

Qifa Zhang

List of Publications by Year in descending order

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170
papers

26,603
citations

5569

82
h-index

6294

158
g-index

176
all docs

176
docs citations

176
times ranked

15547
citing authors

#	ARTICLE	IF	CITATIONS
1	From Green Super Rice to green agriculture: Reaping the promise of functional genomics research. <i>Molecular Plant</i> , 2022, 15, 9-26.	3.9	44
2	Understanding the genetic and molecular constitutions of heterosis for developing hybrid rice. <i>Journal of Genetics and Genomics</i> , 2022, 49, 385-393.	1.7	22
3	Parental variation in CHG methylation is associated with allelic-specific expression in elite hybrid rice. <i>Plant Physiology</i> , 2021, 186, 1025-1041.	2.3	31
4	Purple Tomatoes, Black Rice and Food Security. <i>Nature Reviews Genetics</i> , 2021, 22, 414-414.	7.7	24
5	Designing Future Crops: Genomics-Assisted Breeding Comes of Age. <i>Trends in Plant Science</i> , 2021, 26, 631-649.	4.3	244
6	Two gap-free reference genomes and a global view of the centromere architecture in rice. <i>Molecular Plant</i> , 2021, 14, 1757-1767.	3.9	133
7	The RING E3 ligase CLG1 targets GS3 for degradation via the endosome pathway to determine grain size in rice. <i>Molecular Plant</i> , 2021, 14, 1699-1713.	3.9	41
8	Bract suppression regulated by the miR156/529-SPLs-NL1-PLA1 module is required for the transition from vegetative to reproductive branching in rice. <i>Molecular Plant</i> , 2021, 14, 1168-1184.	3.9	35
9	Hybrid breeding of rice via genomic selection. <i>Plant Biotechnology Journal</i> , 2020, 18, 57-67.	4.1	87
10	Genomic Breeding of Green Super Rice Varieties and Their Deployment in Asia and Africa. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1427-1442.	1.8	53
11	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
12	Integrative analysis of reference epigenomes in 20 rice varieties. <i>Nature Communications</i> , 2020, 11, 2658.	5.8	86
13	Artificial Selection in Domestication and Breeding Prevents Speciation in Rice. <i>Molecular Plant</i> , 2020, 13, 650-657.	3.9	12
14	5Gs for crop genetic improvement. <i>Current Opinion in Plant Biology</i> , 2020, 56, 190-196.	3.5	134
15	The versatile functions of OsALDH2B1 provide a genic basis for growth“defense trade-offs in rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 3867-3873.	3.3	52
16	Crop genetics research in Asia: improving food security and nutrition. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1339-1344.	1.8	4
17	Chromatin loops associated with active genes and heterochromatin shape rice genome architecture for transcriptional regulation. <i>Nature Communications</i> , 2019, 10, 3640.	5.8	75
18	Mapping quantitative trait loci using binned genotypes. <i>Journal of Genetics and Genomics</i> , 2019, 46, 343-352.	1.7	2

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19	Patterns of genome-wide allele-specific expression in hybrid rice and the implications on the genetic basis of heterosis. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 5653-5658.	3.3	130
20	A G-protein pathway determines grain size in rice. Nature Communications, 2018, 9, 851.	5.8	195
21	Rice Functional Genomics Research: Past Decade and Future. Molecular Plant, 2018, 11, 359-380.	3.9	113
22	Cis-directed cleavage and nonstoichiometric abundances of 21 nucleotide reproductive phased small interfering RNA</scps>s in grasses. New Phytologist, 2018, 220, 865-877.	3.5	38
23	Genetic and molecular characterization of photoperiod and thermo-sensitive male sterility in rice. Plant Reproduction, 2018, 31, 3-14.	1.3	59
24	The molecular and evolutionary basis of reproductive isolation in plants. Journal of Genetics and Genomics, 2018, 45, 613-620.	1.7	26
25	The rice genome revolution: from an ancient grain to Green Super Rice. Nature Reviews Genetics, 2018, 19, 505-517.	7.7	251
26	Processes Underlying a Reproductive Barrier in <i>indica</i>-<i>japonica</i> Rice Hybrids Revealed by Transcriptome Analysis. Plant Physiology, 2017, 174, 1683-1696.	2.3	22
27	Boosting Rice Yield by Fine-Tuning SPL Gene Expression. Trends in Plant Science, 2017, 22, 643-646.	4.3	72
28	Three representative inter and intra-subspecific crosses reveal the genetic architecture of reproductive isolation in rice. Plant Journal, 2017, 92, 349-362.	2.8	33
29	Metabolomic prediction of yield in hybrid rice. Plant Journal, 2016, 88, 219-227.	2.8	120
30	PMS1T</i>, producing phased small-interfering RNAs, regulates photoperiod-sensitive male sterility in rice. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 15144-15149.	3.3	234
31	Genetic Components of Heterosis for Seedling Traits in an Elite Rice Hybrid Analyzed Using an Immortalized F2 Population. Journal of Genetics and Genomics, 2016, 43, 87-97.	1.7	49
32	Origination and Establishment of a Trigenic Reproductive Isolation System in Rice. Molecular Plant, 2016, 9, 1542-1545.	3.9	18
33	Extensive sequence divergence between the reference genomes of two elite <i>indica</i> rice varieties Zhenshan 97 and Minghui 63. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E5163-71.	3.3	211
34	Allelic diversity in an NLR gene <i>BPH9</i> enables rice to combat planthopper variation. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 12850-12855.	3.3	196
35	Building two indica rice reference genomes with PacBio long-read and Illumina paired-end sequencing data. Scientific Data, 2016, 3, 160076.	2.4	34
36	Stacking S5-n and f5-n to overcome sterility in indica-japonica hybrid rice. Theoretical and Applied Genetics, 2016, 129, 563-575.	1.8	37

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37	Differential expression of GS5 regulates grain size in rice. <i>Journal of Experimental Botany</i> , 2015, 66, 2611-2623.	2.4	119
38	Breeding signatures of rice improvement revealed by a genomic variation map from a large germplasm collection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E5411-9.	3.3	165
39	Coordinated regulation of vegetative and reproductive branching in rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 15504-15509.	3.3	218
40	Genetic basis of sRNA quantitative variation analyzed using an experimental population derived from an elite rice hybrid. <i>ELife</i> , 2015, 4, e04250.	2.8	12
41	Understanding a key gene for thermosensitive genic male sterility in rice. <i>Science China Life Sciences</i> , 2014, 57, 1241-1242.	2.3	4
42	<i>Grain Number</i> , <i>Plant Height</i> , and <i>Heading Date</i> Is a Central Regulator of Growth, Development, and Stress Response. <i>Plant Physiology</i> , 2014, 164, 735-747.	2.3	198
43	A whole-genome SNP array (RICE6K) for genomic breeding in rice. <i>Plant Biotechnology Journal</i> , 2014, 12, 28-37.	4.1	163
44	Comparative BAC-based physical mapping of <i>Oryza sativa</i> ssp. <i>indica</i> var. 9311 and evaluation of the two rice reference sequence assemblies. <i>Plant Journal</i> , 2014, 77, 795-805.	2.8	16
45	Combining high-throughput phenotyping and genome-wide association studies to reveal natural genetic variation in rice. <i>Nature Communications</i> , 2014, 5, 5087.	5.8	490
46	Predicting hybrid performance in rice using genomic best linear unbiased prediction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 12456-12461.	3.3	194
47	Global Genomic Diversity of <i>Oryza sativa</i> Varieties Revealed by Comparative Physical Mapping. <i>Genetics</i> , 2014, 196, 937-949.	1.2	10
48	An expression quantitative trait loci-guided co-expression analysis for constructing regulatory network using a rice recombinant inbred line population. <i>Journal of Experimental Botany</i> , 2014, 65, 1069-1079.	2.4	74
49	A High-Density SNP Genotyping Array for Rice Biology and Molecular Breeding. <i>Molecular Plant</i> , 2014, 7, 541-553.	3.9	251
50	OsAP65, a rice aspartic protease, is essential for male fertility and plays a role in pollen germination and pollen tube growth. <i>Journal of Experimental Botany</i> , 2013, 64, 3351-3360.	2.4	52
51	Mutant Resources for the Functional Analysis of the Rice Genome. <i>Molecular Plant</i> , 2013, 6, 596-604.	3.9	112
52	Genome studies and molecular genetics: understanding the functional genome based on the rice model. <i>Current Opinion in Plant Biology</i> , 2013, 16, 129-132.	3.5	13
53	Heterosis in elite hybrid rice: speculation on the genetic and biochemical mechanisms. <i>Current Opinion in Plant Biology</i> , 2013, 16, 221-227.	3.5	68
54	Understanding Reproductive Isolation Based on the Rice Model. <i>Annual Review of Plant Biology</i> , 2013, 64, 111-135.	8.6	116

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55	Genetic analysis of the metabolome exemplified using a rice population. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 20320-20325.	3.3	155
56	Heterosis. , 2013, , 255-268.		0
57	Dynamic Intra-Japonica Subspecies Variation and Resource Application. Molecular Plant, 2012, 5, 218-230.	3.9	23
58	Genetic composition of yield heterosis in an elite rice hybrid. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 15847-15852.	3.3	214
59	CHD3 protein recognizes and regulates methylated histone H3 lysines 4 and 27 over a subset of targets in the rice genome. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 5773-5778.	3.3	93
60	A long noncoding RNA regulates photoperiod-sensitive male sterility, an essential component of hybrid rice. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 2654-2659.	3.3	572
61	A Killer-Protector System Regulates Both Hybrid Sterility and Segregation Distortion in Rice. Science, 2012, 337, 1336-1340.	6.0	263
62	RNA-Directed DNA Methylation Is Involved in Regulating Photoperiod-Sensitive Male Sterility in Rice. Molecular Plant, 2012, 5, 1210-1216.	3.9	127
63	Rice functional genomics research: Progress and implications for crop genetic improvement. Biotechnology Advances, 2012, 30, 1059-1070.	6.0	100
64	The Rice HGW Gene Encodes a Ubiquitin-Associated (UBA) Domain Protein That Regulates Heading Date and Grain Weight. PLoS ONE, 2012, 7, e34231.	1.1	83
65	XIAO is involved in the control of organ size by contributing to the regulation of signaling and homeostasis of brassinosteroids and cell cycling in rice. Plant Journal, 2012, 70, 398-408.	2.8	87
66	Natural variation in GS5 plays an important role in regulating grain size and yield in rice. Nature Genetics, 2011, 43, 1266-1269.	9.4	821
67	Complex evolution of <i>S5</i> , a major reproductive barrier regulator, in the cultivated rice <i>Oryza sativa</i> and its wild relatives. New Phytologist, 2011, 191, 275-287.	3.5	33
68	OsBC1L4 encodes a COBRA-like protein that affects cellulose synthesis in rice. Plant Molecular Biology, 2011, 75, 333-345.	2.0	67
69	Rice APOPTOSIS INHIBITOR5 Coupled with Two DEAD-Box Adenosine 5'-Triphosphate-Dependent RNA Helicases Regulates Tapetum Degeneration. Plant Cell, 2011, 23, 1416-1434.	3.1	129
70	Heterosis in Rice Seedlings: Its Relationship to Gibberellin Content and Expression of Gibberellin Metabolism and Signaling Genes. Plant Physiology, 2011, 156, 1905-1920.	2.3	47
71	Gains in QTL Detection Using an Ultra-High Density SNP Map Based on Population Sequencing Relative to Traditional RFLP/SSR Markers. PLoS ONE, 2011, 6, e17595.	1.1	228
72	Transcriptomic analysis of rice responses to low phosphorus stress. Science Bulletin, 2010, 55, 251-258.	1.7	25

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73	Co-suppressed glutamine synthetase2 gene modifies nitrogen metabolism and plant growth in rice. Science Bulletin, 2010, 55, 823-833.	1.7	25
74	Hybrid sterility in plant: stories from rice. Current Opinion in Plant Biology, 2010, 13, 186-192.	3.5	93
75	A dynamic gene expression atlas covering the entire life cycle of rice. Plant Journal, 2010, 61, 752-766.	2.8	326
76	A global analysis of QTLs for expression variations in rice shoots at the early seedling stage. Plant Journal, 2010, 63, 1063-1074.	2.8	69
77	Parent-independent genotyping for constructing an ultrahigh-density linkage map based on population sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 10578-10583.	3.3	299
78	Linking differential domain functions of the GS3 protein to natural variation of grain size in rice. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 19579-19584.	3.3	580
79	Genetic and Molecular Bases of Rice Yield. Annual Review of Plant Biology, 2010, 61, 421-442.	8.6	762
80	Replication Protein A (RPA1a) Is Required for Meiotic and Somatic DNA Repair But Is Dispensable for DNA Replication and Homologous Recombination in Rice. Plant Physiology, 2009, 151, 2162-2173.	2.3	78
81	Mutant Resources in Rice for Functional Genomics of the Grasses. Plant Physiology, 2009, 149, 165-170.	2.3	167
82	FLEXIBLE CULM 1 encoding a cinnamyl-alcohol dehydrogenase controls culm mechanical strength in rice. Plant Molecular Biology, 2009, 69, 685-697.	2.0	124
83	Comprehensive sequence and expression profile analysis of Hsp20 gene family in rice. Plant Molecular Biology, 2009, 70, 341-357.	2.0	95
84	The ankyrin repeat gene family in rice: genome-wide identification, classification and expression profiling. Plant Molecular Biology, 2009, 71, 207-226.	2.0	47
85	Molecular characterization, expression pattern, and function analysis of the OsBC1L family in rice. Plant Molecular Biology, 2009, 71, 469-481.	2.0	29
86	Advances in the understanding of inter-subspecific hybrid sterility and wide-compatibility in rice. Science Bulletin, 2009, 54, 2332-2341.	1.7	55
87	Review and prospect of transgenic rice research. Science Bulletin, 2009, 54, 4049-4068.	1.7	46
88	Over-expression of aspartate aminotransferase genes in rice resulted in altered nitrogen metabolism and increased amino acid content in seeds. Theoretical and Applied Genetics, 2009, 118, 1381-1390.	1.8	115
89	Single feature polymorphisms between two rice cultivars detected using a median polish method. Theoretical and Applied Genetics, 2009, 119, 151-164.	1.8	13
90	Overexpressed glutamine synthetase gene modifies nitrogen metabolism and abiotic stress responses in rice. Plant Cell Reports, 2009, 28, 527-537.	2.8	203

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91	Molecular analyses of the rice glutamate dehydrogenase gene family and their response to nitrogen and phosphorous deprivation. <i>Plant Cell Reports</i> , 2009, 28, 1115-1126.	2.8	47
92	Mutation of the rice gene <i>PAIR3</i> results in lack of bivalent formation in meiosis. <i>Plant Journal</i> , 2009, 59, 303-315.	2.8	64
93	Aspartic proteases gene family in rice: Gene structure and expression, predicted protein features and phylogenetic relation. <i>Gene</i> , 2009, 442, 108-118.	1.0	63
94	Sequence and expression analysis of the C3HC4-type RING finger gene family in rice. <i>Gene</i> , 2009, 444, 33-45.	1.0	59
95	Fine mapping of a major quantitative trait loci, qSSP7, controlling the number of spikelets per panicle as a single Mendelian factor in rice. <i>Theoretical and Applied Genetics</i> , 2008, 116, 789-796.	1.8	83
96	Sequence and expression analysis of the thioredoxin protein gene family in rice. <i>Molecular Genetics and Genomics</i> , 2008, 280, 139-51.	1.0	58
97	KT/HAK/KUP potassium transporters gene family and their whole-life cycle expression profile in rice (<i>Oryza sativa</i>). <i>Molecular Genetics and Genomics</i> , 2008, 280, 437-52.	1.0	129
98	Natural variation in <i>Ghd7</i> is an important regulator of heading date and yield potential in rice. <i>Nature Genetics</i> , 2008, 40, 761-767.	9.4	1,666
99	RICD: A rice indica cDNA database resource for rice functional genomics. <i>BMC Plant Biology</i> , 2008, 8, 118.	1.6	24
100	Comprehensive sequence and expression profile analysis of PEX11 gene family in rice. <i>Gene</i> , 2008, 412, 59-70.	1.0	29
101	Effect of Transgenic <i>Bacillus thuringiensis</i> Rice Lines on Mortality and Feeding Behavior of Rice Stem Borers (Lepidoptera: Crambidae). <i>Journal of Economic Entomology</i> , 2008, 101, 182-189.	0.8	48
102	Rice 2020: A Call For An International Coordinated Effort In Rice Functional Genomics. <i>Molecular Plant</i> , 2008, 1, 715-719.	3.9	104
103	<i>RID1</i> , encoding a Cys2/His2-type zinc finger transcription factor, acts as a master switch from vegetative to floral development in rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 12915-12920.	3.3	207
104	A triallelic system of <i>S5</i> is a major regulator of the reproductive barrier and compatibility of indica-japonica hybrids in rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 11436-11441.	3.3	257
105	Rice Genome Research: Current Status and Future Perspectives. <i>Plant Genome</i> , 2008, 1, .	1.6	7
106	Strategies for developing Green Super Rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 16402-16409.	3.3	653
107	Rice functional genomics research in China. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2007, 362, 1009-1021.	1.8	28
108	The Rice YABBY1 Gene Is Involved in the Feedback Regulation of Gibberellin Metabolism. <i>Plant Physiology</i> , 2007, 144, 121-133.	2.3	168

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109	Non-random distribution of T-DNA insertions at various levels of the genome hierarchy as revealed by analyzing 13804 T-DNA flanking sequences from an enhancer-trap mutant library. <i>Plant Journal</i> , 2007, 49, 947-959.	2.8	107
110	Genetic basis of 17 traits and viscosity parameters characterizing the eating and cooking quality of rice grain. <i>Theoretical and Applied Genetics</i> , 2007, 115, 463-476.	1.8	148
111	The QTL controlling amino acid content in grains of rice (<i>Oryza sativa</i>) are co-localized with the regions involved in the amino acid metabolism pathway. <i>Molecular Breeding</i> , 2007, 21, 127-137.	1.0	69
112	Analysis of rice genes induced by striped stemborer (<i>Chilo suppressalis</i>) attack identified a promoter fragment highly specifically responsive to insect feeding. <i>Plant Molecular Biology</i> , 2007, 65, 519-530.	2.0	24
113	Rapid genome evolution in Pms1 region of rice revealed by comparative sequence analysis. <i>Science Bulletin</i> , 2007, 52, 912-921.	1.7	2
114	Genomics-based strategies for the development of "green super rice". , 2007, , .		0
115	Plant Nutriomics in China: An Overview. <i>Annals of Botany</i> , 2006, 98, 473-482.	1.4	167
116	Overexpressing a NAM, ATAF, and CUC (NAC) transcription factor enhances drought resistance and salt tolerance in rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 12987-12992.	3.3	1,371
117	Establishment of a patterned GAL4-VP16 transactivation system for discovering gene function in rice. <i>Plant Journal</i> , 2006, 46, 1059-1072.	2.8	33
118	Expression Profiles of 10,422 Genes at Early Stage of Low Nitrogen Stress in Rice Assayed using a cDNA Microarray. <i>Plant Molecular Biology</i> , 2006, 60, 617-631.	2.0	167
119	Heterosis and polymorphisms of gene expression in an elite rice hybrid as revealed by a microarray analysis of 9198 unique ESTs. <i>Plant Molecular Biology</i> , 2006, 62, 579-591.	2.0	104
120	Development of insect-resistant transgenic indica rice with a synthetic cry1C* gene. <i>Molecular Breeding</i> , 2006, 18, 1-10.	1.0	192
121	Fine mapping of f5-Du, a gene conferring wide-compatibility for pollen fertility in inter-subspecific hybrids of rice (<i>Oryza sativa</i> L.). <i>Theoretical and Applied Genetics</i> , 2006, 112, 382-387.	1.8	38
122	Targeting xa13, a recessive gene for bacterial blight resistance in rice. <i>Theoretical and Applied Genetics</i> , 2006, 112, 455-461.	1.8	178
123	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
124	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
125	Comparative analysis of gene expression at early seedling stage between a rice hybrid and its parents using a cDNA microarray of 9198 uni-sequences. <i>Science in China Series C: Life Sciences</i> , 2006, 49, 519-529.	1.3	8
126	RMD: a rice mutant database for functional analysis of the rice genome. <i>Nucleic Acids Research</i> , 2006, 34, D745-D748.	6.5	200

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127	Promoter mutations of an essential gene for pollen development result in disease resistance in rice. <i>Genes and Development</i> , 2006, 20, 1250-1255.	2.7	457
128	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
129	Isolation and annotation of 10828 putative full length cDNAs from indica rice. <i>Science in China Series C: Life Sciences</i> , 2005, 48, 445.	1.3	17
130	Features of the expressed sequences revealed by a large-scale analysis of ESTs from a normalized cDNA library of the elite indica rice cultivar Minghui 63. <i>Plant Journal</i> , 2005, 42, 772-780.	2.8	39
131	Optimising the tissue culture conditions for high efficiency transformation of indica rice. <i>Plant Cell Reports</i> , 2005, 23, 540-547.	2.8	308
132	Genetic dissection of embryo sac fertility, pollen fertility, and their contributions to spikelet fertility of intersubspecific hybrids in rice. <i>Theoretical and Applied Genetics</i> , 2005, 110, 205-211.	1.8	72
133	Delimitation of the rice wide compatibility gene S5 n to a 40-kb DNA fragment. <i>Theoretical and Applied Genetics</i> , 2005, 111, 1080-1086.	1.8	53
134	Transgenic indica rice plants harboring a synthetic cry2A* gene of <i>Bacillus thuringiensis</i> exhibit enhanced resistance against lepidopteran rice pests. <i>Theoretical and Applied Genetics</i> , 2005, 111, 1330-1337.	1.8	196
135	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
136	The main effects, epistatic effects and environmental interactions of QTLs on the cooking and eating quality of rice in a doubled-haploid line population. <i>Theoretical and Applied Genetics</i> , 2005, 110, 1445-1452.	1.8	153
137	Identification and confirmation of three neutral alleles conferring wide compatibility in inter-subspecific hybrids of rice (<i>Oryza sativa</i> L.) using near-isogenic lines. <i>Theoretical and Applied Genetics</i> , 2005, 111, 702-710.	1.8	26
138	How Can We Use Genomics to Improve Cereals with Rice as a Reference Genome?. <i>Plant Molecular Biology</i> , 2005, 59, 7-26.	2.0	59
139	A Diagnostic Analysis of Genetic Differentiation Among Subpopulations of a Barley Composite Cross Using Isozyme Markers. <i>Hereditas</i> , 2004, 118, 63-70.	0.5	2
140	RFLPs in Cultivated Barley and Their Application in the Evaluation of Malting Quality Cultivars. <i>Hereditas</i> , 2004, 121, 21-29.	0.5	8
141	Rice Mutant Resources for Gene Discovery. <i>Plant Molecular Biology</i> , 2004, 54, 325-334.	2.0	221
142	Male and female gamete abortions, and reduced affinity between the uniting gametes as the causes for sterility in an indica/japonica hybrid in rice. <i>Sexual Plant Reproduction</i> , 2004, 17, 55.	2.2	40
143	Xa26, a gene conferring resistance to <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> in rice, encodes an LRR receptor kinase-like protein. <i>Plant Journal</i> , 2004, 37, 517-527.	2.8	446
144	Development of enhancer trap lines for functional analysis of the rice genome. <i>Plant Journal</i> , 2003, 35, 418-427.	2.8	237

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145	Comparative analyses of genomic locations and race specificities of loci for quantitative resistance to <i>Pyricularia grisea</i> in rice and barley. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 2544-2549.	3.3	122
146	Single-locus heterotic effects and dominance by dominance interactions can adequately explain the genetic basis of heterosis in an elite rice hybrid. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 2574-2579.	3.3	367
147	New Gene for Bacterial Blight Resistance in Rice Located on Chromosome 12 Identified from Minghui 63, an Elite Restorer Line. Phytopathology, 2002, 92, 750-754.	1.1	133
148	The defense-responsive genes showing enhanced and repressed expression after pathogen infection in rice (<i>Oryza sativa</i> L.). Science in China Series C: Life Sciences, 2002, 45, 449.	1.3	35
149	Development and Mapping of 2240 New SSR Markers for Rice (<i>Oryza sativa</i> L.). DNA Research, 2002, 9, 199-207.	1.5	1,203
150	Identification of quantitative trait loci and epistatic interactions for plant height and heading date in rice. Theoretical and Applied Genetics, 2002, 104, 619-625.	1.8	118
151	Genetic Dissection of an Elite Rice Hybrid Revealed That Heterozygotes Are Not Always Advantageous for Performance. Genetics, 2002, 162, 1885-1895.	1.2	240
152	Pathotypes of <i>Pyricularia grisea</i> in Rice Fields of Central and Southern China. Plant Disease, 2001, 85, 843-850.	0.7	66
153	Identification of an 85-kb DNA fragment containing <i>pms1</i> , a locus for photoperiod-sensitive genic male sterility in rice. Molecular Genetics and Genomics, 2001, 266, 271-275.	1.0	49
154	Title is missing!. Euphytica, 2001, 119, 343-348.	0.6	18
155	Improvement of Bacterial Blight Resistance of "Minghui 63"™, an Elite Restorer Line of Hybrid Rice, by Molecular Marker-Assisted Selection. Crop Science, 2000, 40, 239-244.	0.8	174
156	Analyzing quantitative trait loci for yield using a vegetatively replicated F2 population from a cross between the parents of an elite rice hybrid. Theoretical and Applied Genetics, 2000, 101, 248-254.	1.8	75
157	Genetic bases of appearance quality of rice grains in Shanyou 63, an elite rice hybrid. Theoretical and Applied Genetics, 2000, 101, 823-829.	1.8	263
158	Field performance of transgenic elite commercial hybrid rice expressing <i>Bacillus thuringiensis</i> δ -endotoxin. Nature Biotechnology, 2000, 18, 1101-1104.	9.4	412
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