

# Yongzhong Xing

## List of Publications by Year in descending order

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137  
papers

13,850  
citations

47409

49  
h-index

25230

113  
g-index

143  
all docs

143  
docs citations

143  
times ranked

9455  
citing authors

#	ARTICLE	IF	CITATIONS
1	Assembly of yield heterosis of an elite rice hybrid is promising by manipulating dominant quantitative trait loci. <i>Journal of Integrative Plant Biology</i> , 2022, 64, 688-701.	4.1	7
2	Conservation and divergence: Regulatory networks underlying reproductive branching in rice and maize. <i>Journal of Advanced Research</i> , 2022, 41, 179-190.	4.4	10
3	A long transcript mutant of the rubisco activase gene <i>RCA</i> upregulated by the transcription factor <i>Ghd2</i> enhances drought tolerance in rice. <i>Plant Journal</i> , 2022, 110, 673-687.	2.8	2
4	Rice functional genomics: decades' efforts and roads ahead. <i>Science China Life Sciences</i> , 2022, 65, 33-92.	2.3	107
5	Fixation of hybrid sterility genes and favorable alleles of key yield-related genes with dominance contribute to the high yield of the Yongyou series of intersubspecific hybrid rice. <i>Journal of Genetics and Genomics</i> , 2022, 49, 448-457.	1.7	2
6	Introgression Lines: Valuable Resources for Functional Genomics Research and Breeding in Rice ( <i>Oryza sativa</i> L.). <i>Frontiers in Plant Science</i> , 2022, 13, 863789.	1.7	7
7	NAD <sup>+</sup> -capped RNAs are widespread in rice ( <i>Oryza sativa</i> ) and spatiotemporally modulated during development. <i>Science China Life Sciences</i> , 2022, 65, 2121-2124.	2.3	4
8	Five plants per RIL for phenotyping traits of high or moderate heritability ensure the power of QTL mapping in a rice MAGIC population. <i>Molecular Breeding</i> , 2022, 42, .	1.0	3
9	Meeting partners at the right time promises varied flowering. <i>Molecular Plant</i> , 2022, , .	3.9	0
10	Genetic analyses of lodging resistance and yield provide insights into post-Green Revolution breeding in rice. <i>Plant Biotechnology Journal</i> , 2021, 19, 814-829.	4.1	25
11	Bin-based genome-wide association studies reveal superior alleles for improvement of appearance quality using a 4-way MAGIC population in rice. <i>Journal of Advanced Research</i> , 2021, 28, 183-194.	4.4	20
12	The heading-date gene <i>Ghd7</i> inhibits seed germination by modulating the balance between abscisic acid and gibberellins. <i>Crop Journal</i> , 2021, 9, 297-304.	2.3	8
13	Global analysis of CCT family knockout mutants identifies four genes involved in regulating heading date in rice. <i>Journal of Integrative Plant Biology</i> , 2021, 63, 913-923.	4.1	25
14	The transcriptional repressor <i>OsPRR73</i> links circadian clock and photoperiod pathway to control heading date in rice. <i>Plant, Cell and Environment</i> , 2021, 44, 842-855.	2.8	29
15	<i>OsPRR37</i> Alternatively Promotes Heading Date Through Suppressing the Expression of <i>Ghd7</i> in the Japonica Variety Zhonghua 11 under Natural Long-Day Conditions. <i>Rice</i> , 2021, 14, 20.	1.7	10
16	The chromosome-scale reference genome of safflower ( <i>Carthamus tinctorius</i> ) provides insights into linoleic acid and flavonoid biosynthesis. <i>Plant Biotechnology Journal</i> , 2021, 19, 1725-1742.	4.1	60
17	Breeding by design for future rice: Genes and genome technologies. <i>Crop Journal</i> , 2021, 9, 491-496.	2.3	9
18	Combinations of <i>Ghd7</i> , <i>Ghd8</i> , and <i>Hd1</i> determine strong heterosis of commercial rice hybrids in diverse ecological regions. <i>Journal of Experimental Botany</i> , 2021, 72, 6963-6976.	2.4	9

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19	BSA-seq-based identification of a major additive plant height QTL with an effect equivalent to that of Semi-dwarf 1 in a large rice F2 population. <i>Crop Journal</i> , 2021, 9, 1428-1437.	2.3	12
20	Root-to-Shoot Long-Distance Mobile miRNAs Identified from <i>Nicotiana</i> Rootstocks. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12821.	1.8	12
21	Bin-based genome-wide association analyses improve power and resolution in QTL mapping and identify favorable alleles from multiple parents in a four-way MAGIC rice population. <i>Theoretical and Applied Genetics</i> , 2020, 133, 59-71.	1.8	18
22	<i>Wide Grain 7</i> increases grain width by enhancing H3K4me3 enrichment in the <i>OsMADS1</i> promoter in rice ( <i>Oryza sativa</i> L.). <i>Plant Journal</i> , 2020, 102, 517-528.	2.8	25
23	An ethyl methanesulfonate-induced neutral mutant bridging method efficiently identifies spontaneously mutated genes in rice. <i>Plant Journal</i> , 2020, 104, 1129-1141.	2.8	3
24	Structural Insight into DNA Recognition by CCT/NF-YB/YC Complexes in Plant Photoperiodic Flowering. <i>Plant Cell</i> , 2020, 32, 3469-3484.	3.1	46
25	<i>OsHOX1</i> and <i>OsHOX28</i> Redundantly Shape Rice Tiller Angle by Reducing <i>HSFA2D</i> Expression and Auxin Content. <i>Plant Physiology</i> , 2020, 184, 1424-1437.	2.3	44
26	Conserved Imprinted Genes between Intra-Subspecies and Inter-Subspecies Are Involved in Energy Metabolism and Seed Development in Rice. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9618.	1.8	8
27	Dominant complementary interaction between <i>OsC1</i> and two tightly linked genes, <i>Rb1</i> and <i>Rb2</i> , controls the purple leaf sheath in rice. <i>Theoretical and Applied Genetics</i> , 2020, 133, 2555-2566.	1.8	14
28	A minor QTL, <i>SG3</i> , encoding an R2R3-MYB protein, negatively controls grain length in rice. <i>Theoretical and Applied Genetics</i> , 2020, 133, 2387-2399.	1.8	25
29	<i>OsMFT2</i> is involved in the regulation of ABA signaling-mediated seed germination through interacting with <i>OsZIP23/66/72</i> in rice. <i>Plant Journal</i> , 2020, 103, 532-546.	2.8	58
30	Minor Effects of 11 Dof Family Genes Contribute to the Missing Heritability of Heading Date in Rice ( <i>Oryza sativa</i> L.). <i>Frontiers in Plant Science</i> , 2020, 10, 1739.	1.7	11
31	CCT domain-containing genes in cereal crops: flowering time and beyond. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1385-1396.	1.8	30
32	Development of Whole-Genome Agarose-Resolvable LlnDel Markers in Rice. <i>Rice</i> , 2020, 13, 1.	1.7	73
33	Genetic Interactions Among <i>Ghd7</i> , <i>Ghd8</i> , <i>OsPRR37</i> and <i>Hd1</i> Contribute to Large Variation in Heading Date in Rice. <i>Rice</i> , 2019, 12, 48.	1.7	57
34	Nitrogen, phosphorus, and potassium fertilization affects the flowering time of rice ( <i>Oryza sativa</i> L.). <i>Global Ecology and Conservation</i> , 2019, 20, e00753.	1.0	55
35	<i>Hd1</i> function conversion in regulating heading is dependent on gene combinations of <i>Ghd7</i> , <i>Ghd8</i> , and <i>Ghd7.1</i> under long-day conditions in rice. <i>Molecular Breeding</i> , 2019, 39, 1.	1.0	26
36	Beyond heading time: <i>FT</i> -like genes and spike development in cereals. <i>Journal of Experimental Botany</i> , 2019, 70, 1-3.	2.4	12

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37	Natural variation in the <i>HAN1</i> gene confers chilling tolerance in rice and allowed adaptation to a temperate climate. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 3494-3501.	3.3	139
38	Lessons from natural variations: artificially induced heading date variations for improvement of regional adaptation in rice. Theoretical and Applied Genetics, 2019, 132, 383-394.	1.8	25
39	<i>PALE-GREEN LEAF12</i> Encodes a Novel Pentatricopeptide Repeat Protein Required for Chloroplast Development and 16S rRNA Processing in Rice. Plant and Cell Physiology, 2019, 60, 587-598.	1.5	24
40	<i>Short Panicle 3</i> controls panicle architecture by upregulating <i>APO2/RFL</i> and increasing cytokinin content in rice. Journal of Integrative Plant Biology, 2019, 61, 987-999.	4.1	35
41	Overexpression of an auxin receptor OsAFB6 significantly enhanced grain yield by increasing cytokinin and decreasing auxin concentrations in rice panicle. Scientific Reports, 2018, 8, 14051.	1.6	24
42	Genes Contributing to Domestication of Rice Seed Traits and Its Global Expansion. Genes, 2018, 9, 489.	1.0	20
43	Gene diagnosis and targeted breeding for blast-resistant Kongyu 131 without changing regional adaptability. Journal of Genetics and Genomics, 2018, 45, 539-547.	1.7	16
44	Genome-Wide Association Studies Reveal the Genetic Basis of Ionomic Variation in Rice. Plant Cell, 2018, 30, 2720-2740.	3.1	164
45	OsMFT1 increases spikelets per panicle and delays heading date in rice by suppressing Ehd1, FZP and SEPALLATA-like genes. Journal of Experimental Botany, 2018, 69, 4283-4293.	2.4	50
46	Genome-wide association studies reveal that members of bHLH subfamily 16 share a conserved function in regulating flag leaf angle in rice ( <i>Oryza sativa</i> ). PLoS Genetics, 2018, 14, e1007323.	1.5	52
47	Next-Generation Sequencing Promoted the Release of Reference Genomes and Discovered Genome Evolution in Cereal Crops. Current Issues in Molecular Biology, 2018, 27, 37-50.	1.0	5
48	A Rice Genetic Improvement Boom by Next Generation Sequencing. Current Issues in Molecular Biology, 2018, 27, 109-126.	1.0	10
49	QTLs for heading date and plant height under multiple environments in rice. Genetica, 2017, 145, 67-77.	0.5	19
50	Duplication of an upstream silencer of FZP increases grain yield in rice. Nature Plants, 2017, 3, 885-893.	4.7	121
51	Alternative functions of Hd1 in repressing or promoting heading are determined by Ghd7 status under long-day conditions. Scientific Reports, 2017, 7, 5388.	1.6	81
52	Auxin Binding Protein 1 Reinforces Resistance to Sugarcane Mosaic Virus in Maize. Molecular Plant, 2017, 10, 1357-1360.	3.9	33
53	The CCT domain-containing gene family has large impacts on heading date, regional adaptation, and grain yield in rice. Journal of Integrative Agriculture, 2017, 16, 2686-2697.	1.7	12
54	Intragenic recombination between two non-functional semi-dwarf 1 alleles produced a functional SD1 allele in a tall recombinant inbred line in rice. PLoS ONE, 2017, 12, e0190116.	1.1	11

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55	Genome-Wide Association Analysis Reveals Different Genetic Control in Panicle Architecture Between <i>Indica</i> and <i>Japonica</i> Rice. <i>Plant Genome</i> , 2016, 9, plantgenome2015.11.0115.	1.6	57
56	Genome-Wide Association Studies Reveal that Diverse Heading Date Genes Respond to Short and Long Day Lengths between <i>Indica</i> and <i>Japonica</i> Rice. <i>Frontiers in Plant Science</i> , 2016, 7, 1270.	1.7	40
57	Regulatory role of FZP in the determination of panicle branching and spikelet formation in rice. <i>Scientific Reports</i> , 2016, 6, 19022.	1.6	72
58	Genome-wide association mapping revealed a diverse genetic basis of seed dormancy across subpopulations in rice ( <i>Oryza sativa</i> L.). <i>BMC Genetics</i> , 2016, 17, 28.	2.7	64
59	Extensive sequence divergence between the reference genomes of two elite <i>indica</i> rice varieties Zhenshan 97 and Minghui 63. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E5163-71.	3.3	211
60	Genome-wide association analysis reveals flowering-related genes regulating rachis length in rice. <i>Plant Breeding</i> , 2016, 135, 677-682.	1.0	6
61	Building two indica rice reference genomes with PacBio long-read and Illumina paired-end sequencing data. <i>Scientific Data</i> , 2016, 3, 160076.	2.4	34
62	Genomewide association analysis for awn length linked to the seed shattering gene qSH1 in rice. <i>Journal of Genetics</i> , 2016, 95, 639-646.	0.4	10
63	Duplication of <i>OsHAP</i> family genes and their association with heading date in rice. <i>Journal of Experimental Botany</i> , 2016, 67, 1759-1768.	2.4	34
64	Nucleotide Diversity and Molecular Evolution of the ALK Gene in Cultivated Rice and its Wild Relatives. <i>Plant Molecular Biology Reporter</i> , 2016, 34, 923-930.	1.0	11
65	A Novel Tiller Angle Gene, TAC3, together with TAC1 and D2 Largely Determine the Natural Variation of Tiller Angle in Rice Cultivars. <i>PLoS Genetics</i> , 2016, 12, e1006412.	1.5	106
66	Progress in understanding molecular genetic basis of heterosis in rice. <i>Chinese Science Bulletin</i> , 2016, 61, 3842-3849.	0.4	2
67	Combinations of the <i>Ghd7</i> , <i>Ghd8</i> and <i>Hd1</i> genes largely define the ecogeographical adaptation and yield potential of cultivated rice. <i>New Phytologist</i> , 2015, 208, 1056-1066.	3.5	126
68	RiceVarMap: a comprehensive database of rice genomic variations. <i>Nucleic Acids Research</i> , 2015, 43, D1018-D1022.	6.5	219
69	Three CCT domain-containing genes were identified to regulate heading date by candidate gene-based association mapping and transformation in rice. <i>Scientific Reports</i> , 2015, 5, 7663.	1.6	61
70	QTL mapping for thermo-sensitive heading date in rice. <i>Euphytica</i> , 2015, 205, 51-62.	0.6	3
71	Genetic Architecture of Natural Variation in Rice Chlorophyll Content Revealed by a Genome-Wide Association Study. <i>Molecular Plant</i> , 2015, 8, 946-957.	3.9	106
72	Loss of function of <i>OsMADS3</i> via the insertion of a novel retrotransposon leads to recessive male sterility in rice ( <i>Oryza sativa</i> ). <i>Plant Science</i> , 2015, 238, 188-197.	1.7	14

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73	Two quantitative trait loci for grain yield and plant height on chromosome 3 are tightly linked in coupling phase in rice. <i>Molecular Breeding</i> , 2015, 35, 1.	1.0	18
74	The regulatory network mediated by circadian clock genes is related to heterosis in rice. <i>Journal of Integrative Plant Biology</i> , 2015, 57, 300-312.	4.1	19
75	Two Novel QTLs for Heading Date Are Identified Using a Set of Chromosome Segment Substitution Lines in Rice ( <i>Oryza sativa</i> L.). <i>Journal of Genetics and Genomics</i> , 2014, 41, 659-662.	1.7	14
76	Identification and fine mapping of quantitative trait loci for seed vigor in germination and seedling establishment in rice. <i>Journal of Integrative Plant Biology</i> , 2014, 56, 749-759.	4.1	91
77	<i>Ghd7</i> Is a Central Regulator of Growth, Development, and Stress Response in Rice. <i>Plant Physiology</i> , 2014, 164, 735-747.	2.3	198
78	Chalk5 encodes a vacuolar H <sup>+</sup> -translocating pyrophosphatase influencing grain chalkiness in rice. <i>Nature Genetics</i> , 2014, 46, 398-404.	9.4	281
79	Dominance and epistasis are the main contributors to heterosis for plant height in rice. <i>Plant Science</i> , 2014, 215-216, 11-18.	1.7	51
80	Validation and Characterization of <i>Ghd7.1</i> , a Major Quantitative Trait Locus with Pleiotropic Effects on Spikelets per Panicle, Plant Height, and Heading Date in Rice ( <i>Oryza sativa</i> ). <i>Journal of Genetics and Genomics</i> , 2013, 40, 629-638.	1.7	21
81	Natural variation and artificial selection in four genes determine grain shape in rice. <i>New Phytologist</i> , 2013, 200, 1269-1280.	3.5	70
82	QTL Scanning for Rice Yield Using a Whole Genome SNP Array. <i>Journal of Genetics and Genomics</i> , 2013, 40, 629-638.	1.7	21
83	Expression patterns of photoperiod and temperature regulated heading date genes in <i>Oryza sativa</i> . <i>Computational Biology and Chemistry</i> , 2013, 45, 36-41.	1.1	5
84	Molecular Diagnostics in Rice ( <i>Oryza sativa</i> )., 2013, , 443-465.		0
85	Identification of genomic loci associated with crown rust resistance in perennial ryegrass ( <i>Lolium perenne</i> ). <i>Journal of Genetics and Genomics</i> , 2013, 40, 629-638.	1.7	21
86	Identification and validation of a yield-enhancing QTL cluster in rice ( <i>Oryza sativa</i> L.). <i>Euphytica</i> , 2013, 192, 145-153.	0.6	9
87	Natural variation in <i>Ghd7.1</i> plays an important role in grain yield and adaptation in rice. <i>Cell Research</i> , 2013, 23, 969-971.	5.7	222
88	Genome Mapping, Markers and QTLs. , 2013, , 35-54.		1
89	Genetic composition of yield heterosis in an elite rice hybrid. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 15847-15852.	3.3	214
90	Comparative mapping reveals similar linkage of functional genes to QTL of yield-related traits between <i>Brassica napus</i> and <i>Oryza sativa</i> . <i>Journal of Genetics</i> , 2012, 91, 163-170.	0.4	6

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91	Improving rice yield and quality by QTL pyramiding. <i>Molecular Breeding</i> , 2012, 29, 903-913.	1.0	30
92	Yield-related QTLs and Their Applications in Rice Genetic Improvement<sup>F</sup>. <i>Journal of Integrative Plant Biology</i> , 2012, 54, 300-311.	4.1	94
93	Evolution and Association Analysis of Ghd7 in Rice. <i>PLoS ONE</i> , 2012, 7, e34021.	1.1	100
94	Natural variation in GS5 plays an important role in regulating grain size and yield in rice. <i>Nature Genetics</i> , 2011, 43, 1266-1269.	9.4	821
95	Quantitative trait loci for seed dormancy in rice. <i>Euphytica</i> , 2011, 178, 427-435.	0.6	22
96	Impact of seasonal changes on spikelets per panicle, panicle length and plant height in rice ( <i>Oryza</i> ) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	0.6	17
97	Epistasis and complementary gene action adequately account for the genetic bases of transgressive segregation of kilo-grain weight in rice. <i>Euphytica</i> , 2011, 180, 261-271.	0.6	28
98	Identification and characterization of quantitative trait loci for grain yield and its components under different nitrogen fertilization levels in rice ( <i>Oryza sativa</i> L.). <i>Molecular Breeding</i> , 2011, 28, 495-509.	1.0	24
99	Two complementary recessive genes in duplicated segments control etiolation in rice. <i>Theoretical and Applied Genetics</i> , 2011, 122, 373-383.	1.8	20
100	Candidacy of a chitin-inducible gibberellin-responsive gene for a major locus affecting plant height in rice that is closely linked to Green Revolution gene sd1. <i>Theoretical and Applied Genetics</i> , 2011, 123, 705-714.	1.8	41
101	Quantitative trait loci for rice yield-related traits using recombinant inbred lines derived from two diverse cultivars. <i>Journal of Genetics</i> , 2011, 90, 209-215.	0.4	63
102	Comparison of quantitative trait loci for rice yield, panicle length and spikelet density across three connected populations. <i>Journal of Genetics</i> , 2011, 90, 377-382.	0.4	36
103	A Major QTL, Ghd8, Plays Pleiotropic Roles in Regulating Grain Productivity, Plant Height, and Heading Date in Rice. <i>Molecular Plant</i> , 2011, 4, 319-330.	3.9	498
104	Quantitative trait loci for the number of grains per panicle dependent on or independent of heading date in rice ( <i>Oryza sativa</i> L.). <i>Breeding Science</i> , 2011, 61, 142-150.	0.9	11
105	Gains in QTL Detection Using an Ultra-High Density SNP Map Based on Population Sequencing Relative to Traditional RFLP/SSR Markers. <i>PLoS ONE</i> , 2011, 6, e17595.	1.1	228
106	Mapping and validation of quantitative trait loci for spikelets per panicle and 1,000-grain weight in rice ( <i>Oryza sativa</i> L.). <i>Theoretical and Applied Genetics</i> , 2010, 120, 933-942.	1.8	54
107	Genetic and physical fine mapping of Scmv2, a potyvirus resistance gene in maize. <i>Theoretical and Applied Genetics</i> , 2010, 120, 1621-1634.	1.8	35
108	Molecular dissection of genetic basis of significant correlation among five morphological traits in rice ( <i>Oryza sativa</i> L.). <i>Science Bulletin</i> , 2010, 55, 3154-3160.	1.7	14



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109	Comparison of quantitative trait loci for 1,000-grain weight and spikelets per panicle across three connected rice populations. <i>Euphytica</i> , 2010, 175, 383-394.	0.6	15
110	Genetic dissection of rice grain shape using a recombinant inbred line population derived from two contrasting parents and fine mapping a pleiotropic quantitative trait locus qGL7. <i>BMC Genetics</i> , 2010, 11, 16.	2.7	162
111	A global analysis of QTLs for expression variations in rice shoots at the early seedling stage. <i>Plant Journal</i> , 2010, 63, 1063-1074.	2.8	69
112	Parent-independent genotyping for constructing an ultrahigh-density linkage map based on population sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 10578-10583.	3.3	299
113	Genetic and Molecular Bases of Rice Yield. <i>Annual Review of Plant Biology</i> , 2010, 61, 421-442.	8.6	762
114	Expression of CENH3 alleles in synthesized allopolyploid <i>Oryza</i> species. <i>Journal of Genetics and Genomics</i> , 2010, 37, 703-711.	1.7	7
115	Additive and additive $\times$ additive interaction make important contributions to spikelets per panicle in rice near isogenic ( <i>Oryza sativa</i> L.) lines. <i>Journal of Genetics and Genomics</i> , 2010, 37, 795-803.	1.7	11
116	A causal C $\rightarrow$ A mutation in the second exon of GS3 highly associated with rice grain length and validated as a functional marker. <i>Theoretical and Applied Genetics</i> , 2009, 118, 465-472.	1.8	160
117	Four rice QTL controlling number of spikelets per panicle expressed the characteristics of single Mendelian gene in near isogenic backgrounds. <i>Theoretical and Applied Genetics</i> , 2009, 118, 1035-1044.	1.8	54
118	Fine mapping SPP1, a QTL controlling the number of spikelets per panicle, to a BAC clone in rice ( <i>Oryza</i> ) Tj ETQq0 0.0 rgBT /Overlock 10	1.8	66
119	Mapping QTLs for seedling characteristics under different water supply conditions in rice (<i>Oryza) Tj ETQq1 1 0.784314 rgBT /Overlock	2.6	39
120	Natural variation in Ghd7 is an important regulator of heading date and yield potential in rice. <i>Nature Genetics</i> , 2008, 40, 761-767.	9.4	1,666
121	Identification of quantitative trait loci for four morphologic traits under water stress in rice ( <i>Oryza</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock	1.7	35
122	Nucleotide diversity and linkage disequilibrium in 11 expressed resistance candidate genes in <i>Lolium perenne</i> . <i>BMC Plant Biology</i> , 2007, 7, 43.	1.6	62
123	A major QTL associated with cold tolerance at seedling stage in rice ( <i>Oryza sativa</i> L.). <i>Euphytica</i> , 2007, 158, 87-94.	0.6	125
124	Analysis of sugarcane mosaic virus resistance in maize in an isogenic dihybrid crossing scheme and implications for breeding potyvirus-resistant maize hybrids. <i>Genome</i> , 2006, 49, 1274-1282.	0.9	27
125	Molecular Marker-Assisted Dissection of Quantitative Trait Loci for seven Morphological Traits in Rice ( <i>Oryza Sativa</i> L.). <i>Euphytica</i> , 2006, 150, 131-139.	0.6	17
126	GS3, a major QTL for grain length and weight and minor QTL for grain width and thickness in rice, encodes a putative transmembrane protein. <i>Theoretical and Applied Genetics</i> , 2006, 112, 1164-1171.	1.8	1,252



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127	Quantitative trait loci for panicle size, heading date and plant height co-segregating in trait-performance derived near-isogenic lines of rice ( <i>Oryza sativa</i> ). <i>Theoretical and Applied Genetics</i> , 2006, 113, 361-368.	1.8	85
128	Molecular dissection of developmental behavior of tiller number and plant height and their relationship in rice ( <i>Oryza sativa</i> L.). <i>Hereditas</i> , 2006, 143, 236-245.	0.5	43
129	Genetic Basis of Drought Resistance at Reproductive Stage in Rice: Separation of Drought Tolerance From Drought Avoidance. <i>Genetics</i> , 2006, 172, 1213-1228.	1.2	359
130	QTL mapping of vernalization response in perennial ryegrass ( <i>Lolium perenne</i> L.) reveals co-location with an orthologue of wheat VRN1. <i>Theoretical and Applied Genetics</i> , 2005, 110, 527-536.	1.8	147
131	Genetic analysis for drought resistance of rice at reproductive stage in field with different types of soil. <i>Theoretical and Applied Genetics</i> , 2005, 111, 1127-1136.	1.8	106
132	QTLs for low nitrogen tolerance at seedling stage identified using a recombinant inbred line population derived from an elite rice hybrid. <i>Theoretical and Applied Genetics</i> , 2005, 112, 85-96.	1.8	127
133	Comparative analyses of genomic locations and race specificities of loci for quantitative resistance to <i>Pyricularia grisea</i> in rice and barley. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 2544-2549.	3.3	122
134	Single-locus heterotic effects and dominance by dominance interactions can adequately explain the genetic basis of heterosis in an elite rice hybrid. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 2574-2579.	3.3	367
135	Development and Mapping of 2240 New SSR Markers for Rice ( <i>Oryza sativa</i> L.) (Supplement). <i>DNA Research</i> , 2002, 9, 257-279.	1.5	121
136	Development and Mapping of 2240 New SSR Markers for Rice ( <i>Oryza sativa</i> L.). <i>DNA Research</i> , 2002, 9, 199-207.	1.5	1,203
137	Quantitative Genetic Basis of Gelatinization Temperature of Rice. <i>Cereal Chemistry</i> , 2001, 78, 666-674.	1.1	6