

A QTL for rice grain width and weight encodes a previously identified ubiquitin ligase

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Strategies for developing Green Super Rice. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 16402-16409.	3.3	653
2	A quantitative trait locus regulating rice grain width. Nature Genetics, 2007, 39, 583-584.	9.4	9
3	Recent Progress on Rice Genetics in China. Journal of Integrative Plant Biology, 2007, 49, 776-790.	4.1	16
4	New insights into the history of rice domestication. Trends in Genetics, 2007, 23, 578-587.	2.9	443
5	Identification and stability of QTLs for fruit quality traits in apple. Tree Genetics and Genomes, 2008, 4, 647-661.	0.6	182
6	Fine mapping of a yield-enhancing QTL cluster associated with transgressive variation in an <i>Oryza sativa</i> – <i>O. rufipogon</i> cross. Theoretical and Applied Genetics, 2008, 116, 613-622.	1.8	142
7	Genetic dissection and pyramiding of quantitative traits for panicle architecture by using chromosomal segment substitution lines in rice. Theoretical and Applied Genetics, 2008, 116, 881-890.	1.8	140
8	Genetic dissection of a thousand-grain weight quantitative trait locus on rice chromosome 1. Science Bulletin, 2008, 53, 2326-2332.	4.3	21
9	Toward An Optimum Return From Crop Plants. Rice, 2008, 1, 135-143.	1.7	14
10	Comparative Analysis of Rice Genome Sequence to Understand the Molecular Basis of Genome Evolution. Rice, 2008, 1, 119-126.	1.7	6
11	SSR based linkage and mapping analysis of <i>C</i> , a yellow cocoon gene in the silkworm, <i>Bombyx mori</i> . Insect Science, 2008, 15, 399-404.	1.5	9
12	Isolation and initial characterization of GW5, a major QTL associated with rice grain width and weight. Cell Research, 2008, 18, 1199-1209.	5.7	583
13	Natural variation in Ghd7 is an important regulator of heading date and yield potential in rice. Nature Genetics, 2008, 40, 761-767.	9.4	1,666
14	Deletion in a gene associated with grain size increased yields during rice domestication. Nature Genetics, 2008, 40, 1023-1028.	9.4	794
15	Control of rice grain-filling and yield by a gene with a potential signature of domestication. Nature Genetics, 2008, 40, 1370-1374.	9.4	706
16	Genetic approaches to crop improvement: responding to environmental and population changes. Nature Reviews Genetics, 2008, 9, 444-457.	7.7	396
17	Mapping quantitative trait loci associated with arsenic accumulation in rice (<i>Oryza sativa</i>). New Phytologist, 2008, 177, 350-356.	3.5	108
18	Applying modelling experiences from the past to shape crop systems biology: the need to converge crop physiology and functional genomics. New Phytologist, 2008, 179, 629-642.	3.5	81

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19	Towards molecular breeding of reproductive traits in cereal crops. <i>Plant Biotechnology Journal</i> , 2008, 6, 529-559.	4.1	34
20	Yield assessment of integumentâ€ed seed growth following targeted repair of <i>auxin response factor 2</i>. <i>Plant Biotechnology Journal</i> , 2008, 6, 758-769.	4.1	33
21	Genetic variation in rice. <i>Current Opinion in Plant Biology</i> , 2008, 11, 144-148.	3.5	23
22	Identifying and exploiting grain yield genes in rice. <i>Current Opinion in Plant Biology</i> , 2008, 11, 209-214.	3.5	255
23	Conditional and unconditional mapping of quantitative trait loci underlying plant height and tiller number in rice (<i>Oryza sativa</i> L.) grown at two nitrogen levels. <i>Progress in Natural Science: Materials International</i> , 2008, 18, 1539-1547.	1.8	18
24	Prospect of the QTL-qSB-9Tq utilized in molecular breeding program of japonica rice against sheath blight. <i>Journal of Genetics and Genomics</i> , 2008, 35, 499-505.	1.7	47
25	Genetic analysis and fine-mapping of a dwarfing with withered leaf-tip mutant in rice. <i>Journal of Genetics and Genomics</i> , 2008, 35, 715-721.	1.7	4
26	Fine Mapping of Spr3, a Locus for Spreading Panicle from African Cultivated Rice (<i>Oryza glaberrima</i>) Tj ETQq1 1 0.784314 rgBT /Overloc	3.9	25
27	Quantitative Trait Loci for Grain Yield and Adaptation of Durum Wheat (<i>Triticum durum</i> Desf.) Across a Wide Range of Water Availability. <i>Genetics</i> , 2008, 178, 489-511.	1.2	397
28	COP1-Mediated Ubiquitination of CONSTANS Is Implicated in Cryptochrome Regulation of Flowering in<i>Arabidopsis</i>. <i>Plant Cell</i> , 2008, 20, 292-306.	3.1	355
29	Quantitative Trait Loci (QTL) Analysis For Rice Grain Width and Fine Mapping of an Identified QTL Allele <i>gw-5</i> in a Recombination Hotspot Region on Chromosome 5. <i>Genetics</i> , 2008, 179, 2239-2252.	1.2	133
30	Molecular Markers and Their Use in Markerâ€Assisted Selection in Rice. <i>Crop Science</i> , 2008, 48, 1266-1276.	0.8	222
31	Rice Genome Research: Current Status and Future Perspectives. <i>Plant Genome</i> , 2008, 1, .	1.6	7
32	Highly Specific Gene Silencing by Artificial miRNAs in Rice. <i>PLoS ONE</i> , 2008, 3, e1829.	1.1	295
33	Intellectual Property Protection for Plant Varieties in the 21st Century. <i>Crop Science</i> , 2008, 48, 1277-1290.	0.8	17
34	Local maternal control of seed size by <i>KLUH</i> / <i>CYP78A5</i> -dependent growth signaling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 20115-20120.	3.3	230
35	Unraveling the Complex Trait of Crop Yield With Quantitative Trait Loci Mapping in <i>Brassica napus</i>. <i>Genetics</i> , 2009, 182, 851-861.	1.2	362
36	Towards the Understanding of Complex Traits in Rice: Substantially or Superficially?. <i>DNA Research</i> , 2009, 16, 141-154.	1.5	119

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37	PosMed-plus: An Intelligent Search Engine that Inferentially Integrates Cross-Species Information Resources for Molecular Breeding of Plants. <i>Plant and Cell Physiology</i> , 2009, 50, 1249-1259.	1.5	17
38	Loss of 26S Proteasome Function Leads to Increased Cell Size and Decreased Cell Number in Arabidopsis Shoot Organs. <i>Plant Physiology</i> , 2009, 150, 178-189.	2.3	117
39	Natural Variation in an ABC Transporter Gene Associated with Seed Size Evolution in Tomato Species. <i>PLoS Genetics</i> , 2009, 5, e1000347.	1.5	63
40	DNA changes tell us about rice domestication. <i>Current Opinion in Plant Biology</i> , 2009, 12, 185-192.	3.5	77
41	QTL mapping of grain quality traits in rice. <i>Journal of Cereal Science</i> , 2009, 50, 145-151.	1.8	87
42	Identification and characterization of a novel Waxy allele from a Yunnan rice landrace. <i>Plant Molecular Biology</i> , 2009, 71, 609-626.	2.0	95
43	Development of gene-tagged markers for quantitative trait loci underlying rice yield components. <i>Euphytica</i> , 2009, 169, 215-226.	0.6	33
44	Review and prospect of transgenic rice research. <i>Science Bulletin</i> , 2009, 54, 4049-4068.	1.7	46
45	Genetic Relationships Among Panicle Characteristics of Rice (<i>Oryza sativa</i> L.) Using Unconditional and Conditional QTL Analyses. <i>Journal of Plant Biology</i> , 2009, 52, 259-267.	0.9	11
46	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
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49	The ethylene response factors SNORKEL1 and SNORKEL2 allow rice to adapt to deep water. <i>Nature</i> , 2009, 460, 1026-1030.	13.7	840
50	Natural variation at the DEP1 locus enhances grain yield in rice. <i>Nature Genetics</i> , 2009, 41, 494-497.	9.4	858
51	Genetic Analysis and Fine Mapping of Two Genes for Grain Shape and Weight in Rice. <i>Journal of Integrative Plant Biology</i> , 2009, 51, 45-51.	4.1	58
52	Overexpression of the rice <i>LRK1</i> gene improves quantitative yield components. <i>Plant Biotechnology Journal</i> , 2009, 7, 611-620.	4.1	57
53	Deletion in a Quantitative Trait Gene <i>qPE9-1</i> Associated With Panicle Erectness Improves Plant Architecture During Rice Domestication. <i>Genetics</i> , 2009, 183, 315-324.	1.2	180
54	Evolutionary History of <i>GS3</i> , a Gene Conferring Grain Length in Rice. <i>Genetics</i> , 2009, 182, 1323-1334.	1.2	305

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56	Characterization of the genome expression trends in the heading-stage panicle of six rice lineages. Genomics, 2009, 93, 169-178.	1.3	11
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60	QTL mapping of 1000-kernel weight, kernel length, and kernel width in bread wheat (<i>Triticum aestivum</i>) Tj ETQq1	1.0	200
61	Cloning and characterization of a putative GS3 ortholog involved in maize kernel development. Theoretical and Applied Genetics, 2010, 120, 753-763.	1.8	126
62	A gene controlling the number of primary rachis branches also controls the vascular bundle formation and hence is responsible to increase the harvest index and grain yield in rice. Theoretical and Applied Genetics, 2010, 120, 875-893.	1.8	152
63	Mapping and validation of quantitative trait loci for spikelets per panicle and 1,000-grain weight in rice (<i>Oryza sativa</i> L.). Theoretical and Applied Genetics, 2010, 120, 933-942.	1.8	54
64	Fine mapping Fhb4, a major QTL conditioning resistance to Fusarium infection in bread wheat (<i>Triticum</i>) Tj ETQq1	1.8	112
65	Genetic diversity and population structure of a diverse set of rice germplasm for association mapping. Theoretical and Applied Genetics, 2010, 121, 475-487.	1.8	172
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70	Identification of main effects, epistatic effects and their environmental interactions of QTLs for yield traits in rice. Genes and Genomics, 2010, 32, 37-45.	0.5	15
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73	GmRFP1 encodes a previously unknown RING-type E3 ubiquitin ligase in Soybean (<i>Glycine max</i>). <i>Molecular Biology Reports</i> , 2010, 37, 685-693.	1.0	30
74	Fruit size QTL analysis of an F1 population derived from a cross between a domesticated sweet cherry cultivar and a wild forest sweet cherry. <i>Tree Genetics and Genomes</i> , 2010, 6, 25-36.	0.6	105
75	Developing high throughput genotyped chromosome segment substitution lines based on population whole-genome re-sequencing in rice (<i>Oryza sativa</i> L.). <i>BMC Genomics</i> , 2010, 11, 656.	1.2	96
76	Relationship, evolutionary fate and function of two maize co-orthologs of rice GW2 associated with kernel size and weight. <i>BMC Plant Biology</i> , 2010, 10, 143.	1.6	179
77	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
78	OsSPL14 promotes panicle branching and higher grain productivity in rice. <i>Nature Genetics</i> , 2010, 42, 545-549.	9.4	1,187
79	Comparative mapping of QTLs determining glume, pistil and stamen sizes in cultivated rice (<i>Oryza</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.6	20
80	QTL analysis for heading date and yield traits using recombinant inbred lines of <i>indica</i> rice grown in different cropping seasons. <i>Plant Breeding</i> , 2010, 129, 676-682.	1.0	10
81	Germplasm-regression-combined marker-trait association identification in plants. <i>African Journal of Biotechnology</i> , 2010, 9, 573-580.	0.3	12
82	A Novel Kinesin 13 Protein Regulating Rice Seed Length. <i>Plant and Cell Physiology</i> , 2010, 51, 1315-1329.	1.5	125
83	High-Throughput Genetic Mapping of Mutants via Quantitative Single Nucleotide Polymorphism Typing. <i>Genetics</i> , 2010, 184, 19-26.	1.2	66
84	Halophyte Improvement for a Salinized World. <i>Critical Reviews in Plant Sciences</i> , 2010, 29, 329-359.	2.7	151
85	Construction of a new set of rice chromosome segment substitution lines and identification of grain weight and related traits QTLs. <i>Breeding Science</i> , 2010, 60, 305-313.	0.9	40
86	Germplasm-regression-combined (GRC) marker-trait association identification in plant breeding: a challenge for plant biotechnological breeding under soil water deficit conditions. <i>Critical Reviews in Biotechnology</i> , 2010, 30, 192-199.	5.1	8
87	Comparison Between QTLs for Chlorophyll Content and Genes Controlling Chlorophyll Biosynthesis and Degradation in Japonica Rice. <i>Acta Agronomica Sinica</i> , 2010, 36, 376-384.	0.3	8
88	Mapping QTLs for Grain Weight and Shape Using Four Sister Near Isogenic Lines of Rice. <i>Acta Agronomica Sinica</i> , 2010, 36, 1310-1317.	0.3	3
89	Linking differential domain functions of the GS3 protein to natural variation of grain size in rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 19579-19584.	3.3	580
90	Genetic and Molecular Bases of Rice Yield. <i>Annual Review of Plant Biology</i> , 2010, 61, 421-442.	8.6	762

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94	Cloning and Expression Level Analysis of Two BnaANT Candidate Genes in Brassica napus. Agricultural Sciences in China, 2010, 9, 488-496.	0.6	6
95	Identification of Quantitative Trait Loci for Grain Traits in Japonica Rice. Agricultural Sciences in China, 2010, 9, 929-936.	0.6	15
96	Relationship Between Heterosis and Parental Genetic Distance Based on Molecular Markers for Functional Genes Related to Yield Traits in Rice. Rice Science, 2010, 17, 288-295.	1.7	33
97	Transgenics for Increasing Productivity of Crops. Journal of Plant Biochemistry and Biotechnology, 2010, 19, 1-7.	0.9	9
98	<i>DTH8</i> Suppresses Flowering in Rice, Influencing Plant Height and Yield Potential Simultaneously. Plant Physiology, 2010, 153, 1747-1758.	2.3	549
99	A Genetic Framework for Grain Size and Shape Variation in Wheat. Plant Cell, 2010, 22, 1046-1056.	3.1	397
100	Differential expression of the microRNAs in superior and inferior spikelets in rice (<i>Oryza sativa</i>). Journal of Experimental Botany, 2011, 62, 4943-4954.	2.4	95
101	Rice RING protein OsBBI1 with E3 ligase activity confers broad-spectrum resistance against <i>Magnaporthe oryzae</i> by modifying the cell wall defence. Cell Research, 2011, 21, 835-848.	5.7	80
102	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
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106	Development of upland rice introgression lines and identification of QTLs for basal root thickness under different water regimes. Journal of Genetics and Genomics, 2011, 38, 547-556.	1.7	21
107	Characterization of a single recessive yield trait mutant with elevated endogenous ABA concentration and deformed grains, spikelets and leaves. Plant Science, 2011, 180, 306-312.	1.7	10
108	The role of QTLs in the breeding of high-yielding rice. Trends in Plant Science, 2011, 16, 319-326.	4.3	171

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109	QTL Detection for Rice Grain Shape Using Chromosome Single Segment Substitution Lines. <i>Rice Science</i> , 2011, 18, 273-278.	1.7	3
110	Functional Genomics of Rice Pollen and Seed Development by Genome-wide Transcript Profiling and <i><i>Ds</i></i> Insertion Mutagenesis. <i>International Journal of Biological Sciences</i> , 2011, 7, 28-40.	2.6	8
111	Molecular mapping of quantitative trait loci for kernel morphology traits in a non-1BL.1RS—1BL.1RS wheat cross. <i>Crop and Pasture Science</i> , 2011, 62, 625.	0.7	20
112	A loss-of-function mutation of rice DENSE PANICLE 1 causes semi-dwarfness and slightly increased number of spikelets. <i>Breeding Science</i> , 2011, 61, 17-25.	0.9	45
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115	Modelling the size and composition of fruit, grain and seed by process-based simulation models. <i>New Phytologist</i> , 2011, 191, 601-618.	3.5	42
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117	Making the most of "omics"™ for crop breeding. <i>Trends in Biotechnology</i> , 2011, 29, 33-40.	4.9	199
118	Exploring molecular backgrounds of quality traits in rice by predictive models based on high-coverage metabolomics. <i>BMC Systems Biology</i> , 2011, 5, 176.	3.0	37
119	Physiological characterization of introgression lines derived from an indica rice cultivar, IR64, adapted to drought and water-saving irrigation. <i>Field Crops Research</i> , 2011, 123, 130-138.	2.3	44
120	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
121	Mapping QTLs for improving grain yield using the USDA rice mini-core collection. <i>Planta</i> , 2011, 234, 347-361.	1.6	72
122	Diverse approaches to achieving grain yield in wheat. <i>Functional and Integrative Genomics</i> , 2011, 11, 37-48.	1.4	35
123	Identification and development of a functional marker of TaGW2 associated with grain weight in bread wheat (<i>Triticum aestivum</i> L.). <i>Theoretical and Applied Genetics</i> , 2011, 122, 211-223.	1.8	392
124	Mapping 49 quantitative trait loci at high resolution through sequencing-based genotyping of rice recombinant inbred lines. <i>Theoretical and Applied Genetics</i> , 2011, 122, 327-340.	1.8	134
125	Mapping quantitative trait loci for seed size traits in soybean (<i>Glycine max</i> L. Merr.). <i>Theoretical and Applied Genetics</i> , 2011, 122, 581-594.	1.8	82
126	QTL consistency and meta-analysis for grain yield components in three generations in maize. <i>Theoretical and Applied Genetics</i> , 2011, 122, 771-782.	1.8	71

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127	Functional markers developed from multiple loci in GS3 for fine marker-assisted selection of grain length in rice. <i>Theoretical and Applied Genetics</i> , 2011, 122, 905-913.	1.8	97
128	QTL analysis for yield components and kernel-related traits in maize across multi-environments. <i>Theoretical and Applied Genetics</i> , 2011, 122, 1305-1320.	1.8	143
129	Tomato fruit weight 11.3 maps close to fasciated on the bottom of chromosome 11. <i>Theoretical and Applied Genetics</i> , 2011, 123, 465-474.	1.8	66
130	Map-based cloning proves qGC-6, a major QTL for gel consistency of japonica/indica cross, responds by Waxy in rice (<i>Oryza sativa</i> L.). <i>Theoretical and Applied Genetics</i> , 2011, 123, 859-867.	1.8	75
131	Precise mapping Fhb5, a major QTL conditioning resistance to Fusarium infection in bread wheat (<i>Triticum aestivum</i> L.). <i>Theoretical and Applied Genetics</i> , 2011, 123, 1055-1063.	1.8	125
132	Seed size is determined by the combinations of the genes controlling different seed characteristics in rice. <i>Theoretical and Applied Genetics</i> , 2011, 123, 1173-1181.	1.8	80
133	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
134	Studies on Ancient Rice—Where Botanists, Agronomists, Archeologists, Linguists, and Ethnologists Meet. <i>Rice</i> , 2011, 4, 178-183.	1.7	18
135	Genetic and Molecular Insights into the Enhancement of Rice Yield Potential. <i>Journal of Plant Biology</i> , 2011, 54, 1-9.	0.9	48
136	Fine mapping of grain weight QTL, <i>tgw11</i> using near isogenic lines from a cross between <i>Oryza sativa</i> and <i>O. grandiglumis</i> . <i>Genes and Genomics</i> , 2011, 33, 259-265.	0.5	21
137	Field transcriptome revealed critical developmental and physiological transitions involved in the expression of growth potential in japonicarice. <i>BMC Plant Biology</i> , 2011, 11, 10.	1.6	130
139	A Major QTL, <i>Chd8</i> , 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
140	Genome-Wide Association Study Identifies Candidate Genes That Affect Plant Height in Chinese Elite Maize (<i>Zea mays</i> L.) Inbred Lines. <i>PLoS ONE</i> , 2011, 6, e29229.	1.1	110
141	VpRFP1, a novel C4C4-type RING finger protein gene from Chinese wild <i>Vitis pseudoreticulata</i> , functions as a transcriptional activator in defence response of grapevine. <i>Journal of Experimental Botany</i> , 2011, 62, 5671-5682.	2.4	43
142	Detection of epistatic interaction of two QTLs, <i>gw8.1</i> and <i>gw9.1</i> , underlying grain weight using nearly isogenic lines in rice. <i>Breeding Science</i> , 2011, 61, 69-75.	0.9	8
143	Detection of QTLs for grain length from large grain rice (<i>Oryza sativa</i> L.). <i>Breeding Science</i> , 2011, 61, 269-274.	0.9	32
144	Genetic Effects of Background-Independent Loci for Grain Weight and Shape Identified using Advanced Reciprocal Introgression Lines from Lemont — Teqing in Rice. <i>Crop Science</i> , 2011, 51, 2525-2534.	0.8	19
145	<i>SmartGrain</i> : High-Throughput Phenotyping Software for Measuring Seed Shape through Image Analysis. <i>Plant Physiology</i> , 2012, 160, 1871-1880.	2.3	325

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146	An atypical bHLH protein encoded by <i>POSITIVE REGULATOR OF GRAIN LENGTH 2</i> is involved in controlling grain length and weight of rice through interaction with a typical bHLH protein APG. <i>Breeding Science</i> , 2012, 62, 133-141.	0.9	84
147	The BnGRF2 gene (GRF2-like gene from <i>Brassica napus</i>) enhances seed oil production through regulating cell number and plant photosynthesis. <i>Journal of Experimental Botany</i> , 2012, 63, 3727-3740.	2.4	123
148	Molecular and environmental factors determining grain quality in rice. <i>Food and Energy Security</i> , 2012, 1, 111-132.	2.0	118
149	Overexpression of a Rice TIFY Gene Increases Grain Size through Enhanced Accumulation of Carbohydrates in the Stem. <i>Bioscience, Biotechnology and Biochemistry</i> , 2012, 76, 2129-2134.	0.6	41
150	Identification of Quantitative Trait Loci for Lipid Metabolism in Rice Seeds. <i>Molecular Plant</i> , 2012, 5, 865-875.	3.9	50
151	Transcriptome-wide mining of the differentially expressed transcripts for natural variation of floral organ size in <i>Physalis philadelphica</i> . <i>Journal of Experimental Botany</i> , 2012, 63, 6457-6465.	2.4	9
152	<i>SHORT GRAIN1</i> Decreases Organ Elongation and Brassinosteroid Response in Rice. <i>Plant Physiology</i> , 2012, 158, 1208-1219.	2.3	90
153	Evidence from principal component analysis for improvement of grain shape- and spikelet morphology-related traits after hexaploid wheat speciation. <i>Genes and Genetic Systems</i> , 2012, 87, 299-310.	0.2	36
154	Loose Plant Architecture1, an INDETERMINATE DOMAIN Protein Involved in Shoot Gravitropism, Regulates Plant Architecture in Rice. <i>Plant Physiology</i> , 2012, 161, 317-329.	2.3	150
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319	Homologous haplotypes, expression, genetic effects and geographic distribution of the wheat yield gene TaGW2. <i>BMC Plant Biology</i> , 2014, 14, 107.	1.6	117
320	Genome-wide association for grain morphology in synthetic hexaploid wheats using digital imaging analysis. <i>BMC Plant Biology</i> , 2014, 14, 128.	1.6	102
321	Quantitative trait loci identification, fine mapping and gene expression profiling for ovicidal response to whitebacked planthopper (<i>Sogatella furcifera</i> Horvath) in rice (<i>Oryza sativa</i> L.). <i>BMC Plant Biology</i> , 2014, 14, 145.	1.6	39
322	Regulatory change at <i>Physalis</i> Organ Size 1 correlates to natural variation in tomatillo reproductive organ size. <i>Nature Communications</i> , 2014, 5, 4271.	5.8	24
323	The <i>ZmCLA4</i> gene in the qLA4-1 QTL controls leaf angle in maize (<i>Zea mays</i> L.). <i>Journal of Experimental Botany</i> , 2014, 65, 5063-5076.	2.4	69
324	Development of a TILLING resource in durum wheat for reverse- and forward-genetic analyses. <i>Crop and Pasture Science</i> , 2014, 65, 112.	0.7	33
325	QTL Mapping for Hull Thickness and Related Traits in Hybrid Rice Xieyou 9308. <i>Rice Science</i> , 2014, 21, 29-38.	1.7	4
326	Molecular Improvement of Grain Weight and Yield in Rice by Using <i>CW6</i> Gene. <i>Rice Science</i> , 2014, 21, 127-132.	1.7	6
327	Genotype × Environment Interactions for Agronomic Traits of Rice Revealed by Association Mapping. <i>Rice Science</i> , 2014, 21, 133-141.	1.7	27
328	Three-dimensional Seed Size and Shape QTL in Hexaploid Wheat (<i>Triticum aestivum</i> L.) Populations. <i>Crop Science</i> , 2014, 54, 98-110.	0.8	79
329	Rice <i>PCR1</i> influences grain weight and <i>Zn</i> accumulation in grains. <i>Plant, Cell and Environment</i> , 2015, 38, 2327-2339.	2.8	56
330	Maize orthologs of rice <i>GS5</i> and their trans-regulator are associated with kernel development. <i>Journal of Integrative Plant Biology</i> , 2015, 57, 943-953.	4.1	55

#	ARTICLE	IF	CITATIONS
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332	A dense SNP genetic map constructed using restriction site-associated DNA sequencing enables detection of QTLs controlling apple fruit quality. <i>BMC Genomics</i> , 2015, 16, 747.	1.2	83
333	An ultra-high-density map as a community resource for discerning the genetic basis of quantitative traits in maize. <i>BMC Genomics</i> , 2015, 16, 1078.	1.2	55
334	Mapping of qTGW1.1, a Quantitative Trait Locus for 1000-Grain Weight in Rice (<i>Oryza sativa</i> L.). <i>Rice Science</i> , 2015, 22, 9-15.	1.7	4
335	Influence of Multi-Gene Allele Combinations on Grain Size of Rice and Development of a Regression Equation Model to Predict Grain Parameters. <i>Rice</i> , 2015, 8, 33.	1.7	23
336	An evolutionarily conserved gene, <i>OsCYP78A3</i> , plays a role in determining panicle architecture, grain shape and grain weight in rice. <i>Plant Journal</i> , 2015, 83, 427-438.	2.8	68
337	Rice microRNA osa-miR1848 targets the obtusifoliol 14 α -demethylase gene <i>OsCYP51G3</i> and mediates the biosynthesis of phytosterols and brassinosteroids during development and in response to stress. <i>New Phytologist</i> , 2015, 208, 790-802.	3.5	81
338	Unconditional and conditional QTL underlying the genetic interrelationships between soybean seed isoflavone, and protein or oil contents. <i>Plant Breeding</i> , 2015, 134, 300-309.	1.0	58
339	Expression of <i>TaCYP78A3</i> , a gene encoding cytochrome P450 <i>CYP78A3</i> protein in wheat (<i>Triticum aestivum</i> L.), affects seed size. <i>Plant Journal</i> , 2015, 83, 312-325.	2.8	131
340	Relationship between grain yield and quality in rice germplasm grown across different growing areas. <i>Breeding Science</i> , 2015, 65, 226-232.	0.9	45
341	Genetic analysis of grain shape and weight after cutting rice husk. <i>Genetics and Molecular Research</i> , 2015, 14, 17739-17748.	0.3	6
342	Verification and evaluation of grain QTLs using RILs from TD70 x Kasalath in rice. <i>Genetics and Molecular Research</i> , 2015, 14, 14882-14892.	0.3	7
343	Advanced backcross QTL analysis reveals complicated genetic control of rice grain shape in a japonica \times indica cross. <i>Breeding Science</i> , 2015, 65, 308-318.	0.9	56
344	Time-Course Association Mapping of the Grain-Filling Rate in Rice (<i>Oryza sativa</i> L.). <i>PLoS ONE</i> , 2015, 10, e0119959.	1.1	17
345	Genomic Prediction of Biological Shape: Elliptic Fourier Analysis and Kernel Partial Least Squares (PLS) Regression Applied to Grain Shape Prediction in Rice (<i>Oryza sativa</i> L.). <i>PLoS ONE</i> , 2015, 10, e0120610.	1.1	43
346	Identification of Genomic Regions and the Isoamylase Gene for Reduced Grain Chalkiness in Rice. <i>PLoS ONE</i> , 2015, 10, e0122013.	1.1	53
347	Identification of Novel SNP in Promoter Sequence of TaGW2-6A Associated with Grain Weight and Other Agronomic Traits in Wheat (<i>Triticum aestivum</i> L.). <i>PLoS ONE</i> , 2015, 10, e0129400.	1.1	85
348	Differential Proteomic Analysis Using iTRAQ Reveals Alterations in Hull Development in Rice (<i>Oryza</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.1	10

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349	Analysis of main effect QTL for thousand grain weight in European winter wheat (<i>Triticum aestivum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	2.7	129
350	Review of functional markers for improving cooking, eating, and the nutritional qualities of rice. <i>Frontiers in Plant Science</i> , 2015, 6, 832.	1.7	38
351	A Single-Nucleotide Polymorphism of TaGS5 Gene Revealed its Association with Kernel Weight in Chinese Bread Wheat. <i>Frontiers in Plant Science</i> , 2015, 6, 1166.	1.7	76
352	Accuracy and genetic progress of agronomic traits in irrigated rice program in Brazil. <i>African Journal of Agricultural Research Vol Pp</i> , 2015, 10, 4032-4038.	0.2	4
353	Phenotypic Diversity Studies on Selected Kenyan and Tanzanian Rice (<i>Oryza sativa</i> L) Genotypes Based on Grain and Kernel Traits. <i>Rice Research Open Access</i> , 2015, 03, .	0.4	0
354	Functional Marker Development and Effect Analysis of Grain Size Gene GW2 in Extreme Grain Size Germplasm in Rice. <i>Rice Science</i> , 2015, 22, 65-70.	1.7	5
355	Drought Resistance in Crops: Physiological and Genetic Basis of Traits for Crop Productivity. , 2015, , 267-292.		9
356	Rapid Identification of Major QTLs Associated with Rice Grain Weight and Their Utilization. <i>PLoS ONE</i> , 2015, 10, e0122206.	1.1	56
357	High-Density Genetic Linkage Map Construction and QTL Mapping of Grain Shape and Size in the Wheat Population Yanda1817 Å– Beinong6. <i>PLoS ONE</i> , 2015, 10, e0118144.	1.1	167
358	Comparative Genetics of Seed Size Traits in Divergent Cereal Lineages Represented by Sorghum (<i>Panicoidae</i>) and Rice (<i>Oryzoidae</i>). <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1117-1128.	0.8	45
360	Characterization and fine mapping of NGP4c(t), a novel gene controlling the number of grains per panicle in rice. <i>Journal of Genetics</i> , 2015, 94, 513-517.	0.4	2
361	A Mathematical Model of Phloem Sucrose Transport as a New Tool for Designing Rice Panicle Structure for High Grain Yield. <i>Plant and Cell Physiology</i> , 2015, 56, 605-619.	1.5	23
362	Designing climate-resilient rice with ideal grain quality suited for high-temperature stress. <i>Journal of Experimental Botany</i> , 2015, 66, 1737-1748.	2.4	164
363	Patterns of genomic changes with crop domestication and breeding. <i>Current Opinion in Plant Biology</i> , 2015, 24, 47-53.	3.5	83
364	Genomic analysis of hybrid rice varieties reveals numerous superior alleles that contribute to heterosis. <i>Nature Communications</i> , 2015, 6, 6258.	5.8	292
365	Maternal control of seed size in plants. <i>Journal of Experimental Botany</i> , 2015, 66, 1087-1097.	2.4	123
366	Rare allele of a previously unidentified histone H4 acetyltransferase enhances grain weight, yield, and plant biomass in rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 76-81.	3.3	236
367	Genotyping-by-sequencing based intra-specific genetic map refines a â€ˆQTL-hotspotâ€™-region for drought tolerance in chickpea. <i>Molecular Genetics and Genomics</i> , 2015, 290, 559-571.	1.0	180

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369	Molecular functions of genes related to grain shape in rice. <i>Breeding Science</i> , 2015, 65, 120-126.	0.9	20
370	Identification of QTLs for agronomic traits in indica rice using an RIL population. <i>Genes and Genomics</i> , 2015, 37, 809-817.	0.5	6
371	Copy number variation at the GL7 locus contributes to grain size diversity in rice. <i>Nature Genetics</i> , 2015, 47, 944-948.	9.4	485
372	Genetic evidence for differential selection of grain and embryo weight during wheat evolution under domestication. <i>Journal of Experimental Botany</i> , 2015, 66, 5703-5711.	2.4	70
373	A Rare Allele of GS2 Enhances Grain Size and Grain Yield in Rice. <i>Molecular Plant</i> , 2015, 8, 1455-1465.	3.9	382
374	Genetic dissection on rice grain shape by the two-dimensional image analysis in one japonica—indica population consisting of recombinant inbred lines. <i>Theoretical and Applied Genetics</i> , 2015, 128, 1969-1986.	1.8	63
375	Introgression of <i>Agropyron cristatum</i> 6P chromosome segment into common wheat for enhanced thousand-grain weight and spike length. <i>Theoretical and Applied Genetics</i> , 2015, 128, 1827-1837.	1.8	54
376	Population genetic structure of <i>Oryza sativa</i> in East and Southeast Asia and the discovery of elite alleles for grain traits. <i>Scientific Reports</i> , 2015, 5, 11254.	1.6	19
377	Mapping of the genetic determinant for grain size in rice using a recombinant inbred line (RIL) population generated from two elite indica parents. <i>Euphytica</i> , 2015, 206, 159-173.	0.6	7
378	Genetic mapping of a QTL controlling source-sink size and heading date in rice. <i>Gene</i> , 2015, 571, 263-270.	1.0	12
379	<i>OsAGSW1</i> , an ABC1-like kinase gene, is involved in the regulation of grain size and weight in rice. <i>Journal of Experimental Botany</i> , 2015, 66, 5691-5701.	2.4	17
380	Rice RING E3 ligase may negatively regulate gamma-ray response to mediate the degradation of photosynthesis-related proteins. <i>Planta</i> , 2015, 241, 1119-1129.	1.6	23
381	QTL mapping for rice grain quality: a strategy to detect more QTLs within sub-populations. <i>Molecular Breeding</i> , 2015, 35, 1.	1.0	25
382	Genetic diversity and elite gene introgression reveal the japonica rice breeding in northern China. <i>Journal of Integrative Agriculture</i> , 2015, 14, 811-822.	1.7	6
383	Post-transcriptional and post-translational regulations of drought and heat response in plants: a spider's web of mechanisms. <i>Frontiers in Plant Science</i> , 2015, 6, 57.	1.7	136
384	Construction of high-throughput genotyped chromosome segment substitution lines in rice (<i>Oryza</i>) Tj ETQq0.0 rgBT /Overlock 1	1.0	9
385	qRT9, a quantitative trait locus controlling root thickness and root length in upland rice. <i>Journal of Experimental Botany</i> , 2015, 66, 2723-2732.	2.4	64

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387	OsKinesin-13A Is an Active Microtubule Depolymerase Involved in Glume Length Regulation via Affecting Cell Elongation. <i>Scientific Reports</i> , 2015, 5, 9457.	1.6	28
388	Differential expression of GS5 regulates grain size in rice. <i>Journal of Experimental Botany</i> , 2015, 66, 2611-2623.	2.4	119
389	Transcription Factors SOD7/NGAL2 and DPA4/NGAL3 Act Redundantly to Regulate Seed Size by Directly Repressing <i>KLU</i> Expression in <i>Arabidopsis thaliana</i> . <i>Plant Cell</i> , 2015, 27, 620-632.	3.1	77
390	Discovery and mapping of genomic regions governing economically important traits of Basmati rice. <i>BMC Plant Biology</i> , 2015, 15, 207.	1.6	20
391	Enhanced sucrose loading improves rice yield by increasing grain size. <i>Plant Physiology</i> , 2015, 169, pp.01170.2015.	2.3	88
392	Rice Ovate Family Protein 2 (OFP2) alters hormonal homeostasis and vasculature development. <i>Plant Science</i> , 2015, 241, 177-188.	1.7	106
393	The additive effects of GS3 and qGL3 on rice grain length regulation revealed by genetic and transcriptome comparisons. <i>BMC Plant Biology</i> , 2015, 15, 156.	1.6	32
394	The Usefulness of Known Genes/Qtls for Grain Quality Traits in an Indica Population of Diverse Breeding Lines Tested using Association Analysis. <i>Rice</i> , 2015, 8, 29.	1.7	41
395	Fine mapping of qGW1, a major QTL for grain weight in sorghum. <i>Theoretical and Applied Genetics</i> , 2015, 128, 1813-1825.	1.8	40
396	Different effects of DEP1 on vascular bundle- and panicle-related traits under indica and japonica genetic backgrounds. <i>Molecular Breeding</i> , 2015, 35, 1.	1.0	15
397	Natural variation in <i>ARF18</i> gene simultaneously affects seed weight and silique length in polyploid rapeseed. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E5123-32.	3.3	185
398	Activation of <i>Big Grain1</i> significantly improves grain size by regulating auxin transport in rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 11102-11107.	3.3	265
399	Characterization of three wheat grain weight QTLs that differentially affect kernel dimensions. <i>Theoretical and Applied Genetics</i> , 2015, 128, 2437-2445.	1.8	36
400	Natural Variations in <i>SLG7</i> Regulate Grain Shape in Rice. <i>Genetics</i> , 2015, 201, 1591-1599.	1.2	71
401	QTL Identification. , 2015, , 51-94.		0
402	Dissection of qTGW1.2 to three QTLs for grain weight and grain size in rice (<i>Oryza sativa</i> L.). <i>Euphytica</i> , 2015, 202, 119-127.	0.6	16
403	Novel InDel variation in GS3 locus and development of InDel based marker for marker assisted breeding of short grain aromatic rices. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2015, 24, 120-127.	0.9	8

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405	Variations in <i>CYP78A13</i> coding region influence grain size and yield in rice. <i>Plant, Cell and Environment</i> , 2015, 38, 800-811.	2.8	102
406	Breeding challenge: improving yield potential. , 2015, , 397-421.		5
407	RICE Genetics. , 2016, , .		0
408	Quantitative Trait Loci Mapping for Appearance Quality in Short-Grain Rice. <i>Crop Science</i> , 2016, 56, 1484-1492.	0.8	9
409	Identification of variability for agronomically important traits in rice mutant families. <i>Bragantia</i> , 2016, 75, 41-50.	1.3	21
410	Rice: Genetics. , 2016, , 398-406.		0
411	Mapping of QTLs Controlling Grain Shape and Populations Construction Derived from Related Residual Heterozygous Lines in Rice. <i>Journal of Agricultural Science</i> , 2016, 8, 104.	0.1	3
412	The <i>DENSE AND ERECT PANICLE 1</i> (<i>DEP1</i>) gene offering the potential in the breeding of high-yielding rice. <i>Breeding Science</i> , 2016, 66, 659-667.	0.9	68
413	Flowering-Related RING Protein 1 (FRRP1) Regulates Flowering Time and Yield Potential by Affecting Histone H2B Monoubiquitination in Rice (<i>Oryza Sativa</i>). <i>PLoS ONE</i> , 2016, 11, e0150458.	1.1	38
414	Improvement of Rice Biomass Yield through QTL-Based Selection. <i>PLoS ONE</i> , 2016, 11, e0151830.	1.1	25
415	Identification and Validation of Loci Governing Seed Coat Color by Combining Association Mapping and Bulk Segregation Analysis in Soybean. <i>PLoS ONE</i> , 2016, 11, e0159064.	1.1	46
416	Transferring Desirable Genes from <i>Agropyron cristatum</i> 7P Chromosome into Common Wheat. <i>PLoS ONE</i> , 2016, 11, e0159577.	1.1	23
417	Polycomb Protein OsFIE2 Affects Plant Height and Grain Yield in Rice. <i>PLoS ONE</i> , 2016, 11, e0164748.	1.1	33
418	Haplotypes of qGL3 and their roles in grain size regulation with GS3 alleles in rice. <i>Genetics and Molecular Research</i> , 2016, 15, .	0.3	4
419	Overexpression of Peptide-Encoding OsCEP6.1 Results in Pleiotropic Effects on Growth in Rice (O.) Tj ETQq1 1 0.784314 rgBT _{1.7} /Overlock		37
420	Reassessment of the Four Yield-related Genes Gn1a, DEP1, GS3, and IPA1 in Rice Using a CRISPR/Cas9 System. <i>Frontiers in Plant Science</i> , 2016, 7, 377.	1.7	375
421	The Rice Eukaryotic Translation Initiation Factor 3 Subunit f (OsEIF3f) Is Involved in Microgametogenesis. <i>Frontiers in Plant Science</i> , 2016, 7, 532.	1.7	5

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423	Genetic Diversity and Elite Allele Mining for Grain Traits in Rice (<i>Oryza sativa</i> L.) by Association Mapping. <i>Frontiers in Plant Science</i> , 2016, 7, 787.	1.7	26
424	Identification of Key Proteins and Networks Related to Grain Development in Wheat (<i>Triticum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 66. <i>Frontiers in Plant Science</i> , 2016, 7, 922.	1.7	23
425	High-Throughput Sequencing Reveals Single Nucleotide Variants in Longer-Kernel Bread Wheat. <i>Frontiers in Plant Science</i> , 2016, 7, 1193.	1.7	7
426	Development and Evaluation of Chromosome Segment Substitution Lines Carrying Overlapping Chromosome Segments of the Whole Wild Rice Genome. <i>Frontiers in Plant Science</i> , 2016, 7, 1737.	1.7	12
427	Regulatory Role of OsMADS34 in the Determination of Glumes Fate, Grain Yield, and Quality in Rice. <i>Frontiers in Plant Science</i> , 2016, 7, 1853.	1.7	29
428	SWATH-MS Quantitative Analysis of Proteins in the Rice Inferior and Superior Spikelets during Grain Filling. <i>Frontiers in Plant Science</i> , 2016, 7, 1926.	1.7	15
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430	Quantitative trait loci identification and meta-analysis for rice panicle-related traits. <i>Molecular Genetics and Genomics</i> , 2016, 291, 1927-1940.	1.0	39
431	The OsmiR396â€OsGRF4â€OsGIF1 regulatory module determines grain size and yield in rice. <i>Plant Biotechnology Journal</i> , 2016, 14, 2134-2146.	4.1	224
432	Micro<scp>RNA</scp>â€targeted transcription factor gene <i><scp>RDD</scp>1</i> promotes nutrient ion uptake and accumulation in rice. <i>Plant Journal</i> , 2016, 85, 466-477.	2.8	79
433	Dissection of Genetic Factors underlying Wheat Kernel Shape and Size in an Elite Ã– Nonadapted Cross using a High Density SNP Linkage Map. <i>Plant Genome</i> , 2016, 9, plantgenome2015.09.0081.	1.6	116
434	Molecular cloning and functional characterisation of the tomato E3 ubiquitin ligase SIBAH1 gene. <i>Functional Plant Biology</i> , 2016, 43, 1091.	1.1	6
435	Population structure and association analysis of yield and grain quality traits in hybrid rice primal parental lines. <i>Euphytica</i> , 2016, 212, 261-273.	0.6	12
436	Expanding Maize Genetic Resources with Predomestication Alleles: Maizeâ€Teosinte Introgression Populations. <i>Plant Genome</i> , 2016, 9, plantgenome2015.07.0053.	1.6	43
437	Loss of function of OsMADS34 leads to large sterile lemma and low grain yield in rice (<i>Oryza sativa</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 66. <i>Frontiers in Plant Science</i> , 2016, 7, 1926.	1.0	19
438	Genetic Analysis of Kernel Traits in Maize-Teosinte Introgression Populations. G3: Genes, Genomes, Genetics, 2016, 6, 2523-2530.	0.8	32
439	OsSGL, a novel pleiotropic stress-related gene enhances grain length and yield in rice. <i>Scientific Reports</i> , 2016, 6, 38157.	1.6	38

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441	Genetic mapping and confirmation of quantitative trait loci for grain chalkiness in rice. <i>Molecular Breeding</i> , 2016, 36, 1.	1.0	17
442	SMALL GRAIN 11 Controls Grain Size, Grain Number and Grain Yield in Rice. <i>Rice</i> , 2016, 9, 64.	1.7	87
443	<i>GS5</i> a grain size gene selected during wheat improvement for larger kernel and yield. <i>Plant Biotechnology Journal</i> , 2016, 14, 1269-1280.	4.1	217
444	Genome wide association mapping for grain shape traits in indica rice. <i>Planta</i> , 2016, 244, 819-830.	1.6	47
445	Genetic analysis of heterosis for maize grain yield and its components in a set of SSSL testcross populations. <i>Euphytica</i> , 2016, 210, 181-193.	0.6	11
446	Considering causal genes in the genetic dissection of kernel traits in common wheat. <i>Journal of Applied Genetics</i> , 2016, 57, 467-476.	1.0	82
447	Multi-environment QTL analysis of grain morphology traits and fine mapping of a kernel-width QTL in Zheng58AA-ASK maize population. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1465-1477.	1.8	84
448	Expansin genes are candidate markers for the control of fruit weight in peach. <i>Euphytica</i> , 2016, 210, 441-449.	0.6	11
449	OsSET7, a homologue of ARABIDOPSIS TRITHORAX-RELATED protein that plays a role in grain elongation regulation in rice. <i>Agri Gene</i> , 2016, 1, 135-142.	1.9	1
450	Association mapping of quantitative trait loci for yield-related agronomic traits in rice (<i>Oryza sativa</i>)	1.7	12
451	High-resolution QTL mapping for grain appearance traits and co-localization of chalkiness-associated differentially expressed candidate genes in rice. <i>Rice</i> , 2016, 9, 48.	1.7	56
452	The pleiotropic <i>ABNORMAL FLOWER AND DWARF1</i> affects plant height, floral development and grain yield in rice. <i>Journal of Integrative Plant Biology</i> , 2016, 58, 529-539.	4.1	56
453	Detection of Novel QTLs Regulating Grain Size in Extra-Large Grain Rice (<i>Oryza sativa</i> L.) Lines. <i>Rice</i> , 2016, 9, 34.	1.7	16
454	<i>OsGRF4</i> controls grain shape, panicle length and seed shattering in rice. <i>Journal of Integrative Plant Biology</i> , 2016, 58, 836-847.	4.1	137
455	Leaf growth in dicots and monocots: so different yet so alike. <i>Current Opinion in Plant Biology</i> , 2016, 33, 72-76.	3.5	87
456	QTL mapping of grain appearance quality traits and grain weight using a recombinant inbred population in rice (<i>Oryza sativa</i> L.). <i>Journal of Integrative Agriculture</i> , 2016, 15, 1693-1702.	1.7	13
458	Comparison and analysis of QTLs for grain and hull thickness related traits in two recombinant inbred line (RIL) populations in rice (<i>Oryza sativa</i> L.). <i>Journal of Integrative Agriculture</i> , 2016, 15, 2437-2450.	1.7	8

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460	Regulation of OsGRF4 by OsmiR396 controls grain size and yield in rice. <i>Nature Plants</i> , 2016, 2, 15203.	4.7	306
461	An Integrated Genomic Strategy Delineates Candidate Mediator Genes Regulating Grain Size and Weight in Rice. <i>Scientific Reports</i> , 2016, 6, 23253.	1.6	22
462	Identification of rice chromosome segment substitution line Z322-1-10 and mapping QTLs for agronomic traits from the F3 population. <i>Cereal Research Communications</i> , 2016, 44, 370-380.	0.8	11
463	Restricting the above ground sink corrects the root/shoot ratio and substantially boosts the yield potential per panicle in field-grown rice (<i>Oryza sativa</i> L.). <i>Physiologia Plantarum</i> , 2016, 156, 371-386.	2.6	8
464	Regulation of brassinosteroid on pod growth through cell hypertrophy in soybean (<i>Glycine max</i> (L.) Tj ETQq1 1 0.784314 rgBT /Overl	1.8	13
465	Quantitative evaluation of influence of PROSTRATE GROWTH 1 gene on rice canopy structure based on three-dimensional structure model. <i>Field Crops Research</i> , 2016, 194, 65-74.	2.3	10
466	Fine-mapping of qCW4.05, a major QTL for kernel weight and size in maize. <i>BMC Plant Biology</i> , 2016, 16, 81.	1.6	47
467	Fine mapping of qKW7, a major QTL for kernel weight and kernel width in maize, confirmed by the combined analytic approaches of linkage and association analysis. <i>Euphytica</i> , 2016, 210, 221-232.	0.6	21
468	Quantitative trait locus mapping for salt tolerance at maturity stage in indica rice using replicated F2 population. <i>Revista Brasileira De Botanica</i> , 2016, 39, 641-650.	0.5	14
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470	Identification of QTLs for grain size and characterization of the beneficial alleles of grain size genes in large grain rice variety BL129. <i>Journal of Integrative Agriculture</i> , 2016, 15, 1-9.	1.7	4
471	Fine Mapping Identifies a New QTL for Brown Rice Rate in Rice (<i>Oryza Sativa</i> L.). <i>Rice</i> , 2016, 9, 4.	1.7	38
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473	SNP-based analysis of genetic diversity reveals important alleles associated with seed size in rice. <i>BMC Plant Biology</i> , 2016, 16, 93.	1.6	42
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478	Introgression and Exploitation of QTL for Yield and Yield Components from Related Wild Species in Rice Cultivars. <i>Sustainable Development and Biodiversity</i> , 2016, , 171-202.	1.4	2
479	A splice acceptor site mutation in TaGW2-A1 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
480	Single nucleotide polymorphism tightly linked to a major QTL on chromosome 7A for both kernel length and kernel weight in wheat. <i>Molecular Breeding</i> , 2016, 36, 1.	1.0	42
481	Fine mapping of qKL1.07, a major QTL for kernel length in maize. <i>Molecular Breeding</i> , 2016, 36, 1.	1.0	21
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483	An integrated approach to maintaining cereal productivity under climate change. <i>Global Food Security</i> , 2016, 8, 9-18.	4.0	110
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485	Characterization of an IAA-glucose hydrolase gene TaTGW6 associated with grain weight in common wheat (<i>Triticum aestivum</i> L.). <i>Molecular Breeding</i> , 2016, 36, 1.	1.0	218
487	Arabidopsis KLU homologue GmCYP78A72 regulates seed size in soybean. <i>Plant Molecular Biology</i> , 2016, 90, 33-47.	2.0	84
488	Construction of a versatile SNP array for pyramiding useful genes of rice. <i>Plant Science</i> , 2016, 242, 131-139.	1.7	33
489	Progress and challenges in improving the nutritional quality of rice (<i>Oryza sativa</i> L.). <i>Critical Reviews in Food Science and Nutrition</i> , 2017, 57, 2455-2481.	5.4	110
490	Shoot tolerance mechanisms to iron toxicity in rice (<i>Oryza sativa</i> L.). <i>Plant, Cell and Environment</i> , 2017, 40, 570-584.	2.8	107
491	Validation of qGS10, a quantitative trait locus for grain size on the long arm of chromosome 10 in rice (<i>Oryza sativa</i> L.). <i>Journal of Integrative Agriculture</i> , 2017, 16, 16-26.	1.7	17
492	Genome-wide Association Analyses Reveal the Genetic Basis of Stigma Exsertion in Rice. <i>Molecular Plant</i> , 2017, 10, 634-644.	3.9	66
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499	Major genes determining yield-related traits in wheat and barley. <i>Theoretical and Applied Genetics</i> , 2017, 130, 1081-1098.	1.8	175
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502	A single-nucleotide polymorphism causes smaller grain size and loss of seed shattering during African rice domestication. <i>Nature Plants</i> , 2017, 3, 17064.	4.7	133
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504	The enhancer of zeste gene OsIEZ1 is involved in ligule and seed development in rice. <i>Canadian Journal of Plant Science</i> , 0, , .	0.3	0
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507	Molecular dissection of QTL governing grain size traits employing association and linkage mapping in Basmati rice. <i>Molecular Breeding</i> , 2017, 37, 1.	1.0	6
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509	Exiting Already? Molecular Control of Cell-Proliferation Arrest in Leaves: Cutting Edge. <i>Molecular Plant</i> , 2017, 10, 909-911.	3.9	0
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513	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

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515	Genome-wide study of an elite rice pedigree reveals a complex history of genetic architecture for breeding improvement. <i>Scientific Reports</i> , 2017, 7, 45685.	1.6	13
516	Wheat genomics comes of age. <i>Current Opinion in Plant Biology</i> , 2017, 36, 142-148.	3.5	103
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518	Rapid generation of genetic diversity by multiplex CRISPR/Cas9 genome editing in rice. <i>Science China Life Sciences</i> , 2017, 60, 506-515.	2.3	103
519	Quantitative trait loci from identification to exploitation for crop improvement. <i>Plant Cell Reports</i> , 2017, 36, 1187-1213.	2.8	81
520	Natural Variation in the Promoter of GSE5 Contributes to Grain Size Diversity in Rice. <i>Molecular Plant</i> , 2017, 10, 685-694.	3.9	253
521	Identification of quantitative trait loci for panicle length and yield related traits under different water and P application conditions in tropical region in rice (<i>Oryza sativa</i> L.). <i>Euphytica</i> , 2017, 213, 1.	0.6	9
522	Examining two sets of introgression lines reveals background-independent and stably expressed QTL that improve grain appearance quality in rice (<i>Oryza sativa</i> L.). <i>Theoretical and Applied Genetics</i> , 2017, 130, 951-967.	1.8	35
523	Introgression of Yield Component Traits in Rice (<i>Oryza sativa</i> ssp. <i>indica</i>) through Interspecific Hybridization. <i>Crop Science</i> , 2017, 57, 1557-1573.	0.8	21
524	<i>GRAIN INCOMPLETE FILLING 2</i> regulates grain filling and starch synthesis during rice caryopsis development. <i>Journal of Integrative Plant Biology</i> , 2017, 59, 134-153.	4.1	80
525	Duplication of an upstream silencer of FZP increases grain yield in rice. <i>Nature Plants</i> , 2017, 3, 885-893.	4.7	121
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527	Whole genome sequencing-based association study to unravel genetic architecture of cooked grain width and length traits in rice. <i>Scientific Reports</i> , 2017, 7, 12478.	1.6	69
528	Genetic connection between cell-wall composition and grain yield via parallel QTL analysis in indica and japonica subspecies. <i>Scientific Reports</i> , 2017, 7, 12561.	1.6	11
529	Genetic Improvement of Tropical Crops. , 2017, , .		23
530	Genetic dissection of grain traits in Yamadanishiki, an excellent sake-brewing rice cultivar. <i>Theoretical and Applied Genetics</i> , 2017, 130, 2567-2585.	1.8	13
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533	<scp>QTL</scp> for maize grain yield identified by <scp>QTL</scp> mapping in six environments and consensus loci for grain weight detected by meta-analysis. <i>Plant Breeding</i> , 2017, 136, 820-833.	1.0	8
534	The rice TRIANGULAR HULL1 protein acts as a transcriptional repressor in regulating lateral development of spikelet. <i>Scientific Reports</i> , 2017, 7, 13712.	1.6	23
535	TaGW2-6A allelic variation contributes to grain size possibly by regulating the expression of cytokinins and starch-related genes in wheat. <i>Planta</i> , 2017, 246, 1153-1163.	1.6	36
536	Influence of TaGW2-6A on seed development in wheat by negatively regulating gibberellin synthesis. <i>Plant Science</i> , 2017, 263, 226-235.	1.7	29
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539	OsFH15, a class I formin, interacts with microfilaments and microtubules to regulate grain size via affecting cell expansion in rice. <i>Scientific Reports</i> , 2017, 7, 6538.	1.6	36
540	The Conserved and Unique Genetic Architecture of Kernel Size and Weight in Maize and Rice. <i>Plant Physiology</i> , 2017, 175, 774-785.	2.3	114
541	Conditional quantitative trait locus mapping of wheat seed protein-fraction in relation to starch content. <i>Cereal Research Communications</i> , 2017, 45, 478-487.	0.8	3
542	NOG1 increases grain production in rice. <i>Nature Communications</i> , 2017, 8, 1497.	5.8	111
543	Genetic Improvement of Rice (<i>Oryza sativa</i> L.)., 2017, , 111-127.		5
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546	Does the pre-flowering period determine the potential grain weight of sunflower?. <i>Field Crops Research</i> , 2017, 212, 23-33.	2.3	21
547	O8SG2/OsBAK1 regulates grain size and number, and functions differently in Indica and Japonica backgrounds in rice. <i>Rice</i> , 2017, 10, 25.	1.7	52
548	Overexpression of the 16â€œ<scp>kD</scp>a Î±â€œamylase/trypsin inhibitor <scp>RAG</scp>2 improves grain yield and quality of rice. <i>Plant Biotechnology Journal</i> , 2017, 15, 568-580.	4.1	52
549	The art of curation at a biological database: Principles and application. <i>Current Plant Biology</i> , 2017, 11-12, 2-11.	2.3	30
550	Genomics-assisted breeding â€œ A revolutionary strategy for crop improvement. <i>Journal of Integrative Agriculture</i> , 2017, 16, 2674-2685.	1.7	50

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551	Mapping quantitative trait loci associated with starch paste viscosity in rice (<i>Oryza sativa</i> L.) under different environmental conditions. <i>Plant Breeding</i> , 2017, 136, 591-602.	1.0	9
552	GNS4, a novel allele of DWARF11, regulates grain number and grain size in a high-yield rice variety. <i>Rice</i> , 2017, 10, 34.	1.7	55
553	Breeding Rice for Improved Grain Quality. , 2017, , .		11
554	Genetic analysis and fine mapping of the RK4 gene for round kernel in rice (<i>Oryza sativa</i> L.). <i>Czech Journal of Genetics and Plant Breeding</i> , 2017, 53, 153-158.	0.4	1
555	New Candidate Genes Affecting Rice Grain Appearance and Milling Quality Detected by Genome-Wide and Gene-Based Association Analyses. <i>Frontiers in Plant Science</i> , 2016, 7, 1998.	1.7	55
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557	SNP Discovery and Genetic Variation of Candidate Genes Relevant to Heat Tolerance and Agronomic Traits in Natural Populations of Sand Rice (<i>Agriophyllum squarrosum</i>). <i>Frontiers in Plant Science</i> , 2017, 8, 536.	1.7	18
558	Regional Association Analysis of MetaQTLs Delineates Candidate Grain Size Genes in Rice. <i>Frontiers in Plant Science</i> , 2017, 8, 807.	1.7	36
559	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
560	Evolutionary Insights Based on SNP Haplotypes of Red Pericarp, Grain Size and Starch Synthase Genes in Wild and Cultivated Rice. <i>Frontiers in Plant Science</i> , 2017, 8, 972.	1.7	21
561	Insight into MAS: A Molecular Tool for Development of Stress Resistant and Quality of Rice through Gene Stacking. <i>Frontiers in Plant Science</i> , 2017, 8, 985.	1.7	105
562	Whole-Genome Analysis of Candidate genes Associated with Seed Size and Weight in <i>Sorghum bicolor</i> Reveals Signatures of Artificial Selection and Insights into Parallel Domestication in Cereal Crops. <i>Frontiers in Plant Science</i> , 2017, 8, 1237.	1.7	59
563	Genetic analysis for rice seedling vigor and fine mapping of a major QTL <i>qSSL1b</i> ; for seedling shoot length. <i>Breeding Science</i> , 2017, 67, 307-315.	0.9	40
564	Identify QTLs for grain size and weight in common wild rice using chromosome segment substitution lines across six environments. <i>Breeding Science</i> , 2017, 67, 472-482.	0.9	23
565	Identification of putative markers linked to grain plumpness in rice (<i>Oryza sativa</i> L.) via association mapping. <i>BMC Genetics</i> , 2017, 18, 89.	2.7	9
566	Uncovering the Genetic Architecture of Seed Weight and Size in Intermediate Wheatgrass through Linkage and Association Mapping. <i>Plant Genome</i> , 2017, 10, plantgenome2017.03.0022.	1.6	26
567	QTL mapping of agronomically important traits in sorghum (<i>Sorghum bicolor</i> L.). <i>Euphytica</i> , 2017, 213, 1.	0.6	15
568	Overexpression of <i>SRS5</i> improves grain size of brassinosteroid-related dwarf mutants in rice (<i>Oryza sativa</i> L.). <i>Breeding Science</i> , 2017, 67, 393-397.	0.9	25

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571	G-protein $\beta\gamma$ subunits determine grain size through interaction with MADS-domain transcription factors in rice. <i>Nature Communications</i> , 2018, 9, 852.	5.8	219
572	A G-protein pathway determines grain size in rice. <i>Nature Communications</i> , 2018, 9, 851.	5.8	195
573	Temperature-dependent QTLs in indica alleles for improving grain quality in rice: increased prominence of QTLs responsible for reduced chalkiness under high-temperature conditions. <i>Molecular Breeding</i> , 2018, 38, 1.	1.0	3
574	Fine mapping and identification of a novel locus <i>qGL12.2</i> control grain length in wild rice (<i>Oryza</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 1	1.8	22
575	Analysis of the functions of <i>TaGW2</i> homoeologs in wheat grain weight and protein content traits. <i>Plant Journal</i> , 2018, 94, 857-866.	2.8	211
576	Rice Functional Genomics Research: Past Decade and Future. <i>Molecular Plant</i> , 2018, 11, 359-380.	3.9	113
578	Rice Plant Architecture: Molecular Basis and Application in Breeding. , 2018, , 129-154.		4
579	A heading date QTL, <i>qHD7.2</i> , from wild rice (<i>Oryza rufipogon</i>) delays flowering and shortens panicle length under long-day conditions. <i>Scientific Reports</i> , 2018, 8, 2928.	1.6	26
580	Sequence-specific DNA binding activity of the cross-brace zinc finger motif of the piggyBac transposase. <i>Nucleic Acids Research</i> , 2018, 46, 2660-2677.	6.5	22
581	Genotyping by sequencing of rice interspecific backcross inbred lines identifies QTLs for grain weight and grain length. <i>Euphytica</i> , 2018, 214, 1.	0.6	29
582	Divergent functions of the <i>GAGA</i> -binding transcription factor family in rice. <i>Plant Journal</i> , 2018, 94, 32-47.	2.8	22
583	Characterization and fine mapping of <i>qPE12</i> , a new locus controlling rice panicle exertion. <i>Euphytica</i> , 2018, 214, 1.	0.6	4
584	Overexpression of miR164b-resistant <i>OsNAC2</i> improves plant architecture and grain yield in rice. <i>Journal of Experimental Botany</i> , 2018, 69, 1533-1543.	2.4	66
585	Pleiotropic effects of the wheat domestication gene <i>Q</i> on yield and grain morphology. <i>Planta</i> , 2018, 247, 1089-1098.	1.6	40
586	Identification of quantitative trait loci underlying seed shape in soybean across multiple environments. <i>Journal of Agricultural Science</i> , 2018, 156, 3-12.	0.6	5
587	Fine mapping and candidate gene analysis of the quantitative trait locus <i>gw8.1</i> associated with grain length in rice. <i>Genes and Genomics</i> , 2018, 40, 389-397.	0.5	16

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589	GS9 acts as a transcriptional activator to regulate rice grain shape and appearance quality. <i>Nature Communications</i> , 2018, 9, 1240.	5.8	221
590	<i>GRAIN SIZE AND NUMBER1</i> Negatively Regulates the OsMKKK10-OsMKK4-OsMPK6 Cascade to Coordinate the Trade-off between Grain Number per Panicle and Grain Size in Rice. <i>Plant Cell</i> , 2018, 30, 871-888.	3.1	196
591	A Novel QTL qTGW3 Encodes the GSK3/SHAGGY-Like Kinase OsGSK5/OsSK41 that Interacts with OsARF4 to Negatively Regulate Grain Size and Weight in Rice. <i>Molecular Plant</i> , 2018, 11, 736-749.	3.9	201
592	Dissecting the genetic basis of heavy panicle hybrid rice uncovered Gn1a and GS3 as key genes. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1391-1403.	1.8	17
593	Control of grain size in rice. <i>Plant Reproduction</i> , 2018, 31, 237-251.	1.3	188
594	Expression of sorghum gene SbSGL enhances grain length and weight in rice. <i>Molecular Breeding</i> , 2018, 38, 1.	1.0	6
595	Increasing the efficiency of CRISPR-Cas9/QCR precise genome editing in rice. <i>Plant Biotechnology Journal</i> , 2018, 16, 292-297.	4.1	78
596	Overexpression of mutated <i>Zm<sc>DA</sc>1</i> or <i>Zm<sc>DAR</sc>1</i> gene improves maize kernel yield by enhancing starch synthesis. <i>Plant Biotechnology Journal</i> , 2018, 16, 234-244.	4.1	57
597	Chromosomes A07 and A05 associated with stable and major QTLs for pod weight and size in cultivated peanut (<i>Arachis hypogaea</i> L.). <i>Theoretical and Applied Genetics</i> , 2018, 131, 267-282.	1.8	49
598	Meta-expression analysis of unannotated genes in rice and approaches for network construction to suggest the probable roles. <i>Plant Molecular Biology</i> , 2018, 96, 17-34.	2.0	4
599	Harnessing genetic resources and progress in plant genomics for fonio (<i>Digitaria</i> spp.) improvement. <i>Genetic Resources and Crop Evolution</i> , 2018, 65, 373-386.	0.8	17
600	Genome-wide association study of rice grain width variation. <i>Genome</i> , 2018, 61, 233-240.	0.9	7
601	A novel allele of TaGW2-A1 is located in a finely mapped QTL that increases grain weight but decreases grain number in wheat (<i>Triticum aestivum</i> L.). <i>Theoretical and Applied Genetics</i> , 2018, 131, 539-553.	1.8	121
602	Transcriptome Analysis and Functional Identification of Xa13 and Pi&eta Orthologs in <i>Oryza granulata</i> . <i>Plant Genome</i> , 2018, 11, 170097.	1.6	2
603	Overexpression of OsbHLH107, a member of the basic helix-loop-helix transcription factor family, enhances grain size in rice (<i>Oryza sativa</i> L.). <i>Rice</i> , 2018, 11, 41.	1.7	42
604	Grain width 2 (GW2) and its interacting proteins regulate seed development in rice (<i>Oryza sativa</i> L.). , 2018, 59, 23.		26
605	A northern Chinese origin of Austronesian agriculture: new evidence on traditional Formosan cereals. <i>Rice</i> , 2018, 11, 57.	1.7	12

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608	Fine mapping of a major quantitative trait locus, <i>qgnp7(t)</i> , controlling grain number per panicle in African rice (<i>Oryza glaberrima</i> S.). <i>Breeding Science</i> , 2018, 68, 606-613.	0.9	9
609	Notched Belly Grain 4, a Novel Allele of Dwarf 11, Regulates Grain Shape and Seed Germination in Rice (<i>Oryza sativa</i> L.). <i>International Journal of Molecular Sciences</i> , 2018, 19, 4069.	1.8	16
610	QTL mapping of melon fruit quality traits using a high-density GBS-based genetic map. <i>BMC Plant Biology</i> , 2018, 18, 324.	1.6	82
611	Expansin genes expression in growing ovaries and grains of sunflower are tissue-specific and associate with final grain weight. <i>BMC Plant Biology</i> , 2018, 18, 327.	1.6	10
612	Development of High Yielding Glutinous Cytoplasmic Male Sterile Rice (<i>Oryza sativa</i> L.) Lines through CRISPR/Cas9 Based Mutagenesis of <i>Wx</i> and <i>TGW6</i> and Proteomic Analysis of Anther. <i>Agronomy</i> , 2018, 8, 290.	1.3	24
613	Colocalization of QTLs for hull-cracked rice and grain size in elite rice varieties in Japan. <i>Breeding Science</i> , 2018, 68, 449-454.	0.9	9
614	Retrospective and perspective of rice breeding in China. <i>Journal of Genetics and Genomics</i> , 2018, 45, 603-612.	1.7	45
615	<i>SRG1</i> , Encoding a Kinesin-4 Protein, Is an Important Factor for Determining Grain Shape in Rice. <i>Rice Science</i> , 2018, 25, 297-307.	1.7	7
616	Improvement and identification of genes for yield related traits in Indica-type rice. <i>Ikushugaku Kenkyu</i> , 2018, 20, 180-184.	0.1	0
617	QTL Detection for Kernel Size and Weight in Bread Wheat (<i>Triticum aestivum</i> L.) Using a High-Density SNP and SSR-Based Linkage Map. <i>Frontiers in Plant Science</i> , 2018, 9, 1484.	1.7	78
619	Discovery of QTL Alleles for Grain Shape in the Japan-MAGIC Rice Population Using Haplotype Information. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3559-3565.	0.8	34
620	QTL mapping in a maize F2 population using Genotyping-by-Sequencing and a modified fine-mapping strategy. <i>Plant Science</i> , 2018, 276, 171-180.	1.7	16
621	Identification and validation of QTL for grain yield and plant water status under contrasting water treatments in fall-sown spring wheats. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1741-1759.	1.8	90
622	Genome-wide association reveals novel genomic loci controlling rice grain yield and its component traits under water-deficit stress during the reproductive stage. <i>Journal of Experimental Botany</i> , 2018, 69, 4017-4032.	2.4	39
623	The rational design of multiple molecular module-based assemblies for simultaneously improving rice yield and grain quality. <i>Journal of Genetics and Genomics</i> , 2018, 45, 337-341.	1.7	14
624	Dimerization through the RING-Finger Domain Attenuates Excision Activity of the piggyBac Transposase. <i>Biochemistry</i> , 2018, 57, 2913-2922.	1.2	2

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627	Genome-wide transcriptome profiling provides insights into panicle development of rice (<i>Oryza sativa</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 18	1.0	18
628	Life goes on: Archaeobotanical investigations of diet and ritual at Angkor Thom, Cambodia (14thâ€“15th) Tj ETQq0.0,0 rgBT /Overlock 18	0.9	18
629	Genetic Diversity and Genome-Wide Association Study of Major Ear Quantitative Traits Using High-Density SNPs in Maize. <i>Frontiers in Plant Science</i> , 2018, 9, 966.	1.7	46
630	Genomeâ€“Wide Association Analysis of Grain Yieldâ€“Associated Traits in a Panâ€“European Barley Cultivar Collection. <i>Plant Genome</i> , 2018, 11, 170073.	1.6	78
631	Molecular characterization of the TaWTG1 in bread wheat (<i>Triticum aestivum</i> L.). <i>Gene</i> , 2018, 678, 23-32.	1.0	5
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634	Identification of QTLs for rice grain size using a novel set of chromosomal segment substitution lines derived from Yamadanishiki in the genetic background of Koshihikari. <i>Breeding Science</i> , 2018, 68, 210-218.	0.9	19
635	LTBSG1, a New Allele of BRD2, Regulates Panicle and Grain Development in Rice by Brassinosteroid Biosynthetic Pathway. <i>Genes</i> , 2018, 9, 292.	1.0	14
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641	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
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643	Validation and Fine Mapping a Multifunction Region <i>qPCG10</i>/<i>qDC10</i> Conferring Chalkiness and Grain Shape of Rice. <i>Crop Science</i> , 2018, 58, 639-649.	0.8	4

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645	Gene editing and mutagenesis reveal inter-cultivar differences and additivity in the contribution of TaGW2 ² homoeologues to grain size and weight in wheat. <i>Theoretical and Applied Genetics</i> , 2018, 131, 2463-2475.	1.8	142
646	Transcriptome-referenced association study of clove shape traits in garlic. <i>DNA Research</i> , 2018, 25, 587-596.	1.5	31
647	Relationship between QTL for grain shape, grain weight, test weight, milling yield, and plant height in the spring wheat cross RL4452/â€AC Domainâ€™. <i>PLoS ONE</i> , 2018, 13, e0190681.	1.1	66
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651	Mapping and analysis of QTLs related to seed length and seed width in Glycine max. <i>Plant Breeding</i> , 2019, 138, 733-740.	1.0	3
652	The overexpression of rice <i>ACYL</i> â€™ <i>CoA</i> â€™ <i>BINDING PROTEIN</i> 2 increases grain size and bran oil content in transgenic rice. <i>Plant Journal</i> , 2019, 100, 1132-1147.	2.8	28
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654	Molecular insights into the regulation of rice kernel elongation. <i>Critical Reviews in Biotechnology</i> , 2019, 39, 904-923.	5.1	9
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658	Fine-Mapping of qTGW1.2a, a Quantitative Trait Locus for 1000-Grain Weight in Rice. <i>Rice Science</i> , 2019, 26, 220-228.	1.7	10
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660	Using a Mathematical Model of Phloem Transport to Optimize Strategies for Crop Improvement. <i>Methods in Molecular Biology</i> , 2019, 2014, 387-395.	0.4	0
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667	Mapping quantitative trait loci for yield-related traits and predicting candidate genes for grain weight in maize. <i>Scientific Reports</i> , 2019, 9, 16112.	1.6	15
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671	De novo transcriptome assembly and identification of genes related to seed size in common buckwheat (<i>Fagopyrum esculentum</i> ; M.). <i>Breeding Science</i> , 2019, 69, 487-497.	0.9	19
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673	Genome-wide association mapping and candidate gene analysis for seed shape in soybean (<i>Glycine max</i>). <i>Crop and Pasture Science</i> , 2019, 70, 684.	0.7	7
674	Mapping and genetic validation of a grain size QTL qGS7.1 in rice (<i>Oryza sativa</i> L.). <i>Journal of Integrative Agriculture</i> , 2019, 18, 1838-1850.	1.7	6
675	Utilization of Interspecific High-Density Genetic Map of RIL Population for the QTL Detection and Candidate Gene Mining for 100-Seed Weight in Soybean. <i>Frontiers in Plant Science</i> , 2019, 10, 1001.	1.7	31
676	Evaluation of head and broken rice of long grain Indica rice cultivars: Evidence for the role of starch and protein composition to head rice recovery. <i>Food Research International</i> , 2019, 126, 108675.	2.9	7
677	OsSPL18 controls grain weight and grain number in rice. <i>Journal of Genetics and Genomics</i> , 2019, 46, 41-51.	1.7	76
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679	Dissecting the Genetic Basis of Grain Size and Weight in Barley (<i>Hordeum vulgare</i> L.) by QTL and Comparative Genetic Analyses. <i>Frontiers in Plant Science</i> , 2019, 10, 469.	1.7	46

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681	Gene editing of the wheat homologs of <sc>TONNEAU</sc> 1â€recruiting motif encoding gene affects grain shape and weight in wheat. <i>Plant Journal</i> , 2019, 100, 251-264.	2.8	97
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683	Genome mapping of quantitative trait loci (QTL) controlling domestication traits of intermediate wheatgrass (<i>Thinopyrum intermedium</i>). <i>Theoretical and Applied Genetics</i> , 2019, 132, 2325-2351.	1.8	30
684	The PLATZ Transcription Factor GL6 Affects Grain Length and Number in Rice. <i>Plant Physiology</i> , 2019, 180, 2077-2090.	2.3	127
685	A novel rice grain size gene OsSNB was identified by genome-wide association study in natural population. <i>PLoS Genetics</i> , 2019, 15, e1008191.	1.5	72
686	Novel OsGRAS19 mutant, D26, positively regulates grain shape in rice (<i>Oryza sativa</i>). <i>Functional Plant Biology</i> , 2019, 46, 857.	1.1	12
687	OstMAPKKK5, a truncated mitogen-activated protein kinase kinase kinase 5, positively regulates plant height and yield in rice. <i>Crop Journal</i> , 2019, 7, 707-714.	2.3	12
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694	Harnessing Novel Diversity From Landraces to Improve an Elite Barley Variety. <i>Frontiers in Plant Science</i> , 2019, 10, 434.	1.7	28
695	The Genomics of <i>Oryza</i> Species Provides Insights into Rice Domestication and Heterosis. <i>Annual Review of Plant Biology</i> , 2019, 70, 639-665.	8.6	80
696	QTL identification and epistatic effect analysis of seed size- and weight-related traits in <i>Zea mays</i> L. <i>Molecular Breeding</i> , 2019, 39, 1.	1.0	7
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701	One-step genome editing of elite crop germplasm during haploid induction. <i>Nature Biotechnology</i> , 2019, 37, 287-292.	9.4	222
702	Transcriptome analysis reveals important candidate genes involved in grain-size formation at the stage of grain enlargement in common wheat cultivar 'Bainong 4199'. <i>PLoS ONE</i> , 2019, 14, e0214149.	1.1	13
703	OsGASR9 positively regulates grain size and yield in rice (<i>Oryza sativa</i>). <i>Plant Science</i> , 2019, 286, 17-27.	1.7	31
704	Genetic Modification for Wheat Improvement: From Transgenesis to Genome Editing. <i>BioMed Research International</i> , 2019, 2019, 1-18.	0.9	64
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706	¼ CT trait analysis reveals morphometric differences between domesticated temperate small grain cereals and their wild relatives. <i>Plant Journal</i> , 2019, 99, 98-111.	2.8	19
707	Fine mapping of qTGW10-20.8, a QTL having important contribution to grain weight variation in rice. <i>Crop Journal</i> , 2019, 7, 587-597.	2.3	15
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710	Molecular Networks of Seed Size Control in Plants. <i>Annual Review of Plant Biology</i> , 2019, 70, 435-463.	8.6	336
711	Applications of the CRISPR/Cas9 System for Rice Grain Quality Improvement: Perspectives and Opportunities. <i>International Journal of Molecular Sciences</i> , 2019, 20, 888.	1.8	98
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717	Manipulating osa-MIR156f Expression by D18 Promoter to Regulate Plant Architecture and Yield Traits both in Seasonal and Ratoon Rice. <i>Biological Procedures Online</i> , 2019, 21, 21.	1.4	8
718	Molecular, cellular and Yin-Yang regulation of grain size and number in rice. <i>Molecular Breeding</i> , 2019, 39, 1.	1.0	32
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721	Cloning, characterization of TaGS3 and identification of allelic variation associated with kernel traits in wheat (<i>Triticum aestivum</i> L.). <i>BMC Genetics</i> , 2019, 20, 98.	2.7	35
722	A high-density genetic map constructed using specific length amplified fragment (SLAF) sequencing and QTL mapping of seed-related traits in sesame (<i>Sesamum indicum</i> L.). <i>BMC Plant Biology</i> , 2019, 19, 588.	1.6	24
723	Genetic dissection and validation of QTLs for grain shape and weight in rice and fine mapping of qGL1.3, a major QTL for grain length and weight. <i>Molecular Breeding</i> , 2019, 39, 1.	1.0	3
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725	Multiplex QTL editing of grain-related genes improves yield in elite rice varieties. <i>Plant Cell Reports</i> , 2019, 38, 475-485.	2.8	136
726	Association Analysis of Three Diverse Rice (<i>Oryza sativa</i> L.) Germplasm Collections for Loci Regulating Grain Quality Traits. <i>Plant Genome</i> , 2019, 12, 170085.	1.6	33
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729	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
730	<i>GW5-like</i> , a homolog of <i>GW5</i> , negatively regulates grain width, weight and salt resistance in rice. <i>Journal of Integrative Plant Biology</i> , 2019, 61, 1171-1185.	4.1	30
731	Identification of QTLs and Validation of qCd-2 Associated with Grain Cadmium Concentrations in Rice. <i>Rice Science</i> , 2019, 26, 42-49.	1.7	9
732	A Megabase-Scale Deletion is Associated with Phenotypic Variation of Multiple Traits in Maize. <i>Genetics</i> , 2019, 211, 305-316.	1.2	6
733	Rice Grain Quality. <i>Methods in Molecular Biology</i> , 2019, , .	0.4	5
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736	An efficient multi-locus mixed model framework for the detection of small and linked QTLs in F2. <i>Briefings in Bioinformatics</i> , 2019, 20, 1913-1924.	3.2	74
737	OsNF-YC10, a seed preferentially expressed gene regulates grain width by affecting cell proliferation in rice. <i>Plant Science</i> , 2019, 280, 219-227.	1.7	18
738	<i>1</i> TILLERING AND SMALL GRAIN 1 <i>1</i> dominates the tryptophan aminotransferase family required for local auxin biosynthesis in rice. <i>Journal of Integrative Plant Biology</i> , 2020, 62, 581-600.	4.1	37
739	Analysis of the genetic architecture of maize kernel size traits by combined linkage and association mapping. <i>Plant Biotechnology Journal</i> , 2020, 18, 207-221.	4.1	64
740	The rice PLATZ protein SHORT GRAIN6 determines grain size by regulating spikelet hull cell division. <i>Journal of Integrative Plant Biology</i> , 2020, 62, 847-864.	4.1	43
741	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
743	Microbial inactivation in model tissues treated by surface discharge plasma. <i>Journal Physics D: Applied Physics</i> , 2020, 53, 015205.	1.3	5
744	Integrating the dynamics of yield traits in rice in response to environmental changes. <i>Journal of Experimental Botany</i> , 2020, 71, 490-506.	2.4	39
745	Map-based cloning of qBWT-c12 discovered brassinosteroid-mediated control of organ size in cotton. <i>Plant Science</i> , 2020, 291, 110315.	1.7	4
746	Quantitative trait loci identification and genetic diversity analysis of panicle structure and grain shape in rice. <i>Plant Growth Regulation</i> , 2020, 90, 89-100.	1.8	9
747	A putative AGO protein, OsAGO17, positively regulates grain size and grain weight through OsmiR397b in rice. <i>Plant Biotechnology Journal</i> , 2020, 18, 916-928.	4.1	32
748	Linking fundamental science to crop improvement through understanding source and sink traits and their integration for yield enhancement. <i>Journal of Experimental Botany</i> , 2020, 71, 2270-2280.	2.4	36
749	Effects of <i>DEP1</i> on grain yield and grain quality in the background of two <i>japonica</i> rice (<i>Oryza sativa</i>) cultivars. <i>Plant Breeding</i> , 2020, 139, 608-617.	1.0	10
750	<i>TaDA1</i> , a conserved negative regulator of kernel size, has an additive effect with <i>TaGW2</i> in common wheat (<i>Triticum aestivum</i> L.). <i>Plant Biotechnology Journal</i> , 2020, 18, 1330-1342.	4.1	90
751	Rice grain quality—traditional traits for high quality rice and health-plus substances. <i>Molecular Breeding</i> , 2020, 40, 1.	1.0	78
752	<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
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755	Combined Linkage Mapping and Genome-Wide Association Study Identified QTLs Associated with Grain Shape and Weight in Rice (<i>Oryza sativa</i> L.). <i>Agronomy</i> , 2020, 10, 1532.	1.3	11
756	Rapid prediction of head rice yield and grain shape for genome-wide association study in indica rice. <i>Journal of Cereal Science</i> , 2020, 96, 103091.	1.8	12
757	Less Is More, Natural Loss-of-Function Mutation Is a Strategy for Adaptation. <i>Plant Communications</i> , 2020, 1, 100103.	3.6	35
758	Cytochrome P450 family: Genome-wide identification provides insights into the rutin synthesis pathway in Tartary buckwheat and the improvement of agricultural product quality. <i>International Journal of Biological Macromolecules</i> , 2020, 164, 4032-4045.	3.6	29
759	Identification of qLG2, qLG8, and qWG2 as novel quantitative trait loci for grain shape and the allelic analysis in cultivated rice. <i>Planta</i> , 2020, 252, 18.	1.6	2
760	Genetic determinants for agronomic and yield-related traits localized on a GBS-SNP linkage map from a japonica x indica cross in rice. <i>Plant Gene</i> , 2020, 24, 100249.	1.4	8
761	Identification of Rice QTLs for Important Agronomic Traits with Long-Kernel CSSL-Z741 and Three SSSLs. <i>Rice Science</i> , 2020, 27, 414-422.	1.7	10
762	Identification and validation of quantitative trait loci for kernel traits in common wheat (<i>Triticum</i>) Tj ETQqO O O rgBT /Overlock, 10 Tf 50	1.6	23
763	Responses of sub1A quantitative trait locus in rice to salinity in modulation with silver induction. <i>Revista Brasileira De Botanica</i> , 2020, 43, 789-797.	0.5	4
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767	The Selection of Gamma-Ray Irradiated Higher Yield Rice Mutants by Directed Evolution Method. <i>Plants</i> , 2020, 9, 1004.	1.6	9
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773	Genetic and epistatic effects for grain quality and yield of three grain-size QTLs identified in brewing rice (<i>Oryza sativa</i> L.). <i>Molecular Breeding</i> , 2020, 40, 1.	1.0	6
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775	Transcriptome profiling and weighted gene co-expression network analysis of early floral development in <i>Aquilegia coerulea</i> . <i>Scientific Reports</i> , 2020, 10, 19637.	1.6	12
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779	Effects of GS3 and GL3.1 for Grain Size Editing by CRISPR/Cas9 in Rice. <i>Rice Science</i> , 2020, 27, 405-413.	1.7	39
780	Identification of Additive and Epistatic QTLs Conferring Seed Traits in Soybean Using Recombinant Inbred Lines. <i>Frontiers in Plant Science</i> , 2020, 11, 566056.	1.7	10
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783	A quantitative trait locus <i>GW6</i> controls rice grain size and yield through the gibberellin pathway. <i>Plant Journal</i> , 2020, 103, 1174-1188.	2.8	85
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785	Training instance segmentation neural network with synthetic datasets for crop seed phenotyping. <i>Communications Biology</i> , 2020, 3, 173.	2.0	81
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787	RING finger ubiquitin E3 ligase gene <i>TaSDIR1-4A</i> contributes to determination of grain size in common wheat. <i>Journal of Experimental Botany</i> , 2020, 71, 5377-5388.	2.4	43
788	Genome-wide analysis of polymorphisms identified domestication-associated long low diversity region carrying important rice grain size/weight quantitative trait loci. <i>Plant Journal</i> , 2020, 103, 1525-1547.	2.8	9
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799	The Rice Basic Helix-Loop-Helix 79 (<i>OsBHLH079</i>) Determines Leaf Angle and Grain Shape. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2090.	1.8	16
800	Quantitative Trait Loci for Seed Size Variation in Cucurbits – A Review. <i>Frontiers in Plant Science</i> , 2020, 11, 304.	1.7	30
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802	Marker-assisted selection for grain number and yield-related traits of rice (<i>Oryza sativa</i> L.). <i>Physiology and Molecular Biology of Plants</i> , 2020, 26, 885-898.	1.4	21
803	Genome-Wide Identification and Evolutionary Analysis of the Fruit-Weight 2.2-Like Gene Family in Polyploid Oilseed Rape (<i>Brassica napus</i> L.). <i>DNA and Cell Biology</i> , 2020, 39, 766-782.	0.9	3
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815	Divergent selection and genetic introgression shape the genome landscape of heterosis in hybrid rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 4623-4631.	3.3	46
816	High-density genetic linkage-map construction of hawthorn and QTL mapping for important fruit traits. <i>PLoS ONE</i> , 2020, 15, e0229020.	1.1	4
817	Genome-Wide Association Study and QTL Meta-Analysis Identified Novel Genomic Loci Controlling Potassium Use Efficiency and Agronomic Traits in Bread Wheat. <i>Frontiers in Plant Science</i> , 2020, 11, 70.	1.7	31
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820	Genome-wide analysis of <i>Jatropha curcas</i> MADS-box gene family and functional characterization of the JcMADS40 gene in transgenic rice. <i>BMC Genomics</i> , 2020, 21, 325.	1.2	13
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828	Application of Omics Technologies in Crop Breeding. , 2021, , 25-45.		3
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831	Decreased grain size1, a C3HC4-type RING protein, influences grain size in rice (<i>Oryza sativa</i> L.). <i>Plant Molecular Biology</i> , 2021, 105, 405-417.	2.0	10
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842	Genome-wide association study and Mendelian randomization analysis provide insights for improving rice yield potential. <i>Scientific Reports</i> , 2021, 11, 6894.	1.6	9
843	APETALA2 functions as a temporal factor together with BLADE-ON-PETIOLE2 and MADS29 to control flower and grain development in barley. <i>Development (Cambridge)</i> , 2021, 148, .	1.2	18
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846	Identification of eight QTL controlling multiple yield components in a German multi-parental wheat population, including <i>Rht24</i> , <i>WAO-A1</i> , <i>WAO-B1</i> and genetic loci on chromosomes 5A and 6A. <i>Theoretical and Applied Genetics</i> , 2021, 134, 1435-1454.	1.8	20
848	The brassinosteroid biosynthesis gene, <i>ZmD11</i> , increases seed size and quality in rice and maize. <i>Plant Physiology and Biochemistry</i> , 2021, 160, 281-293.	2.8	18
849	CRISPR/Cas9 Guided Mutagenesis of Grain Size 3 Confers Increased Rice (<i>Oryza sativa</i> L.) Grain Length by Regulating Cysteine Proteinase Inhibitor and Ubiquitin-Related Proteins. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3225.	1.8	19
850	The <i>da1</i> mutation in wheat increases grain size under ambient and elevated CO ₂ but not grain yield due to trade-off between grain size and grain number. <i>Plant-Environment Interactions</i> , 2021, 2, 61-73.	0.7	9
851	Control of seed size by jasmonate. <i>Science China Life Sciences</i> , 2021, 64, 1215-1226.	2.3	33
852	CRISPR/Cas9-mediated mutagenesis of <i>CIBG1</i> decreased seed size and promoted seed germination in watermelon. <i>Horticulture Research</i> , 2021, 8, 70.	2.9	38
853	Identification and Pyramiding of QTLs for Rice Grain Size Based on Short-Wide Grain CSSL-Z563 and Fine-Mapping of <i>qGL3</i> . <i>Rice</i> , 2021, 14, 35.	1.7	13
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867	Superior haplotypes towards development of low glycemic index rice with preferred grain and cooking quality. <i>Scientific Reports</i> , 2021, 11, 10082.	1.6	15
869	Comprehensive Transcriptome Analyses Reveal Candidate Genes for Variation in Seed Size/Weight During Peanut (<i>Arachis hypogaea</i> L.) Domestication. <i>Frontiers in Plant Science</i> , 2021, 12, 666483.	1.7	13
870	Genome-wide association study reveals early seedling vigour-associated quantitative trait loci in indica rice. <i>Euphytica</i> , 2021, 217, 1.	0.6	1
871	A novel miR167a-OsARF6-OsAUX3 module regulates grain length and weight in rice. <i>Molecular Plant</i> , 2021, 14, 1683-1698.	3.9	61
872	Loss of Function of OsARG Resulted in Pepper-Shaped Husk in Indica Rice. <i>Life</i> , 2021, 11, 523.	1.1	0
873	Genome-wide analysis of RING-type E3 ligase family identifies potential candidates regulating high amylose starch biosynthesis in wheat (<i>Triticum aestivum</i> L.). <i>Scientific Reports</i> , 2021, 11, 11461.	1.6	8
874	CRISPR/Cas systems: The link between functional genes and genetic improvement. <i>Crop Journal</i> , 2021, 9, 678-687.	2.3	7
875	What happened during domestication of wild to cultivated rice. <i>Crop Journal</i> , 2021, 9, 564-576.	2.3	19
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880	Genetic Mapping and Validation of Loci for Kernel-Related Traits in Wheat (<i>Triticum aestivum</i> L.). <i>Frontiers in Plant Science</i> , 2021, 12, 667493.	1.7	17
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882	Impaired SWEET-mediated sugar transportation impacts starch metabolism in developing rice seeds. <i>Crop Journal</i> , 2022, 10, 98-108.	2.3	17
883	Dynamic formation and transcriptional regulation mediated by phytohormones during chalkiness formation in rice. <i>BMC Plant Biology</i> , 2021, 21, 308.	1.6	10
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887	MULTI-FLORET SPIKELET 4 (MFS4) Regulates Spikelet Development and Grain Size in Rice. <i>Rice Science</i> , 2021, 28, 344-357.	1.7	0
888	Genome-wide association study of grain morphology in wheat. <i>Euphytica</i> , 2021, 217, 1.	0.6	2
889	Genetic and Molecular Factors Determining Grain Weight in Rice. <i>Frontiers in Plant Science</i> , 2021, 12, 605799.	1.7	27
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891	The ubiquitin-interacting motif-type ubiquitin receptor HDR3 interacts with and stabilizes the histone acetyltransferase GW6a to control the grain size in rice. <i>Plant Cell</i> , 2021, 33, 3331-3347.	3.1	38
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899	Dissection of two QTL for grain length linked on the long arm of chromosome 5 in rice. <i>Crop Science</i> , 0, , .	0.8	0
900	Identification and allele mining of new candidate genes underlying rice grain weight and grain shape by genome-wide association study. <i>BMC Genomics</i> , 2021, 22, 602.	1.2	13
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902	Heterologous expression of ZmGS5 enhances organ size and seed weight by regulating cell expansion in <i>Arabidopsis thaliana</i> . <i>Gene</i> , 2021, 793, 145749.	1.0	5

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906	Expression, purification and crystallization of TGW6, which limits grain weight in rice. Protein Expression and Purification, 2021, 188, 105975.	0.6	6
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908	Utilization of a Wheat55K SNP array-derived high-density genetic map for high-resolution mapping of quantitative trait loci for important kernel-related traits in common wheat. Theoretical and Applied Genetics, 2021, 134, 807-821.	1.8	24
909	Source-Sink Relationships and Its Effect on Plant Productivity: Manipulation of Primary Carbon and Starch Metabolism. Concepts and Strategies in Plant Sciences, 2021, , 1-31.	0.6	5
910	OrMKK3 Influences Morphology and Grain Size in Rice. Journal of Plant Biology, 2021, , 1-14.	0.9	7
911	Seed Dispersal and Crop Domestication: Shattering, Germination and Seasonality in Evolution under Cultivation. , 0, , 238-295.		83
912	Common Bean Genomics and Its Applications in Breeding Programs. , 2014, , 185-206.		4
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1189	QTL Analysis of Z414, a Chromosome Segment Substitution Line with Short, Wide Grains, and Substitution Mapping of qGL11 in Rice. <i>Rice</i> , 2022, 15, 25.	1.7	8
1190	<i>OsJAZ11</i> regulates spikelet and seed development in rice. <i>Plant Direct</i> , 2022, 6, e401.	0.8	8
1191	Poaceae Orthologs of Rice OsSGL, DUF1645 Domain-Containing Genes, Positively Regulate Drought Tolerance, Grain Length and Weight in Rice. <i>Rice Science</i> , 2022, 29, 257-267.	1.7	5
1192	Effect of Panicle Morphology on Grain Filling and Rice Yield: Genetic Control and Molecular Regulation. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	11
1193	Transcriptome analysis reveals genes associated with kernel size in apricots cultivated for kernel consumption (<i>Prunus armeniaca</i> — <i>Prunus sibirica</i>). <i>Scientia Horticulturae</i> , 2022, 302, 111141.	1.7	2
1194	N6-Methyladenosine dynamic changes and differential methylation in wheat grain development. <i>Planta</i> , 2022, 255, 125.	1.6	2
1195	<i>OsAT1</i> , an anion transporter, negatively regulates grain size and yield in rice. <i>Physiologia Plantarum</i> , 2022, 174, e13692.	2.6	5

#	ARTICLE	IF	CITATIONS
1196	Genetic mechanism of heterosis for rice milling and appearance quality in an elite rice hybrid. <i>Crop Journal</i> , 2022, 10, 1705-1716.	2.3	7
1197	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
1198	Genes determining panicle morphology and grain quality in rice (<i>Oryza sativa</i>). <i>Functional Plant Biology</i> , 2022, , .	1.1	0
1199	Identifying Quantitative Trait Loci for Thousand Grain Weight in Eggplant by Genome Re-Sequencing Analysis. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	2
1200	OsBSK2, a putative brassinosteroid-signalling kinase, positively controls grain size in rice. <i>Journal of Experimental Botany</i> , 2022, 73, 5529-5542.	2.4	15
1201	Fine Mapping and Cloning of a Major QTL qph12, Which Simultaneously Affects the Plant Height, Panicle Length, Spikelet Number and Yield in Rice (<i>Oryza sativa</i> L.). <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	5
1202	Natural allelic variation of <i>GmST05</i> controlling seed size and quality in soybean. <i>Plant Biotechnology Journal</i> , 2022, 20, 1807-1818.	4.1	44
1203	Characterization of Grain-Related Traits and Pasting and Texture Properties of United State Rice Varieties in Korea. <i>Han'guk Yukchong Hakhoe Chi</i> , 2022, 54, 81-97.	0.2	0
1204	Emerging roles of the ubiquitin-proteasome pathway in enhancing crop yield by optimizing seed agronomic traits. <i>Plant Cell Reports</i> , 2022, 41, 1805-1826.	2.8	9
1205	Origin of the genome editing systems: application for crop improvement. , 2022, 77, 3353-3383.		1
1206	Genome-Wide Association Study of Grain Quality Traits in Rice Detected Genomic Regions of High-Quality Rice for Increasing Rice Consumption. <i>Biosciences, Biotechnology Research Asia</i> , 2022, 19, 333-346.	0.2	1
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1208	Regulation of OsPIL15 on rice quality. <i>Molecular Breeding</i> , 2022, 42, .	1.0	2
1209	Fine Mapping of Two Major Quantitative Trait Loci for Rice Chalkiness With High Temperature-Enhanced Additive Effects. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
1210	Genes Impacting Grain Weight and Number in Wheat (<i>Triticum aestivum</i> L. ssp. <i>aestivum</i>). <i>Plants</i> , 2022, 11, 1772.	1.6	6
1211	Unravelling genetic architecture and development of core set from elite rice lines using yield-related candidate gene markers. <i>Physiology and Molecular Biology of Plants</i> , 2022, 28, 1217-1232.	1.4	3
1212	Natural variation of the BRD2 allele affects plant height and grain size in rice. <i>Planta</i> , 2022, 256, .	1.6	7
1213	Genetic control of grain appearance quality in rice. <i>Biotechnology Advances</i> , 2022, 60, 108014.	6.0	32

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1214	Fine mapping and candidate gene analysis of qGL10 affecting rice grain length. <i>Crop Journal</i> , 2023, 11, 540-548.	2.3	1
1215	GL9 from <i>Oryza glumaepatula</i> controls grain size and chalkiness in rice. <i>Crop Journal</i> , 2023, 11, 198-207.	2.3	8
1216	Rice co-expression network analysis identifies gene modules associated with agronomic traits. <i>Plant Physiology</i> , 2022, 190, 1526-1542.	2.3	6
1217	<i>cis</i> -regulatory variation affecting gene expression contributes to the improvement of maize kernel size. <i>Plant Journal</i> , 0, , .	2.8	2
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1219	Ribonuclease H-like gene <i>SMALL GRAIN2</i> regulates grain size in rice through brassinosteroid signaling pathway. <i>Journal of Integrative Plant Biology</i> , 2022, 64, 1883-1900.	4.1	14
1220	Fine Mapping of qTGW7b, a Minor Effect QTL for Grain Weight in Rice (<i>Oryza sativa</i> L.). <i>International Journal of Molecular Sciences</i> , 2022, 23, 8296.	1.8	4
1221	Functional Analysis and Precise Location of m-1a in Rice. <i>Agronomy</i> , 2022, 12, 1706.	1.3	1
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1225	Genetic and molecular factors in determining grain number per panicle of rice. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	7
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1232	Short grain 5 controls grain length in rice by regulating cell expansion. <i>Plant Science</i> , 2022, 323, 111412.	1.7	1

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1234	Discovery and Validation of Grain Shape Loci in U.S. Rice Germplasm Through Haplotype Characterization. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
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1236	Genome-wide analysis of the JAZ subfamily of transcription factors and functional verification of BnCO8.JAZ1-1 in <i>Brassica napus</i> . , 2022, 15, .		2
1237	Natural variation of GhSI7 increases seed index in cotton. <i>Theoretical and Applied Genetics</i> , 2022, 135, 3661-3672.	1.8	4
1238	TATA-box binding protein-associated factor 2 regulates grain size in rice. <i>Crop Journal</i> , 2023, 11, 438-446.	2.3	0
1239	Large-Grain and Semidwarf Isogenic Rice Koshihikari Integrated with GW2 and sd1. <i>Sustainability</i> , 2022, 14, 11075.	1.6	1
1240	2Gs and plant architecture: breaking grain yield ceiling through breeding approaches for next wave of revolution in rice (<i>Oryza sativa</i> L.). <i>Critical Reviews in Biotechnology</i> , 2024, 44, 139-162.	5.1	16
1241	Low grain weight, a new allele of BRITTLE CULM12, affects grain size through regulating GW7 expression in rice. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
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1243	Genetic dissection of grain traits and their corresponding heterosis in an elite hybrid. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
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1245	Microsatellite diversity analysis and QTL identification among progenies derived from aerobic " basmati rice (<i>Oryza sativa</i>) cross under direct-seeded conditions. , 2020, 90, 1411-1418.		0
1246	èŠ±ç”ŸçŠââŠâ°ç,â...³æ€ŞçŠŸQTLâ®šä1/2ç”ç©Ÿè;â±•. <i>Acta Agronomica Sinica(China)</i> , 2022, 48, 280-291.	0.1	0
1247	Role of cytokinins in seed development in pulses and oilseed crops: Current status and future perspective. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	5
1248	Genome-wide association studies provide genetic insights into natural variation of seed-size-related traits in mungbean. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	7
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1250	Map-based cloning and transcriptome analysis of the more-tiller and small-grain mutant in rice. <i>Planta</i> , 2022, 256, .	1.6	1

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1253	Developing Genetic Engineering Techniques for Control of Seed Size and Yield. <i>International Journal of Molecular Sciences</i> , 2022, 23, 13256.	1.8	8
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1255	Identification and validation of stable quantitative trait loci for yield component traits in wheat. <i>Crop Journal</i> , 2023, 11, 558-563.	2.3	2
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1259	Genetic background- and environment-independent QTL and candidate gene identification of appearance quality in three MAGIC populations of rice. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
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1262	Genetic improvement of rice grain quality. , 2023, , 235-256.		1
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1264	Relationship between rice grain protein content and key phenotype in rice. <i>Agronomy Journal</i> , 0, , .	0.9	0
1265	Control of Grain Weight and Size in Rice (<i>Oryza sativa</i> L.) by OsPUB3 Encoding a U-Box E3 Ubiquitin Ligase. <i>Rice</i> , 2022, 15, .	1.7	3
1266	Co-Overexpression of Two Key Source Genes, <i>OsBMY4</i> and <i>OsISA3</i> , Improves Multiple Key Traits of Rice Seeds. <i>Journal of Agricultural and Food Chemistry</i> , 2023, 71, 615-625.	2.4	7
1267	Marker-trait association analysis for grain shape traits in rice (<i>Oryza sativa</i> L.). <i>Israel Journal of Plant Sciences</i> , 2022, 70, 47-56.	0.3	0
1268	Detecting and pyramiding target QTL for plant- and grain-related traits via chromosomal segment substitution line of rice. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
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1274	Artificially Selected Grain Shape Gene Combinations in Guangdong Simiao Varieties of Rice (<i>Oryza</i>) Tj ETQq1 1 0.784314 rgBT /Overl	1.7	0
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1278	Fine Mapping and Cloning of a qRA2 Affect the Ratooning Ability in Rice (<i>Oryza sativa</i> L.). <i>International Journal of Molecular Sciences</i> , 2023, 24, 967.	1.8	1
1279	Breeding of the Long-Grain Restorer of Indica-Japonica Hybrid Rice by Using the Genetic Effects of Grain Shape QTLs. <i>Agronomy</i> , 2023, 13, 107.	1.3	0
1280	Variations in Grain Traits among Local Rice Varieties Collected More Than Half-Century Ago in Indochinese Countries. <i>Plants</i> , 2023, 12, 133.	1.6	0
1281	AMMI biplot analysis for stability in early maturity group of rice (<i>Oryza sativa</i> L.). <i>Oryza</i> , 2022, 59, 492-503.	0.2	0
1282	Analysis of Domestication Loci in Wild Rice Populations. <i>Plants</i> , 2023, 12, 489.	1.6	0
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1289	Identification, Fine Mapping and Application of Quantitative Trait Loci for Grain Shape Using Single-Segment Substitution Lines in Rice (<i>Oryza sativa</i> L.). <i>Plants</i> , 2023, 12, 892.	1.6	0
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1297	The translational landscape of bread wheat during grain development. <i>Plant Cell</i> , 2023, 35, 1848-1867.	3.1	11
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1302	Novel quantitative trait loci for yield and yield related traits identified in Basmati rice (<i>Oryza sativa</i> L.) cv. ETQq1 1 0.784314. <i>Overlock 10</i>	1.8	0
1303	Genetic Diversity and Association Mapping of Grain-Size Traits in Rice Landraces from the Honghe Hani Rice Terraces System in Yunnan Province. <i>Plants</i> , 2023, 12, 1678.	1.6	2
1304	Genetic dissection and validation of a major QTL for grain weight on chromosome 3B in bread wheat (<i>Triticum aestivum</i> L.). <i>Journal of Integrative Agriculture</i> , 2024, 23, 77-92.	1.7	4
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1306	Cytological, transcriptome and miRNome temporal landscapes decode enhancement of rice grain size. <i>BMC Biology</i> , 2023, 21, .	1.7	0
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1348	Employing Image Processing and Deep Learning in Gradation and Classification of Paddy Grain. <i>Intelligent Systems Reference Library</i> , 2023, , 85-111.	1.0	1
1357	Regulation of seed traits in soybean. <i>ABIOTECH</i> , 2023, 4, 372-385.	1.8	0
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