Plant Genomes</i> , 2018, , 89-107.	0.5	0

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55	Resistance to <i>Rhynchosporium commune</i> in a collection of European spring barley germplasm. <i>Theoretical and Applied Genetics</i> , 2018, 131, 2513-2528.	3.6	17
56	The pseudogenes of barley. <i>Plant Journal</i> , 2018, 93, 502-514.	5.7	14
57	Reducing Stomatal Density in Barley Improves Drought Tolerance without Impacting on Yield. <i>Plant Physiology</i> , 2017, 174, 776-787.	4.8	267
58	A chromosome conformation capture ordered sequence of the barley genome. <i>Nature</i> , 2017, 544, 427-433.	27.8	1,365
59	Construction of a map-based reference genome sequence for barley, <i>Hordeum vulgare</i> L.. <i>Scientific Data</i> , 2017, 4, 170044.	5.3	130
60	Barley SIX-ROWED SPIKE3 encodes a putative Jumonji C-type H3K9me2/me3 demethylase that represses lateral spikelet fertility. <i>Nature Communications</i> , 2017, 8, 936.	12.8	78
61	Extreme Suppression of Lateral Floret Development by a Single Amino Acid Change in the VRS1 Transcription Factor. <i>Plant Physiology</i> , 2017, 175, 1720-1731.	4.8	49
62	Evaluation and improvement of the regulatory inference for large co-expression networks with limited sample size. <i>BMC Systems Biology</i> , 2017, 11, 62.	3.0	14
63	Observation of Extensive Chromosome Axis Remodeling during the "Diffuse-Phase" of Meiosis in Large Genome Cereals. <i>Frontiers in Plant Science</i> , 2017, 8, 1235.	3.6	30
64	Development and Evaluation of a Barley 50k iSelect SNP Array. <i>Frontiers in Plant Science</i> , 2017, 8, 1792.	3.6	257
65	Levels of Intra-specific AFLP Diversity in Tuber-Bearing Potato Species with Different Breeding Systems and Ploidy Levels. <i>Frontiers in Genetics</i> , 2017, 8, 119.	2.3	14
66	A Genome Wide Association Study of arabinoxylan content in 2-row spring barley grain. <i>PLoS ONE</i> , 2017, 12, e0182537.	2.5	29
67	Alternative Splicing of Barley Clock Genes in Response to Low Temperature. <i>PLoS ONE</i> , 2016, 11, e0168028.	2.5	39
68	HvDep1 Is a Positive Regulator of Culm Elongation and Grain Size in Barley and Impacts Yield in an Environment-Dependent Manner. <i>PLoS ONE</i> , 2016, 11, e0168924.	2.5	77
69	SNP-Based QTL Mapping of 15 Complex Traits in Barley under Rain-Fed and Well-Watered Conditions by a Mixed Modeling Approach. <i>Frontiers in Plant Science</i> , 2016, 7, 909.	3.6	46
70	A homolog of Blade-On-Petiole 1 and 2 (BOP1/2) controls internode length and homeotic changes of the barley inflorescence. <i>Plant Physiology</i> , 2016, 171, pp.00124.2016.	4.8	41
71	Exome sequencing of geographically diverse barley landraces and wild relatives gives insights into environmental adaptation. <i>Nature Genetics</i> , 2016, 48, 1024-1030.	21.4	259
72	Genomic analysis of 6,000-year-old cultivated grain illuminates the domestication history of barley. <i>Nature Genetics</i> , 2016, 48, 1089-1093.	21.4	122

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73	A spontaneous mutation in MutLâ€Homolog 3 (Hv<sc>MLH</sc>3) affects synapsis and crossover resolution in the barley desynaptic mutant <i>des10</i>. <i>New Phytologist</i> , 2016, 212, 693-707.	7.3	44
74	The Dynamics of Transcript Abundance during Cellularization of Developing Barley Endosperm. <i>Plant Physiology</i> , 2016, 170, 1549-1565.	4.8	47
75	The INDETERMINATE DOMAIN Protein BROAD LEAF1 Limits Barley Leaf Width by Restricting Lateral Proliferation. <i>Current Biology</i> , 2016, 26, 903-909.	3.9	37
76	The Maltase Involved in Starch Metabolism in Barley Endosperm Is Encoded by a Single Gene. <i>PLoS ONE</i> , 2016, 11, e0151642.	2.5	19
77	Genetic Diversity and Genome Wide Association Study of Î²-Glucan Content in Tetraploid Wheat Grains. <i>PLoS ONE</i> , 2016, 11, e0152590.	2.5	40
78	The effect of temperature on the male and female recombination landscape of barley. <i>New Phytologist</i> , 2015, 208, 421-429.	7.3	105
79	The Barley <i>Ucn4</i> Gene Encodes a BLADE-ON-PETIOLE-Like Protein That Controls Tillering and Leaf Patterning. <i>Plant Physiology</i> , 2015, 168, 164-174.	4.8	85
80	Evolutionary Relationships Among Barley and Arabidopsis Core Circadian Clock and Clock-Associated Genes. <i>Journal of Molecular Evolution</i> , 2015, 80, 108-119.	1.8	59
81	Evolution of the Grain Dispersal System in Barley. <i>Cell</i> , 2015, 162, 527-539.	28.9	265
82	Evolutionary Dynamics of the Cellulose Synthase Gene Superfamily in Grasses. <i>Plant Physiology</i> , 2015, 168, 968-983.	4.8	55
83	A whole-genome shotgun approach for assembling and anchoring the hexaploid bread wheat genome. <i>Genome Biology</i> , 2015, 16, 26.	8.8	256
84	Barley: a translational model for adaptation to climate change. <i>New Phytologist</i> , 2015, 206, 913-931.	7.3	257
85	A Genome-Wide Association Study for Culm Cellulose Content in Barley Reveals Candidate Genes Co-Expressed with Members of the CELLULOSE SYNTHASE A Gene Family. <i>PLoS ONE</i> , 2015, 10, e0130890.	2.5	24
86	Genome Wide Association Mapping for Arabinoxylan Content in a Collection of Tetraploid Wheats. <i>PLoS ONE</i> , 2015, 10, e0132787.	2.5	56
87	The USDA Barley Core Collection: Genetic Diversity, Population Structure, and Potential for Genome-Wide Association Studies. <i>PLoS ONE</i> , 2014, 9, e94688.	2.5	188
88	The Synaptonemal Complex Protein ZYP1 Is Required for Imposition of Meiotic Crossovers in Barley. <i>Plant Cell</i> , 2014, 26, 729-740.	6.6	88
89	The lowâ€recombining pericentromeric region of barley restricts gene diversity and evolution but not gene expression. <i>Plant Journal</i> , 2014, 79, 981-992.	5.7	30
90	Modulation of Meiotic Recombination. <i>Biotechnology in Agriculture and Forestry</i> , 2014, , 311-329.	0.2	10

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91	A genome wide association scan for (1,3;1,4)- β -glucan content in the grain of contemporary 2-row Spring and Winter barleys. BMC Genomics, 2014, 15, 907.	2.8	57
92	Barley has two peroxisomal ABC transporters with multiple functions in β -oxidation. Journal of Experimental Botany, 2014, 65, 4833-4847.	4.8	26
93	An evaluation of genotyping by sequencing (GBS) to map the Breviaristatum-e (ari-e) locus in cultivated barley. BMC Genomics, 2014, 15, 104.	2.8	145
94	In silico identification and characterization of conserved plant microRNAs in barley. Open Life Sciences, 2014, 9, 841-852.	1.4	1
95	A Sequence-Ready Physical Map of Barley Anchored Genetically by Two Million Single-Nucleotide Polymorphisms. Plant Physiology, 2014, 164, 412-423.	4.8	77
96	Genetic Diversity and Ecological Niche Modelling of Wild Barley: Refugia, Large-Scale Post-LGM Range Expansion and Limited Mid-Future Climate Threats?. PLoS ONE, 2014, 9, e86021.	2.5	46
97	The Barley Genome Sequence Assembly Reveals Three Additional Members of the CslF (1,3;1,4)- β -Glucan Synthase Gene Family. PLoS ONE, 2014, 9, e90888.	2.5	39
98	Barley whole exome capture: a tool for genomic research in the genus <i>Hordeum</i> and beyond. Plant Journal, 2013, 76, 494-505.	5.7	260
99	Anchoring and ordering NGS contig assemblies by population sequencing (POPSEQ). Plant Journal, 2013, 76, 718-727.	5.7	264
100	FR-H3: a new QTL to assist in the development of fall-sown barley with superior low temperature tolerance. Theoretical and Applied Genetics, 2013, 126, 335-347.	3.6	49
101	Feeding the future. Nature, 2013, 499, 23-24.	27.8	464
102	Variation in the interaction between alleles of <i>HvAPETALA2</i> and microRNA172 determines the density of grains on the barley inflorescence. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 16675-16680.	7.1	121
103	A physical, genetic and functional sequence assembly of the barley genome. Nature, 2012, 491, 711-716.	27.8	1,416
104	Spatiotemporal Asymmetry of the Meiotic Program Underlies the Predominantly Distal Distribution of Meiotic Crossovers in Barley. Plant Cell, 2012, 24, 4096-4109.	6.6	185
105	Natural variation in a homolog of Antirrhinum CENTRORADIALIS contributed to spring growth habit and environmental adaptation in cultivated barley. Nature Genetics, 2012, 44, 1388-1392.	21.4	477
106	Induced mutations in circadian clock regulator <i>Mat-a</i> facilitated short-season adaptation and range extension in cultivated barley. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 4326-4331.	7.1	163
107	Analysis of the barley bract suppression gene Trd1. Theoretical and Applied Genetics, 2012, 125, 33-45.	3.6	35
108	Genome-wide association mapping of agronomic and morphologic traits in highly structured populations of barley cultivars. Theoretical and Applied Genetics, 2012, 124, 233-246.	3.6	122

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109	High resolution mapping of Dense spike-ar (dsp.ar) to the genetic centromere of barley chromosome 7H. <i>Theoretical and Applied Genetics</i> , 2012, 124, 373-384.	3.6	39
110	Genetic Dissection of Barley Morphology and Development. <i>Plant Physiology</i> , 2011, 155, 617-627.	4.8	188
111	Genome sequence and analysis of the tuber crop potato. <i>Nature</i> , 2011, 475, 189-195.	27.8	1,912
112	Unlocking the Barley Genome by Chromosomal and Comparative Genomics. <i>Plant Cell</i> , 2011, 23, 1249-1263.	6.6	448
113	Highly parallel gene-to-BAC addressing using microarrays. <i>BioTechniques</i> , 2011, 50, 165-174.	1.8	8
114	An exceptionally high nucleotide and haplotype diversity and a signature of positive selection for the eIF4E resistance gene in barley are revealed by allele mining and phylogenetic analyses of natural populations. <i>Molecular Ecology</i> , 2011, 20, no-no.	3.9	48
115	Analysis of >1000 single nucleotide polymorphisms in geographically matched samples of landrace and wild barley indicates secondary contact and chromosome-level differences in diversity around domestication genes. <i>New Phytologist</i> , 2011, 191, 564-578.	7.3	84
116	INTERMEDIUM-C, a modifier of lateral spikelet fertility in barley, is an ortholog of the maize domestication gene TEOSINTE BRANCHED 1. <i>Nature Genetics</i> , 2011, 43, 169-172.	21.4	302
117	Patterns of polymorphism and linkage disequilibrium in cultivated barley. <i>Theoretical and Applied Genetics</i> , 2011, 122, 523-531.	3.6	41
118	Combining genetical genomics and bulked segregant analysis-based differential expression: an approach to gene localization. <i>Theoretical and Applied Genetics</i> , 2011, 122, 1375-1383.	3.6	20
119	Crops that feed the world 4. Barley: a resilient crop? Strengths and weaknesses in the context of food security. <i>Food Security</i> , 2011, 3, 141-178.	5.3	216
120	Exploiting induced variation to dissect quantitative traits in barley. <i>Biochemical Society Transactions</i> , 2010, 38, 683-688.	3.4	11
121	Expression quantitative trait loci analysis in plants. <i>Plant Biotechnology Journal</i> , 2010, 8, 10-27.	8.3	90
122	An eQTL Analysis of Partial Resistance to <i>Puccinia hordei</i> in Barley. <i>PLoS ONE</i> , 2010, 5, e8598.	2.5	77
123	Genome-wide association mapping to candidate polymorphism resolution in the unsequenced barley genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 21611-21616.	7.1	259
124	An Integrated Resource for Barley Linkage Map and Malting Quality QTL Alignment. <i>Plant Genome</i> , 2009, 2, .	2.8	116
125	The International Barley Sequencing Consortium "At the Threshold of Efficient Access to the Barley Genome". <i>Plant Physiology</i> , 2009, 149, 142-147.	4.8	195
126	Robust Detection and Genotyping of Single Feature Polymorphisms from Gene Expression Data. <i>PLoS Computational Biology</i> , 2009, 5, e1000317.	3.2	16

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127	The emergence of whole genome association scans in barley. <i>Current Opinion in Plant Biology</i> , 2009, 12, 218-222.	7.1	138
128	Development and implementation of high-throughput SNP genotyping in barley. <i>BMC Genomics</i> , 2009, 10, 582.	2.8	570
129	The 172-kb genomic DNA region of the <i>O. rufipogon</i> yld1.1 locus: comparative sequence analysis with <i>O. sativa</i> ssp. <i>japonica</i> and <i>O. sativa</i> ssp. <i>indica</i> . <i>Functional and Integrative Genomics</i> , 2009, 9, 97-108.	3.5	3
130	Reconstruction of monocotelydoneous proto-chromosomes reveals faster evolution in plants than in animals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 14908-14913.	7.1	144
131	QTL mapping of yield, agronomic and quality traits in tetraploid potato (<i>Solanum tuberosum</i> subsp.) Tj ETQq1 1 0.784314 rgBT / Over	3.6	148
132	Exploiting regulatory variation to identify genes underlying quantitative resistance to the wheat stem rust pathogen <i>Puccinia graminis</i> f. sp. <i>tritici</i> in barley. <i>Theoretical and Applied Genetics</i> , 2008, 117, 261-272.	3.6	43
133	Gene expression quantitative trait locus analysis of 16,000 barley genes reveals a complex pattern of genome-wide transcriptional regulation. <i>Plant Journal</i> , 2008, 53, 90-101.	5.7	158
134	Tissue-dependent limited pleiotropy affects gene expression in barley. <i>Plant Journal</i> , 2008, 56, 287-296.	5.7	26
135	Cereal breeding takes a walk on the wild side. <i>Trends in Genetics</i> , 2008, 24, 24-32.	6.7	355
136	Meeting Report The Aaronsohn-ITMI International Conference. <i>Israel Journal of Plant Sciences</i> , 2007, 55, 315-319.	0.5	1
137	Harvesting the potential of induced biological diversity. <i>Trends in Plant Science</i> , 2006, 11, 71-79.	8.8	54
138	An atlas of gene expression from seed to seed through barley development. <i>Functional and Integrative Genomics</i> , 2006, 6, 202-211.	3.5	138
139	Construction of a 10,000-Marker Ultradense Genetic Recombination Map of Potato: Providing a Framework for Accelerated Gene Isolation and a Genomewide Physical Map. <i>Genetics</i> , 2006, 173, 1075-1087.	2.9	212
140	Recent history of artificial outcrossing facilitates whole-genome association mapping in elite inbred crop varieties. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 18656-18661.	7.1	309
141	Evidence that the recessive bymovirus resistance locus <i>rym4</i> in barley corresponds to the eukaryotic translation initiation factor 4E gene. <i>Molecular Plant Pathology</i> , 2005, 6, 449-458.	4.2	115
142	Characterisation and functional analysis of two barley caleosins expressed during barley caryopsis development. <i>Planta</i> , 2005, 221, 513-522.	3.2	27
143	Genome-wide SNP discovery and linkage analysis in barley based on genes responsive to abiotic stress. <i>Molecular Genetics and Genomics</i> , 2005, 274, 515-527.	2.1	250
144	Direct targeting and rapid isolation of BAC clones spanning a defined chromosome region. <i>Functional and Integrative Genomics</i> , 2005, 5, 97-103.	3.5	47

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145	A comparative analysis of transcript abundance using SAGE and Affymetrix arrays. <i>Functional and Integrative Genomics</i> , 2005, 5, 163-174.	3.5	36
146	A single domestication for potato based on multilocus amplified fragment length polymorphism genotyping. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 14694-14699.	7.1	382
147	Interval Mapping of Quantitative Trait Loci for Resistance to Late Blight [<i>Phytophthora infestans</i> (Mont.) de Bary], Height and Maturity in a Tetraploid Population of Potato (<i>Solanum tuberosum</i> subsp.) <i>Tj ETQq1 20.7843140gBT /O</i>	2.9	140
148	A structured mutant population for forward and reverse genetics in Barley (<i>Hordeum vulgare</i>) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf</i>	5.7	339
149	A barley cultivation-associated polymorphism conveys resistance to powdery mildew. <i>Nature</i> , 2004, 430, 887-891.	27.8	202
150	Dissection and analysis of quantitative disease resistance in tetraploid potato. <i>Euphytica</i> , 2004, 137, 13-18.	1.2	15
151	Genetical dissection of H3-mediated polygenic PCN resistance in a heterozygous autotetraploid potato population. <i>Molecular Breeding</i> , 2004, 14, 105-116.	2.1	45
152	HAPPY mapping in a plant genome: reconstruction and analysis of a high-resolution physical map of a 1.9-Mbp region of <i>Arabidopsis thaliana</i> chromosome 4. <i>Plant Biotechnology Journal</i> , 2003, 1, 23-31.	8.3	30
153	Toward a Marker-Dense Meiotic Map of the Potato Genome: Lessons From Linkage Group I. <i>Genetics</i> , 2003, 165, 2107-2116.	2.9	63
154	Title is missing!. <i>Molecular Breeding</i> , 2000, 6, 553-568.	2.1	124
155	UK CropNet: a collection of databases and bioinformatics resources for crop plant genomics. <i>Nucleic Acids Research</i> , 2000, 28, 104-107.	14.5	16
156	Computational and Experimental Characterization of Physically Clustered Simple Sequence Repeats in Plants. <i>Genetics</i> , 2000, 156, 847-854.	2.9	369
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