

Cristobal Uauy

List of Publications by Year in descending order

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Version: 2024-02-01

135
papers

18,659
citations

18887

64
h-index

16791

127
g-index

179
all docs

179
docs citations

179
times ranked

14010
citing authors

#	ARTICLE	IF	CITATIONS
1	Pathogenomic analyses of <i>Puccinia striiformis</i> f. sp. <i>tritici</i> supports a close genetic relationship between South and East Africa. <i>Plant Pathology</i> , 2022, 71, 279-288.	1.2	5
2	Distribution of <i>Puccinia striiformis</i> f. sp. <i>tritici</i> Races and Virulence in Wheat Growing Regions of Kenya from 1970 to 2014. <i>Plant Disease</i> , 2022, 106, 701-710.	0.7	3
3	Population genomic analysis of <i>Aegilops tauschii</i> identifies targets for bread wheat improvement. <i>Nature Biotechnology</i> , 2022, 40, 422-431.	9.4	102
4	Characterization of wheat lacking B-type starch granules. <i>Journal of Cereal Science</i> , 2022, 104, 103398.	1.8	8
5	High expression of the MADS-box gene <i>VRT2</i> increases the number of rudimentary basal spikelets in wheat. <i>Plant Physiology</i> , 2022, 189, 1536-1552.	2.3	17
6	Trend, population structure, and trait mapping from 15 years of national varietal trials of UK winter wheat. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	5
7	Pathogen-induced biosynthetic pathways encode defense-related molecules in bread wheat. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2123299119.	3.3	30
8	MicroRNA-resistant alleles of <i>HOMEBOX DOMAIN-2</i> modify inflorescence branching and increase grain protein content of wheat. <i>Science Advances</i> , 2022, 8, eabn5907.	4.7	19
9	The <i>Triticum ispahanicum</i> elongated glume locus P2 maps to chromosome 6A and is associated with the ectopic expression of SVP-A1. <i>Theoretical and Applied Genetics</i> , 2022, , .	1.8	4
10	FANCM promotes class I interfering crossovers and suppresses class II non-interfering crossovers in wheat meiosis. <i>Nature Communications</i> , 2022, 13, .	5.8	21
11	New insights into homoeologous copy number variations in the hexaploid wheat genome. <i>Plant Genome</i> , 2021, 14, e20069.	1.6	16
12	Identification of <i>Fusarium</i> head blight resistance loci in two Brazilian wheat mapping populations. <i>PLoS ONE</i> , 2021, 16, e0248184.	1.1	7
13	Evaluation of the susceptibility of modern, wild, ancestral, and mutational wheat lines to <i>Septoria tritici</i> blotch disease. <i>Plant Pathology</i> , 2021, 70, 1123-1137.	1.2	2
14	Wheat root systems as a breeding target for climate resilience. <i>Theoretical and Applied Genetics</i> , 2021, 134, 1645-1662.	1.8	74
15	The membrane-localized protein kinase MAP4K4/TOT3 regulates thermomorphogenesis. <i>Nature Communications</i> , 2021, 12, 2842.	5.8	30
16	Genome-wide association mapping identifies yellow rust resistance loci in Ethiopian durum wheat germplasm. <i>PLoS ONE</i> , 2021, 16, e0243675.	1.1	12
17	Ectopic expression of <i>Triticum polonicum</i> <i>VRT-A2</i> underlies elongated glumes and grains in hexaploid wheat in a dosage-dependent manner. <i>Plant Cell</i> , 2021, 33, 2296-2319.	3.1	36
18	A robust KASP marker for selection of four pairs of linked leaf rust and stripe rust resistance genes introgressed on chromosome arm 5DS from different wheat genomes. <i>Molecular Biology Reports</i> , 2021, 48, 5209-5216.	1.0	2

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19	<i>ENHANCED GRAVITROPISM 2</i> encodes a STERILE ALPHA MOTIF-containing protein that controls root growth angle in barley and wheat. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	32
20	Crossover-active regions of the wheat genome are distinguished by DMC1, the chromosome axis, H3K27me3, and signatures of adaptation. <i>Genome Research</i> , 2021, 31, 1614-1628.	2.4	18
21	Wheat in vivo RNA structure landscape reveals a prevalent role of RNA structure in modulating translational subgenome expression asymmetry. <i>Genome Biology</i> , 2021, 22, 326.	3.8	12
22	<i>Aegilops umbellulata</i> introgression carrying leaf rust and stripe rust resistance genes Lr76 and Yr70 located to 9.47-Mb region on 5DS telomeric end through a combination of chromosome sorting and sequencing. <i>Theoretical and Applied Genetics</i> , 2020, 133, 903-915.	1.8	26
23	Yield reduction historically associated with the <i>Aegilops ventricosa</i> 7DV introgression is genetically and physically distinct from the eyespot resistance gene Pch1. <i>Theoretical and Applied Genetics</i> , 2020, 133, 707-717.	1.8	4
24	Insights into the resistance of a synthetically-derived wheat to <i>Septoria tritici</i> blotch disease: less is more. <i>BMC Plant Biology</i> , 2020, 20, 407.	1.6	6
25	A heat-shock inducible system for flexible gene expression in cereals. <i>Plant Methods</i> , 2020, 16, 137.	1.9	5
26	A carbohydrate-binding protein, B-GRANULE CONTENT 1, influences starch granule size distribution in a dose-dependent manner in polyploid wheat. <i>Journal of Experimental Botany</i> , 2020, 71, 105-115.	2.4	36
27	Allelic diversity study of functional genes in East Africa bread wheat highlights opportunities for genetic improvement. <i>Molecular Breeding</i> , 2020, 40, 1.	1.0	4
28	Multiple wheat genomes reveal global variation in modern breeding. <i>Nature</i> , 2020, 588, 277-283.	13.7	513
29	A haplotype-led approach to increase the precision of wheat breeding. <i>Communications Biology</i> , 2020, 3, 712.	2.0	68
30	Comparative Genomics and Functional Studies of Wheat BED-NLR Loci. <i>Genes</i> , 2020, 11, 1406.	1.0	7
31	The Wheat GENIE3 Network Provides Biologically-Relevant Information in Polyploid Wheat. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3675-3686.	0.8	21
32	Copy number variation of <i>TdDof</i> controls solid-stemmed architecture in wheat. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 28708-28718.	3.3	33
33	Dissecting the genetic basis of wheat blast resistance in the Brazilian wheat cultivar BR 18-Terena. <i>BMC Plant Biology</i> , 2020, 20, 398.	1.6	30
34	Diversity analysis of 80,000 wheat accessions reveals consequences and opportunities of selection footprints. <i>Nature Communications</i> , 2020, 11, 4572.	5.8	129
35	Strategies to improve wheat for human health. <i>Nature Food</i> , 2020, 1, 475-480.	6.2	54
36	Genetic Characterization of a Wheat Association Mapping Panel Relevant to Brazilian Breeding Using a High-Density Single Nucleotide Polymorphism Array. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2229-2239.	0.8	12

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37	Discovery and characterisation of a new leaf rust resistance gene introgressed in wheat from wild wheat <i>Aegilops peregrina</i> . <i>Scientific Reports</i> , 2020, 10, 7573.	1.6	13
38	The NLR-Annotator Tool Enables Annotation of the Intracellular Immune Receptor Repertoire. <i>Plant Physiology</i> , 2020, 183, 468-482.	2.3	147
39	Enabling reusability of plant phenomic datasets with MIAPPE 1.1. <i>New Phytologist</i> , 2020, 227, 260-273.	3.5	84
40	Agricultural Selection of Wheat Has Been Shaped by Plant-Microbe Interactions. <i>Frontiers in Microbiology</i> , 2020, 11, 132.	1.5	53
41	Exome sequencing of bulked segregants identified a novel TaMKK3-A allele linked to the wheat ERA8 ABA-hypersensitive germination phenotype. <i>Theoretical and Applied Genetics</i> , 2020, 133, 719-736.	1.8	17
42	LYS3 encodes a prolamins-box-binding transcription factor that controls embryo growth in barley and wheat. <i>Journal of Cereal Science</i> , 2020, 93, 102965.	1.8	14
43	A roadmap for gene functional characterisation in crops with large genomes: Lessons from polyploid wheat. <i>ELife</i> , 2020, 9, .	2.8	78
44	Applying the latest advances in genomics and phenomics for trait discovery in polyploid wheat. <i>Plant Journal</i> , 2019, 97, 56-72.	2.8	83
45	Genetic Screening for Mutants with Altered Seminal Root Numbers in Hexaploid Wheat Using a High-Throughput Root Phenotyping Platform. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2799-2809.	0.8	17
46	Development of mlo-based resistance in tetraploid wheat against wheat powdery mildew. <i>Theoretical and Applied Genetics</i> , 2019, 132, 3009-3022.	1.8	16
47	Identification of a Dominant Chlorosis Phenotype Through a Forward Screen of the <i>Triticum turgidum</i> cv. Kronos TILLING Population. <i>Frontiers in Plant Science</i> , 2019, 10, 963.	1.7	18
48	A Co-Expression Network in Hexaploid Wheat Reveals Mostly Balanced Expression and Lack of Significant Gene Loss of Homeologous Meiotic Genes Upon Polyploidization. <i>Frontiers in Plant Science</i> , 2019, 10, 1325.	1.7	24
49	Conserved residues in the wheat (<i>Triticum aestivum</i>) NAM-A1 NAC domain are required for protein binding and when mutated lead to delayed peduncle and flag leaf senescence. <i>BMC Plant Biology</i> , 2019, 19, 407.	1.6	19
50	Fine mapping of <i>Aegilops peregrina</i> co-segregating leaf and stripe rust resistance genes to distal-most end of 5DS. <i>Theoretical and Applied Genetics</i> , 2019, 132, 1473-1485.	1.8	8
51	Global transcriptome analysis uncovers the gene co-expression regulation network and key genes involved in grain development of wheat (<i>Triticum aestivum</i> L.). <i>Functional and Integrative Genomics</i> , 2019, 19, 853-866.	1.4	14
52	Identification of Transcription Factors Regulating Senescence in Wheat through Gene Regulatory Network Modelling. <i>Plant Physiology</i> , 2019, 180, 1740-1755.	2.3	73
53	Improving wheat as a source of iron and zinc for global nutrition. <i>Nutrition Bulletin</i> , 2019, 44, 53-59.	0.8	69
54	Genome-Wide Association Mapping of Grain Micronutrients Concentration in <i>Aegilops tauschii</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 54.	1.7	45

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55	A reductionist approach to dissecting grain weight and yield in wheat. <i>Journal of Integrative Plant Biology</i> , 2019, 61, 337-358.	4.1	122
56	Hotspots in the genomic architecture of field drought responses in wheat as breeding targets. <i>Functional and Integrative Genomics</i> , 2019, 19, 295-309.	1.4	40
57	Wheat receptor-kinase-like protein <i>Stb6</i> controls gene-for-gene resistance to fungal pathogen <i>Zymoseptoria tritici</i> . <i>Nature Genetics</i> , 2018, 50, 368-374.	9.4	215
58	Speed breeding is a powerful tool to accelerate crop research and breeding. <i>Nature Plants</i> , 2018, 4, 23-29.	4.7	770
59	<i>Rht18</i> Semidwarfism in Wheat Is Due to Increased <i>GA 2-oxidase9</i> Expression and Reduced GA Content. <i>Plant Physiology</i> , 2018, 177, 168-180.	2.3	128
60	Speed breeding in growth chambers and glasshouses for crop breeding and model plant research. <i>Nature Protocols</i> , 2018, 13, 2944-2963.	5.5	286
61	Genome-Wide Transcription During Early Wheat Meiosis Is Independent of Synapsis, Ploidy Level, and the <i>Ph1</i> Locus. <i>Frontiers in Plant Science</i> , 2018, 9, 1791.	1.7	44
62	Heat in Wheat: Exploit Reverse Genetic Techniques to Discover New Alleles Within the <i>Triticum durum</i> <i>sHsp26</i> Family. <i>Frontiers in Plant Science</i> , 2018, 9, 1337.	1.7	38
63	Final grain weight is not limited by the activity of key starch-synthesising enzymes during grain filling in wheat. <i>Journal of Experimental Botany</i> , 2018, 69, 5461-5475.	2.4	38
64	Ubiquitin-related genes are differentially expressed in isogenic lines contrasting for pericarp cell size and grain weight in hexaploid wheat. <i>BMC Plant Biology</i> , 2018, 18, 22.	1.6	29
65	Barley <i>lys3</i> mutants are unique amongst shrunken-endosperm mutants in having abnormally large embryos. <i>Journal of Cereal Science</i> , 2018, 82, 16-24.	1.8	18
66	Gene editing and mutagenesis reveal inter-cultivar differences and additivity in the contribution of <i>TaGW2</i> homologues to grain size and weight in wheat. <i>Theoretical and Applied Genetics</i> , 2018, 131, 2463-2475.	1.8	142
67	BED-domain-containing immune receptors confer diverse resistance spectra to yellow rust. <i>Nature Plants</i> , 2018, 4, 662-668.	4.7	194
68	The transcriptional landscape of polyploid wheat. <i>Science</i> , 2018, 361, .	6.0	768
69	Shifting the limits in wheat research and breeding using a fully annotated reference genome. <i>Science</i> , 2018, 361, .	6.0	2,424
70	Impact of transposable elements on genome structure and evolution in bread wheat. <i>Genome Biology</i> , 2018, 19, 103.	3.8	226
71	Uncovering hidden variation in polyploid wheat. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E913-E921.	3.3	554
72	An improved assembly and annotation of the allohexaploid wheat genome identifies complete families of agronomic genes and provides genomic evidence for chromosomal translocations. <i>Genome Research</i> , 2017, 27, 885-896.	2.4	464

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73	Increased pericarp cell length underlies a major quantitative trait locus for grain weight in hexaploid wheat. <i>New Phytologist</i> , 2017, 215, 1026-1038.	3.5	103
74	Wheat genomics comes of age. <i>Current Opinion in Plant Biology</i> , 2017, 36, 142-148.	3.5	103
75	Genomic innovation for crop improvement. <i>Nature</i> , 2017, 543, 346-354.	13.7	301
76	Genome sequence and genetic diversity of European ash trees. <i>Nature</i> , 2017, 541, 212-216.	13.7	166
77	Plant Genomics: Unlocking the Genome of Wheat's Progenitor. <i>Current Biology</i> , 2017, 27, R1122-R1124.	1.8	6
78	Combining Traditional Mutagenesis with New High-Throughput Sequencing and Genome Editing to Reveal Hidden Variation in Polyploid Wheat. <i>Annual Review of Genetics</i> , 2017, 51, 435-454.	3.2	100
79	Exploiting the ZIP4 homologue within the wheat Ph1 locus has identified two lines exhibiting homoeologous crossover in wheat-wild relative hybrids. <i>Molecular Breeding</i> , 2017, 37, 95.	1.0	126
80	Genome-Wide Sequence and Expression Analysis of the NAC Transcription Factor Family in Polyploid Wheat. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3019-3029.	0.8	59
81	Wheat Vacuolar Iron Transporter TaVIT2 Transports Fe and Mn and Is Effective for Biofortification. <i>Plant Physiology</i> , 2017, 174, 2434-2444.	2.3	206
82	The eyespot resistance genes Pch1 and Pch2 of wheat are not homoeoloci. <i>Theoretical and Applied Genetics</i> , 2017, 130, 91-107.	1.8	15
83	Transfer of a starch phenotype from wild wheat to bread wheat by deletion of a locus controlling B-type starch granule content. <i>Journal of Experimental Botany</i> , 2017, 68, 5497-5509.	2.4	22
84	Genome-Wide Association Study of Grain Architecture in Wild Wheat <i>Aegilops tauschii</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 886.	1.7	114
85	Haplotype Analysis of the Pre-harvest Sprouting Resistance Locus Phs-A1 Reveals a Causal Role of TaMKK3-A in Global Germplasm. <i>Frontiers in Plant Science</i> , 2017, 8, 1555.	1.7	50
86	Systematic Investigation of FLOWERING LOCUS T-Like Poaceae Gene Families Identifies the Short-Day Expressed Flowering Pathway Gene, TaFT3 in Wheat (<i>Triticum aestivum</i> L.). <i>Frontiers in Plant Science</i> , 2016, 7, 857.	1.7	37
87	A Metabolic Gene Cluster in the Wheat <i>W1</i> and the Barley <i>Cer-cqu</i> Loci Determines Î²-Diketone Biosynthesis and Glaucousness. <i>Plant Cell</i> , 2016, 28, 1440-1460.	3.1	123
88	The host-pathogen interaction between wheat and yellow rust induces temporally coordinated waves of gene expression. <i>BMC Genomics</i> , 2016, 17, 380.	1.2	105
89	Identification and mapping of resistance to stem rust in the European winter wheat cultivars Spark and Rialto. <i>Molecular Breeding</i> , 2016, 36, 1.	1.0	2
90	A saturated SNP linkage map for the orange wheat blossom midge resistance gene Sm1. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1507-1517.	1.8	15

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91	The <i>Cer-cqu</i> gene cluster determines three key players in a β^2 -diketone synthase polyketide pathway synthesizing aliphatics in epicuticular waxes. <i>Journal of Experimental Botany</i> , 2016, 67, 2715-2730.	2.4	81
92	The wheat <i>Phs-A1</i> pre-harvest sprouting resistance locus delays the rate of seed dormancy loss and maps 0.3 cM distal to the <i>PM19</i> genes in UK germplasm. <i>Journal of Experimental Botany</i> , 2016, 67, 4169-4178.	2.4	53
93	A splice acceptor site mutation in <i>TaGW2-A1</i> increases thousand grain weight in tetraploid and hexaploid wheat through wider and longer grains. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1099-1112.	1.8	179
94	expVIP: a Customizable RNA-seq Data Analysis and Visualization Platform. <i>Plant Physiology</i> , 2016, 170, 2172-2186.	2.3	403
95	Genomics as the key to unlocking the polyploid potential of wheat. <i>New Phytologist</i> , 2015, 208, 1008-1022.	3.5	151
96	The Genetic Basis of Composite Spike Form in Barley and "Miracle-Wheat"™. <i>Genetics</i> , 2015, 201, 155-165.	1.2	109
97	Mutation Scanning in Wheat by Exon Capture and Next-Generation Sequencing. <i>PLoS ONE</i> , 2015, 10, e0137549.	1.1	65
98	Induction of targeted, heritable mutations in barley and <i>Brassica oleracea</i> using RNA-guided Cas9 nuclease. <i>Genome Biology</i> , 2015, 16, 258.	3.8	490
99	PolyMarker: A fast polyploid primer design pipeline. <i>Bioinformatics</i> , 2015, 31, 2038-2039.	1.8	202
100	Wheat Stripe Rust Resistance Protein WKS1 Reduces the Ability of the Thylakoid-Associated Ascorbate Peroxidase to Detoxify Reactive Oxygen Species. <i>Plant Cell</i> , 2015, 27, 1755-1770.	3.1	133
101	Field pathogenomics reveals the emergence of a diverse wheat yellow rust population. <i>Genome Biology</i> , 2015, 16, 23.	3.8	185
102	RNA-seq bulked segregant analysis enables the identification of high-resolution genetic markers for breeding in hexaploid wheat. <i>Plant Biotechnology Journal</i> , 2015, 13, 613-624.	4.1	202
103	Wheat Grain Filling Is Limited by Grain Filling Capacity rather than the Duration of Flag Leaf Photosynthesis: A Case Study Using NAM RNAi Plants. <i>PLoS ONE</i> , 2015, 10, e0134947.	1.1	73
104	Next Generation Sequencing Enabled Genetics in Hexaploid Wheat. , 2015, , 201-209.		0
105	Biofortification of wheat grain with iron and zinc: integrating novel genomic resources and knowledge from model crops. <i>Frontiers in Plant Science</i> , 2014, 5, 53.	1.7	171
106	A change in temperature modulates defence to yellow (stripe) rust in wheat line UC1041 independently of resistance gene <i>Yr36</i> . <i>BMC Plant Biology</i> , 2014, 14, 10.	1.6	41
107	Functional characterization of <i>GPC-1</i> genes in hexaploid wheat. <i>Planta</i> , 2014, 239, 313-324.	1.6	85
108	Identification and independent validation of a stable yield and thousand grain weight QTL on chromosome 6A of hexaploid wheat (<i>Triticum aestivum</i> L.). <i>BMC Plant Biology</i> , 2014, 14, 191.	1.6	161

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109	<i>Yr36</i> Confers Partial Resistance at Temperatures Below 18°C to U.K. Isolates of <i>Puccinia striiformis</i> . <i>Phytopathology</i> , 2014, 104, 871-878.	1.1	11
110	Genome analyses of the wheat yellow (stripe) rust pathogen <i>Puccinia striiformis</i> f. sp. <i>tritici</i> reveal polymorphic and haustorial expressed secreted proteins as candidate effectors. <i>BMC Genomics</i> , 2013, 14, 270.	1.2	235
111	Strategy for exploiting exotic germplasm using genetic, morphological, and environmental diversity: the <i>Aegilops tauschii</i> Coss. example. <i>Theoretical and Applied Genetics</i> , 2013, 126, 1793-1808.	1.8	62
112	Genomics reveals new landscapes for crop improvement. <i>Genome Biology</i> , 2013, 14, 206.	3.8	99
113	Discovery and development of exome-based, co-dominant single nucleotide polymorphism markers in hexaploid wheat (<i>Triticum aestivum</i> L.). <i>Plant Biotechnology Journal</i> , 2013, 11, 279-295.	4.1	161
114	Application of TILLING for Orphan Crop Improvement. , 2013, , 83-113.		20
115	The inhibitor of wax 1 locus (<i>W1</i>) prevents formation of α - and β -diketones in wheat cuticular waxes and maps to a sub-M interval on chromosome arm 2BS. <i>Plant Journal</i> , 2013, 74, 989-1002.	2.8	82
116	Separating homeologs by phasing in the tetraploid wheat transcriptome. <i>Genome Biology</i> , 2013, 14, R66.	3.8	126
117	Reduced height alleles (<i>Rht</i>) and Hagberg falling number of wheat. <i>Journal of Cereal Science</i> , 2012, 55, 305-311.	1.8	39
118	TILLING in <i>extremis</i> . <i>Plant Biotechnology Journal</i> , 2012, 10, 761-772.	4.1	109
119	Combining SNP discovery from next-generation sequencing data with bulked segregant analysis (BSA) to fine-map genes in polyploid wheat. <i>BMC Plant Biology</i> , 2012, 12, 14.	1.6	265
120	Divergent functions of orthologous NAC transcription factors in wheat and rice. <i>Plant Molecular Biology</i> , 2012, 78, 515-524.	2.0	70
121	Induced Mutations in the <i>Starch Branching Enzyme II</i> (<i>SBEII</i>) Genes Increase Amylose and Resistant Starch Content in Durum Wheat. <i>Crop Science</i> , 2012, 52, 1754-1766.	0.8	97
122	Effect of the down-regulation of the high Grain Protein Content (GPC) genes on the wheat transcriptome during monocarpic senescence. <i>BMC Genomics</i> , 2011, 12, 492.	1.2	75
123	Discovery of Rare Mutations in Populations: TILLING by Sequencing $\hat{A} \hat{A}$. <i>Plant Physiology</i> , 2011, 156, 1257-1268.	2.3	266
124	Identification of a major QTL controlling the content of B-type starch granules in <i>Aegilops</i> . <i>Journal of Experimental Botany</i> , 2011, 62, 2217-2228.	2.4	59
125	Down-regulation of four putative arabinoxylan feruloyl transferase genes from family PF02458 reduces ester-linked ferulate content in rice cell walls. <i>Planta</i> , 2010, 231, 677-691.	1.6	90
126	A modified TILLING approach to detect induced mutations in tetraploid and hexaploid wheat. <i>BMC Plant Biology</i> , 2009, 9, 115.	1.6	323

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127	Wheat (<i>Triticum aestivum</i>) NAM proteins regulate the translocation of iron, zinc, and nitrogen compounds from vegetative tissues to grain. <i>Journal of Experimental Botany</i> , 2009, 60, 4263-4274.	2.4	300
128	A Kinase-START Gene Confers Temperature-Dependent Resistance to Wheat Stripe Rust. <i>Science</i> , 2009, 323, 1357-1360.	6.0	625
129	Colinearity between the barley grain protein content (GPC) QTL on chromosome arm 6HS and the wheat Gpc-B1 region. <i>Molecular Breeding</i> , 2008, 22, 25-38.	1.0	70
130	RNA interference for wheat functional gene analysis. <i>Transgenic Research</i> , 2007, 16, 689-701.	1.3	76
131	A NAC Gene Regulating Senescence Improves Grain Protein, Zinc, and Iron Content in Wheat. <i>Science</i> , 2006, 314, 1298-1301.	6.0	1,408
132	The high grain protein content gene Gpc-B1 accelerates senescence and has pleiotropic effects on protein content in wheat. <i>Journal of Experimental Botany</i> , 2006, 57, 2785-2794.	2.4	252
133	Physical map of the wheat high grain protein content gene Gpc-B1 and development of a high-throughput molecular marker. <i>New Phytologist</i> , 2006, 169, 753-763.	3.5	150
134	High-temperature adult-plant (HTAP) stripe rust resistance gene Yr36 from <i>Triticum turgidum</i> ssp. <i>dicoccoides</i> is closely linked to the grain protein content locus Gpc-B1. <i>Theoretical and Applied Genetics</i> , 2005, 112, 97-105.	1.8	208
135	Microcolinearity between a 2-cM region encompassing the grain protein content locus Gpc-6B1 on wheat chromosome 6B and a 350-kb region on rice chromosome 2. <i>Functional and Integrative Genomics</i> , 2004, 4, 59-66.	1.4	109