

Qixin Sun

List of Publications by Year in descending order

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144
papers

9,195
citations

41323

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docs citations

148
times ranked

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#	ARTICLE	IF	CITATIONS
1	Identification and characterization of QTL for spike morphological traits, plant height and heading date derived from the D genome of natural and resynthetic allohexaploid wheat. <i>Theoretical and Applied Genetics</i> , 2022, 135, 389-403.	1.8	19
2	Stress granule-associated TaMBF1c confers thermotolerance through regulating specific mRNA translation in wheat (<i>Triticum aestivum</i>). <i>New Phytologist</i> , 2022, 233, 1719-1731.	3.5	31
3	A single nucleotide deletion in the third exon of <i>FT1</i> increases the spikelet number and delays heading date in wheat (<i>Triticum aestivum</i> L.). <i>Plant Biotechnology Journal</i> , 2022, 20, 920-933.	4.1	35
4	ggComp enables dissection of germplasm resources and construction of a multiscale germplasm network in wheat. <i>Plant Physiology</i> , 2022, 188, 1950-1965.	2.3	13
5	Identification of a novel major QTL from Chinese wheat cultivar Ji5265 for Fusarium head blight resistance in greenhouse. <i>Theoretical and Applied Genetics</i> , 2022, 135, 1867-1877.	1.8	8
6	An Improved Inoculation Method to Detect Wheat and Barley Genotypes for Resistance to Fusarium Crown Rot. <i>Plant Disease</i> , 2022, 106, 1122-1127.	0.7	5
7	Shaping polyploid wheat for success: Origins, domestication, and the genetic improvement of agronomic traits. <i>Journal of Integrative Plant Biology</i> , 2022, 64, 536-563.	4.1	26
8	The genetic and molecular basis for improving heat stress tolerance in wheat. <i>ABIOTECH</i> , 2022, 3, 25-39.	1.8	3
9	<i>Heat Stress Tolerance 2</i> confers basal heat stress tolerance in allohexaploid wheat (<i>Triticum aestivum</i> L.). <i>Journal of Experimental Botany</i> , 2022, 73, 6600-6614.	2.4	6
10	Histone acetyltransferase <i>TaHAG1</i> interacts with <i>TaPLATZ5</i> to activate <i>TaPAD4</i> expression and positively contributes to powdery mildew resistance in wheat. <i>New Phytologist</i> , 2022, 236, 590-607.	3.5	16
11	Histone acetyltransferase <i>TaHAG1</i> interacts with <i>TaNACL</i> to promote heat stress tolerance in wheat. <i>Plant Biotechnology Journal</i> , 2022, 20, 1645-1647.	4.1	10
12	Genome-wide association study of six quality-related traits in common wheat (<i>Triticum aestivum</i> L.) under two sowing conditions. <i>Theoretical and Applied Genetics</i> , 2021, 134, 399-418.	1.8	22
13	Genome-wide association study identifies QTL for thousand grain weight in winter wheat under normal- and late-sown stressed environments. <i>Theoretical and Applied Genetics</i> , 2021, 134, 143-157.	1.8	36
14	Phenotypic characterization of the glossy1 mutant and fine mapping of GLOSSY1 in common wheat (<i>Triticum aestivum</i> L.). <i>Theoretical and Applied Genetics</i> , 2021, 134, 835-847.	1.8	6
15	The endosperm-specific transcription factor TaNAC019 regulates glutenin and starch accumulation and its elite allele improves wheat grain quality. <i>Plant Cell</i> , 2021, 33, 603-622.	3.1	88
16	Pleiotropic function of the SQUAMOSA PROMOTER-BINDING PROTEIN-LIKE gene TaSPL14 in wheat plant architecture. <i>Planta</i> , 2021, 253, 44.	1.6	26
17	The Transcriptional and Splicing Changes Caused by Hybridization Can Be Globally Recovered by Genome Doubling during Allopolyploidization. <i>Molecular Biology and Evolution</i> , 2021, 38, 2513-2519.	3.5	10
18	Histone acetyltransferase TaHAG1 acts as a crucial regulator to strengthen salt tolerance of hexaploid wheat. <i>Plant Physiology</i> , 2021, 186, 1951-1969.	2.3	69

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19	Fine mapping of a powdery mildew resistance gene Mllw39 derived from wild emmer wheat (<i>Triticum</i>) Tj ETQq1 1 0.784314 rgBT /Overl	1.8	14
20	<i>FRIZZY PANICLE</i> defines a regulatory hub for simultaneously controlling spikelet formation and awn elongation in bread wheat. <i>New Phytologist</i> , 2021, 231, 814-833.	3.5	41
21	Fine Mapping of the Leaf Rust Resistance Gene Lr65 in Spelt Wheat "Altgold"™. <i>Frontiers in Plant Science</i> , 2021, 12, 666921.	1.7	7
22	The decreased expression of GW2 homologous genes contributed to the increased grain width and thousand-grain weight in wheat- <i>Dasypyrum villosum</i> 6VS-6DL translocation lines. <i>Theoretical and Applied Genetics</i> , 2021, 134, 3873-3894.	1.8	7
23	A Major Quantitative Trait Loci Cluster Controlling Three Components of Yield and Plant Height Identified on Chromosome 4B of Common Wheat. <i>Frontiers in Plant Science</i> , 2021, 12, 799520.	1.7	9
24	Identification and Validation of Stable Quantitative Trait Loci for SDS-Sedimentation Volume in Common Wheat (<i>Triticum aestivum</i> L.). <i>Frontiers in Plant Science</i> , 2021, 12, 747775.	1.7	4
25	Dissection of genetic factors underlying grain size and fine mapping of QTgw.cau-7D in common wheat (<i>Triticum aestivum</i> L.). <i>Theoretical and Applied Genetics</i> , 2020, 133, 149-162.	1.8	42
26	Heat shock transcription factor A1b regulates heat tolerance in wheat and <i>Arabidopsis</i> through <i>OPR3</i> and jasmonate signalling pathway. <i>Plant Biotechnology Journal</i> , 2020, 18, 1109-1111.	4.1	36
27	A Collinearity-Incorporating Homology Inference Strategy for Connecting Emerging Assemblies in the Triticeae Tribe as a Pilot Practice in the Plant Pangenomic Era. <i>Molecular Plant</i> , 2020, 13, 1694-1708.	3.9	126
28	Origin and adaptation to high altitude of Tibetan semi-wild wheat. <i>Nature Communications</i> , 2020, 11, 5085.	5.8	104
29	Changes in Alternative Splicing in Response to Domestication and Polyploidization in Wheat. <i>Plant Physiology</i> , 2020, 184, 1955-1968.	2.3	34
30	Dissection and validation of a QTL cluster linked to Rht-B1 locus controlling grain weight in common wheat (<i>Triticum aestivum</i> L.) using near-isogenic lines. <i>Theoretical and Applied Genetics</i> , 2020, 133, 2639-2653.	1.8	26
31	SnpHub: an easy-to-set-up web server framework for exploring large-scale genomic variation data in the post-genomic era with applications in wheat. <i>GigaScience</i> , 2020, 9, .	3.3	43
32	A Single Amino Acid Substitution in STKc_GSK3 Kinase Conferring Semispherical Grains and Its Implications for the Origin of <i>Triticum sphaerococcum</i> . <i>Plant Cell</i> , 2020, 32, 923-934.	3.1	78
33	The semidominant mutation w5 impairs epicuticular wax deposition in common wheat (<i>Triticum</i>) Tj ETQq1 1 0.784314 rgBT /Overl	1.8	6
34	Glycerol-Induced Powdery Mildew Resistance in Wheat by Regulating Plant Fatty Acid Metabolism, Plant Hormones Cross-Talk, and Pathogenesis-Related Genes. <i>International Journal of Molecular Sciences</i> , 2020, 21, 673.	1.8	28
35	Pleiotropic QTL influencing spikelet number and heading date in common wheat (<i>Triticum aestivum</i> L.). <i>Theoretical and Applied Genetics</i> , 2020, 133, 1825-1838.	1.8	53
36	Characterization of a major quantitative trait locus on the short arm of chromosome 4B for spike number per unit area in common wheat (<i>Triticum aestivum</i> L.). <i>Theoretical and Applied Genetics</i> , 2020, 133, 2259-2269.	1.8	12

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37	Importance of small RNA in plant seed germination. , 2020, , 117-123.		1
38	Histone acetyltransferase <scp>GCN</scp>5 contributes to cell wall integrity and salt stress tolerance by altering the expression of cellulose synthesis genes. Plant Journal, 2019, 97, 587-602.	2.8	99
39	Frequent intra- and inter-species introgression shapes the landscape of genetic variation in bread wheat. Genome Biology, 2019, 20, 136.	3.8	148
40	High Molecular Weight Glutenin Subunits 1Bx7 and 1By9 Encoded by <i>Glu-B1</i> Locus Affect Wheat Dough Properties and Sponge Cake Quality. Journal of Agricultural and Food Chemistry, 2019, 67, 11796-11804.	2.4	23
41	Wheat <i>TaSPL8</i> Modulates Leaf Angle Through Auxin and Brassinosteroid Signaling. Plant Physiology, 2019, 181, 179-194.	2.3	69
42	Use of near-isogenic lines to precisely map and validate a major QTL for grain weight on chromosome 4AL in bread wheat (<i>Triticum aestivum</i> L.). Theoretical and Applied Genetics, 2019, 132, 2367-2379.	1.8	32
43	Wheat Responses and Tolerance to High Temperature. , 2019, , 139-147.		5
44	Hybrid sequencing reveals insight into heat sensing and signaling of bread wheat. Plant Journal, 2019, 98, 1015-1032.	2.8	73
45	Dissection of two quantitative trait loci with pleiotropic effects on plant height and spike length linked in coupling phase on the short arm of chromosome 2D of common wheat (<i>Triticum aestivum</i> L.). Theoretical and Applied Genetics, 2019, 132, 1815-1831.	1.8	22
46	Wheat powdery mildew resistance gene Pm64 derived from wild emmer (<i>Triticum turgidum</i> var.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3 761-770.	2.3	57
47	Genomic Imprinting Was Evolutionarily Conserved during Wheat Polyploidization. Plant Cell, 2018, 30, 37-47.	3.1	26
48	Wheat miR9678 Affects Seed Germination by Generating Phased siRNAs and Modulating Abscisic Acid/Gibberellin Signaling. Plant Cell, 2018, 30, 796-814.	3.1	75
49	Genetic improvement of heat tolerance in wheat: Recent progress in understanding the underlying molecular mechanisms. Crop Journal, 2018, 6, 32-41.	2.3	103
50	Global profiling of alternative splicing landscape responsive to drought, heat and their combination in wheat (<i>Triticum aestivum</i> L.). Plant Biotechnology Journal, 2018, 16, 714-726.	4.1	161
51	Overexpression of the Wheat (<i>Triticum aestivum</i> L.) TaPEPKR2 Gene Enhances Heat and Dehydration Tolerance in Both Wheat and Arabidopsis. Frontiers in Plant Science, 2018, 9, 1710.	1.7	37
52	Dissection of two quantitative trait loci with pleiotropic effects on plant height and spike length linked in coupling phase on the short arm of chromosome 2D of common wheat (<i>Triticum aestivum</i> L.). Theoretical and Applied Genetics, 2018, 131, 2621-2637.	1.8	51
53	Unconventional splicing of wheat TabZIP60 confers heat tolerance in transgenic Arabidopsis. Plant Science, 2018, 274, 252-260.	1.7	33
54	Three genomes differentially contribute to the seedling lateral root number in allohexaploid wheat: evidence from phenotype evolution and gene expression. Plant Journal, 2018, 95, 976-987.	2.8	35

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55	Simultaneous Transfer of Leaf Rust and Powdery Mildew Resistance Genes from Hexaploid Triticale Cultivar Sorento into Bread Wheat. <i>Frontiers in Plant Science</i> , 2018, 9, 85.	1.7	19
56	Global QTL Analysis Identifies Genomic Regions on Chromosomes 4A and 4B Harboring Stable Loci for Yield-Related Traits Across Different Environments in Wheat (<i>Triticum aestivum</i> L.). <i>Frontiers in Plant Science</i> , 2018, 9, 529.	1.7	132
57	TaWRKY51 promotes lateral root formation through negative regulation of ethylene biosynthesis in wheat (<i>Triticum aestivum</i> L.). <i>Plant Journal</i> , 2018, 96, 372-388.	2.8	55
58	Metabolic adaptation of wheat grains contributes to a stable filling rate under heat stress. <i>Journal of Experimental Botany</i> , 2018, 69, 5531-5545.	2.4	61
59	Overexpression of wheat ferritin gene TaFER-5B enhances tolerance to heat stress and other abiotic stresses associated with the ROS scavenging. <i>BMC Plant Biology</i> , 2017, 17, 14.	1.6	116
60	Ectopic expression of TaOEP16-2-5B, a wheat plastid outer envelope protein gene, enhances heat and drought stress tolerance in transgenic <i>Arabidopsis</i> plants. <i>Plant Science</i> , 2017, 258, 1-11.	1.7	42
61	Isolation and characterization of heat-responsive gene TaGASR1 from wheat (<i>Triticum aestivum</i> L.). <i>Journal of Plant Biology</i> , 2017, 60, 57-65.	0.9	39
62	The E3 Ligase TaSAP5 Alters Drought Stress Responses by Promoting the Degradation of DRIP Proteins. <i>Plant Physiology</i> , 2017, 175, 1878-1892.	2.3	64
63	Altered expression of the TaRSL2 gene contributed to variation in root hair length during allopolyploid wheat evolution. <i>Planta</i> , 2017, 246, 1019-1028.	1.6	14
64	Mutations in eIF5B Confer Thermosensitive and Pleiotropic Phenotypes via Translation Defects in <i>Arabidopsis thaliana</i> . <i>Plant Cell</i> , 2017, 29, 1952-1969.	3.1	43
65	Genome sequence of the progenitor of the wheat D genome <i>Aegilops tauschii</i> . <i>Nature</i> , 2017, 551, 498-502.	13.7	563
66	Massive expansion and differential evolution of small heat shock proteins with wheat (<i>Triticum</i>) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 30</i>	1.6	17
67	Sequencing and comparative analyses of <i>Aegilops tauschii</i> chromosome arm 3DS reveal rapid evolution of Triticeae genomes. <i>Journal of Genetics and Genomics</i> , 2017, 44, 51-61.	1.7	25
68	Molecular and Functional Characterization of Wheat ARGOS Genes Influencing Plant Growth and Stress Tolerance. <i>Frontiers in Plant Science</i> , 2017, 8, 170.	1.7	20
69	Comparative Proteomic Analysis of Flag Leaves Reveals New Insight into Wheat Heat Adaptation. <i>Frontiers in Plant Science</i> , 2017, 8, 1086.	1.7	41
70	Identification of QTL for Grain Size and Shape on the D Genome of Natural and Synthetic Allohexaploid Wheats with Near-Identical AABB Genomes. <i>Frontiers in Plant Science</i> , 2017, 8, 1705.	1.7	49
71	Characterization of wheat MYB genes responsive to high temperatures. <i>BMC Plant Biology</i> , 2017, 17, 208.	1.6	75
72	Genome-Wide Mapping of Targets of Maize Histone Deacetylase HDA101 Reveals Its Function and Regulatory Mechanism during Seed Development. <i>Plant Cell</i> , 2016, 28, 629-645.	3.1	49

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73	Up-regulating the abscisic acid inactivation gene <i>ZmABA8ox1b</i> contributes to seed germination heterosis by promoting cell expansion. <i>Journal of Experimental Botany</i> , 2016, 67, 2889-2900.	2.4	17
74	<i>Haynaldia villosa</i> NAM-V1 is linked with the powdery mildew resistance gene <i>Pm21</i> and contributes to increasing grain protein content in wheat. <i>BMC Genetics</i> , 2016, 17, 82.	2.7	6
75	Identification and mapping of <i>MLIW30</i> , a novel powdery mildew resistance gene derived from wild emmer wheat. <i>Molecular Breeding</i> , 2016, 36, 1.	1.0	13
76	Ectopic expression of the <i>Vigna eylindrica</i> ferritin gene enhanced heat tolerance in transgenic wheat (<i>Triticum aestivum</i> L.). <i>Euphytica</i> , 2016, 209, 23-30.	0.6	3
77	Altered expression of <i>TaRSL4</i> gene by genome interplay shapes root hair length in allopolyploid wheat. <i>New Phytologist</i> , 2016, 209, 721-732.	3.5	71
78	Fine genetic mapping of spot blotch resistance gene <i>Sb3</i> in wheat (<i>Triticum aestivum</i>). <i>Theoretical and Applied Genetics</i> , 2016, 129, 577-589.	1.8	71
79	Proteomic patterns associated with heterosis. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016, 1864, 908-915.	1.1	32
80	Ectopic expression of a maize hybrid up-regulated gene, ErbB-3 binding Protein 1 (<i>ZmEBP1</i>), increases organ size by promoting cell proliferation in <i>Arabidopsis</i> . <i>Plant Science</i> , 2016, 243, 23-34.	1.7	20
81	Characterization of Small RNAs Derived from tRNAs, rRNAs and snoRNAs and Their Response to Heat Stress in Wheat Seedlings. <i>PLoS ONE</i> , 2016, 11, e0150933.	1.1	54
82	Identification and characterization of a high kernel weight mutant induced by gamma radiation in wheat (<i>Triticum aestivum</i> L.). <i>BMC Genetics</i> , 2015, 16, 127.	2.7	35
83	Histone acetyltransferase <i>GCN5</i> is essential for heat stress-responsive gene activation and thermotolerance in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2015, 84, 1178-1191.	2.8	126
84	The wheat transcription factor <i>TaGAMyb</i> recruits histone acetyltransferase and activates the expression of a high-molecular-weight glutenin subunit gene. <i>Plant Journal</i> , 2015, 84, 347-359.	2.8	46
85	Temporal small RNA transcriptome profiling unraveled partitioned miRNA expression in developing maize endosperms between reciprocal crosses. <i>Frontiers in Plant Science</i> , 2015, 6, 744.	1.7	14
86	Temporal transcriptome profiling reveals expression partitioning of homeologous genes contributing to heat and drought acclimation in wheat (<i>Triticum aestivum</i> L.). <i>BMC Plant Biology</i> , 2015, 15, 152.	1.6	343
87	Mapping QTLs associated with root traits using two different populations in wheat (<i>Triticum</i>) <i>Tj ETQq1 1 0.784314 rgBT / Overlock 10</i>	0.8	53
88	Genetic and physical mapping of powdery mildew resistance gene <i>MH1T</i> in Chinese wheat landrace Hulutou. <i>Theoretical and Applied Genetics</i> , 2015, 128, 365-373.	1.8	48
89	Overexpression of heat stress-responsive <i>TaMBF1c</i> , a wheat (<i>Triticum aestivum</i> L.) Multiprotein Bridging Factor, confers heat tolerance in both yeast and rice. <i>Plant Molecular Biology</i> , 2015, 87, 31-45.	2.0	67
90	Ectopic Expression of a Maize Hybrid Down-Regulated Gene <i>ZmARF25</i> Decreases Organ Size by Affecting Cellular Proliferation in <i>Arabidopsis</i> . <i>PLoS ONE</i> , 2014, 9, e94830.	1.1	12

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91	Fine Physical and Genetic Mapping of Powdery Mildew Resistance Gene MlW172 Originating from Wild Emmer (<i>Triticum dicoccoides</i>). PLoS ONE, 2014, 9, e100160.	1.1	36
92	Molecular mapping of a recessive powdery mildew resistance gene in spelt wheat cultivar Hubel. Molecular Breeding, 2014, 34, 491-500.	1.0	17
93	Maize (<i>Zea mays</i> L.) seedling leaf nuclear proteome and differentially expressed proteins between a hybrid and its parental lines. Proteomics, 2014, 14, 1071-1087.	1.3	24
94	Mapping QTLs of yield-related traits using RIL population derived from common wheat and Tibetan semi-wild wheat. Theoretical and Applied Genetics, 2014, 127, 2415-2432.	1.8	97
95	A wheat lipid transfer protein 3 could enhance the basal thermotolerance and oxidative stress resistance of Arabidopsis. Gene, 2014, 550, 18-26.	1.0	49
96	Comparative genetic mapping and genomic region collinearity analysis of the powdery mildew resistance gene Pm41. Theoretical and Applied Genetics, 2014, 127, 1741-1751.	1.8	32
97	Whole-genome discovery of miRNAs and their targets in wheat (<i>Triticum aestivum</i> L.). BMC Plant Biology, 2014, 14, 142.	1.6	120
98	TaWRKY68 responses to biotic stresses are revealed by the orthologous genes from major cereals. Genetics and Molecular Biology, 2014, 37, 73-80.	0.6	5
99	Epigenetic modification contributes to the expression divergence of three <i>TaEXPA1</i> homoeologs in hexaploid wheat (<i>Triticum aestivum</i>) Tj ETQq1 1 0.384314 rgBT /Over		
100	Widespread, abundant, and diverse TE-associated siRNAs in developing wheat grain. Gene, 2013, 522, 1-7.	1.0	23
101	Overexpression of Three <i>TaEXPA1</i> Homoeologous Genes with Distinct Expression Divergence in Hexaploid Wheat Exhibit Functional Retention in Arabidopsis. PLoS ONE, 2013, 8, e63667.	1.1	16
102	Comparative High-Resolution Mapping of the Wax Inhibitors <i>lw1</i> and <i>lw2</i> in Hexaploid Wheat. PLoS ONE, 2013, 8, e84691.	1.1	27
103	Comparative Proteomic Analysis of Embryos between a Maize Hybrid and Its Parental Lines during Early Stages of Seed Germination. PLoS ONE, 2013, 8, e65867.	1.1	71
104	Exploration of small non coding RNAs in wheat (<i>Triticum aestivum</i> L.). Plant Molecular Biology, 2012, 80, 67-73.	2.0	20
105	Transcriptome Comparison of Susceptible and Resistant Wheat in Response to Powdery Mildew Infection. Genomics, Proteomics and Bioinformatics, 2012, 10, 94-106.	3.0	90
106	Identification and comparative mapping of a powdery mildew resistance gene derived from wild emmer (<i>Triticum turgidum</i> var. <i>dicoccoides</i>) on chromosome 2BS. Theoretical and Applied Genetics, 2012, 124, 1041-1049.	1.8	47
107	Suppressed recombination rate in 6VS/6AL translocation region carrying the Pm21 locus introgressed from <i>Haynaldia villosa</i> into hexaploid wheat. Molecular Breeding, 2012, 29, 399-412.	1.0	40
108	TamiR159 Directed Wheat TaGAMYB Cleavage and Its Involvement in Anther Development and Heat Response. PLoS ONE, 2012, 7, e48445.	1.1	158

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109	Expression divergence of TaMBD2 homoeologous genes encoding methyl CpG-binding domain proteins in wheat (<i>Triticum aestivum</i> L.). <i>Gene</i> , 2011, 471, 13-18.	1.0	26
110	Genome-wide identification of gibberellins metabolic enzyme genes and expression profiling analysis during seed germination in maize. <i>Gene</i> , 2011, 482, 34-42.	1.0	47
111	Molecular dissection of plant height QTLs using recombinant inbred lines from hybrids between common wheat (<i>Triticum aestivum</i> L.) and spelt wheat (<i>Triticum spelta</i> L.). <i>Science Bulletin</i> , 2011, 56, 1897-1903.	1.7	19
112	Identification and characterization of wheat long non-protein coding RNAs responsive to powdery mildew infection and heat stress by using microarray analysis and SBS sequencing. <i>BMC Plant Biology</i> , 2011, 11, 61.	1.6	347
113	Genome-wide identification and expression profiling of auxin response factor (ARF) gene family in maize. <i>BMC Genomics</i> , 2011, 12, 178.	1.2	189
114	Genetic and comparative genomics mapping reveals that a powdery mildew resistance gene Ml3D232 originating from wild emmer co-segregates with an NBS-LRR analog in common wheat (<i>Triticum</i>) Tj ETQq0 0 0 rgBT1/Overlock 10 Tf 50 3	1.8	28
115	Non-coding small RNAs responsive to abiotic stress in wheat (<i>Triticum aestivum</i> L.). <i>Functional and Integrative Genomics</i> , 2010, 10, 187-190.	1.4	69
116	Identification and molecular mapping of a leaf rust resistance gene in spelt wheat landrace Altgold. <i>Euphytica</i> , 2010, 174, 371-375.	0.6	13
117	Diverse set of microRNAs are responsive to powdery mildew infection and heat stress in wheat (<i>Triticum aestivum</i> L.). <i>BMC Plant Biology</i> , 2010, 10, 123.	1.6	459
118	Identification and characterization of a novel hybrid upregulated long non-protein coding RNA in maize seedling roots. <i>Plant Science</i> , 2010, 179, 356-363.	1.7	5
119	The relationship of differential expression of genes in GA biosynthesis and response pathways with heterosis of plant height in a wheat diallel cross. <i>Science Bulletin</i> , 2009, 54, 3029-3034.	1.7	6
120	Identification of differentially expressed proteins between hybrid and parents in wheat (<i>Triticum</i>) Tj ETQq0 0 0 rgBT1/Overlock 10 Tf 50 3	1.8	28
121	Identification and genetic mapping of pm42, a new recessive wheat powdery mildew resistance gene derived from wild emmer (<i>Triticum turgidum</i> var. <i>dicoccoides</i>). <i>Theoretical and Applied Genetics</i> , 2009, 119, 223-230.	1.8	141
122	Molecular identification of a new powdery mildew resistance gene Pm41 on chromosome 3BL derived from wild emmer (<i>Triticum turgidum</i> var. <i>dicoccoides</i>). <i>Theoretical and Applied Genetics</i> , 2009, 119, 531-539.	1.8	85
123	Altered circadian rhythms regulate growth vigour in hybrids and allopolyploids. <i>Nature</i> , 2009, 457, 327-331.	13.7	598
124	Identification and genetic mapping of a powdery mildew resistance gene in wild emmer (<i>Triticum</i>) Tj ETQq0 0 0 rgBT1/Overlock 10 Tf 50 3	0.6	68
125	Heat stress-responsive transcriptome analysis in heat susceptible and tolerant wheat (<i>Triticum</i>) Tj ETQq1 1 0.784314 rgBT1/Overlock 10 Tf 50 3	1.2	290
126	Genomic and genic sequence variation in synthetic hexaploid wheat (AABBDD) as compared to their parental species. <i>Progress in Natural Science: Materials International</i> , 2008, 18, 533-538.	1.8	8

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127	Cloning and expression profiles of 15 genes encoding WRKY transcription factor in wheat (<i>Triticum</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf	1.8	79
128	Isolation and comparative expression analysis of six MBD genes in wheat. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2008, 1779, 90-98.	0.9	12
129	Cloning and characterization of microRNAs from wheat (<i>Triticum aestivum</i> L.). <i>Genome Biology</i> , 2007, 8, R96.	13.9	330
130	Gibberellins and heterosis of plant height in wheat (<i>Triticum aestivum</i> L.). <i>BMC Genetics</i> , 2007, 8, 40.	2.7	65
131	Wheat (<i>Triticum aestivum</i> L.) root proteome and differentially expressed root proteins between hybrid and parents. <i>Proteomics</i> , 2007, 7, 3538-3557.	1.3	63
132	Molecular mapping of a dominant non-glaucousness gene from synthetic hexaploid wheat (<i>Triticum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.6	32
133	Molecular identification of Pm12-carrying introgression lines in wheat using genomic and EST-SSR markers. <i>Euphytica</i> , 2007, 158, 95-102.	0.6	20
134	Isolation and characterization of 15 genes encoding ribosomal proteins in wheat (<i>Triticum aestivum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.7	17
135	Wheat Dof transcription factor WPBF interacts with TaQM and activates transcription of an alpha-gliadin gene during wheat seed development. <i>Plant Molecular Biology</i> , 2006, 63, 73-84.	2.0	90
136	Heterosis in root development and differential gene expression between hybrids and their parental inbreds in wheat (<i>Triticum aestivum</i> L.). <i>Theoretical and Applied Genetics</i> , 2006, 113, 1283-1294.	1.8	57
137	Identification of RAPD Markers and Development of SCAR Markers Linked to a Powdery Mildew Resistance Gene, and their Location on Chromosome in Wheat Cultivar Brock. <i>Plant Production Science</i> , 2005, 8, 578-585.	0.9	6
138	Isolation and characterization of 18 genes encoding $\hat{1}^{\pm}$ - and $\hat{1}^2$ -expansins in wheat (<i>Triticum aestivum</i> L.). <i>Molecular Genetics and Genomics</i> , 2005, 274, 548-556.	1.0	49
139	Identification of differentially expressed genes in leaf and root between wheat hybrid and its parental inbreds using PCR-based cDNA subtraction. <i>Plant Molecular Biology</i> , 2005, 58, 367-384.	2.0	73
140	Identification of Random Amplified Polymorphic DNA and Simple Sequence Repeat Markers Linked to Powdery Mildew Resistance in Common Wheat Cultivar Brock. <i>Plant Production Science</i> , 2004, 7, 319-323.	0.9	8
141	Differential gene expression patterns in leaves between hybrids and their parental inbreds are correlated with heterosis in a wheat diallel cross. <i>Plant Science</i> , 2004, 166, 651-657.	1.7	68
142	Title is missing!. <i>Euphytica</i> , 2002, 123, 21-29.	0.6	138
143	Differential gene expression between wheat hybrids and their parental inbreds in seedling leaves. <i>Euphytica</i> , 1999, 106, 117-123.	0.6	32
144	Title is missing!. <i>Euphytica</i> , 1998, 99, 205-211.	0.6	48