

# Bin Han

## List of Publications by Year in descending order

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136  
papers

24,291  
citations

13827

67  
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12558

132  
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141  
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141  
docs citations

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times ranked

17691  
citing authors

#	ARTICLE	IF	CITATIONS
1	NLRs guard metabolism to coordinate pattern- and effector-triggered immunity. <i>Nature</i> , 2022, 601, 245-251.	13.7	66
2	Twenty years of rice genomics research: From sequencing and functional genomics to quantitative genomics. <i>Molecular Plant</i> , 2022, 15, 593-619.	3.9	15
3	Genotype calling and haplotype inference from low coverage sequence data in heterozygous plant genome using HetMap. <i>Theoretical and Applied Genetics</i> , 2022, , .	1.8	0
4	The integrated genomics of crop domestication and breeding. <i>Cell</i> , 2022, 185, 2828-2839.	13.5	47
5	Designing future crops: challenges and strategies for sustainable agriculture. <i>Plant Journal</i> , 2021, 105, 1165-1178.	2.8	110
6	A quantitative genomics map of rice provides genetic insights and guides breeding. <i>Nature Genetics</i> , 2021, 53, 243-253.	9.4	106
7	OryzaGenome2.1: Database of Diverse Genotypes in Wild Oryza Species. <i>Rice</i> , 2021, 14, 24.	1.7	17
8	A route to de novo domestication of wild allotetraploid rice. <i>Cell</i> , 2021, 184, 1156-1170.e14.	13.5	259
9	Chromosome-scale assembly and analysis of biomass crop <i>Miscanthus lutarioriparius</i> genome. <i>Nature Communications</i> , 2021, 12, 2458.	5.8	25
10	Subtelomeric assembly of a multi-gene pathway for antimicrobial defense compounds in cereals. <i>Nature Communications</i> , 2021, 12, 2563.	5.8	51
11	Enhancing rice grain production by manipulating the naturally evolved cis-regulatory element-containing inverted repeat sequence of OsREM20. <i>Molecular Plant</i> , 2021, 14, 997-1011.	3.9	19
12	Understanding the genetic basis of rice heterosis: Advances and prospects. <i>Crop Journal</i> , 2021, 9, 688-692.	2.3	18
13	The magic of genomics in creating hybrid potato. <i>Molecular Plant</i> , 2021, 14, 1237-1238.	3.9	3
14	Cytoplasmic and nuclear genome variations of rice hybrids and their parents inform the trajectory and strategy of hybrid rice breeding. <i>Molecular Plant</i> , 2021, 14, 2056-2071.	3.9	5
15	Genome-wide identification and analysis of heterotic loci in three maize hybrids. <i>Plant Biotechnology Journal</i> , 2020, 18, 185-194.	4.1	39
16	The draft genome of a wild barley genotype reveals its enrichment in genes related to biotic and abiotic stresses compared to cultivated barley. <i>Plant Biotechnology Journal</i> , 2020, 18, 443-456.	4.1	45
17	Advances in genome-wide association studies of complex traits in rice. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1415-1425.	1.8	72
18	Rice Protein Tagging Project: A Call for International Collaborations on Genome-wide In-Locus Tagging of Rice Proteins. <i>Molecular Plant</i> , 2020, 13, 1663-1665.	3.9	11

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19	Genome-wide screen and functional analysis in <i>Xanthomonas</i> reveal a large number of mRNA-derived sRNAs, including the novel RsmA-sequester RsmU. <i>Molecular Plant Pathology</i> , 2020, 21, 1573-1590.	2.0	10
20	Pan-Genome of Wild and Cultivated Soybeans. <i>Cell</i> , 2020, 182, 162-176.e13.	13.5	508
21	Translational Regulation of Plant Response to High Temperature by a Dual-Function tRNAHis Guanylyltransferase in Rice. <i>Molecular Plant</i> , 2019, 12, 1123-1142.	3.9	44
22	The tea plant reference genome and improved gene annotation using long-read and paired-end sequencing data. <i>Scientific Data</i> , 2019, 6, 122.	2.4	29
23	Dissecting a heterotic gene through GradedPool-Seq mapping informs a rice-improvement strategy. <i>Nature Communications</i> , 2019, 10, 2982.	5.8	65
24	Population genetics and evolutionary history of <i>Miscanthus</i> species in China. <i>Journal of Systematics and Evolution</i> , 2019, 57, 530-542.	1.6	12
25	Genome Sequences Provide Insights into the Reticulate Origin and Unique Traits of Woody Bamboos. <i>Molecular Plant</i> , 2019, 12, 1353-1365.	3.9	116
26	<i>Ef-cd</i> locus shortens rice maturity duration without yield penalty. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 18717-18722.	3.3	77
27	The PLATZ Transcription Factor GL6 Affects Grain Length and Number in Rice. <i>Plant Physiology</i> , 2019, 180, 2077-2090.	2.3	127
28	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
29	A noncanonical vacuolar sugar transferase required for biosynthesis of antimicrobial defense compounds in oat. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 27105-27114.	3.3	27
30	Draft genome sequence of <i>Camellia sinensis</i> var. <i>sinensis</i> provides insights into the evolution of the tea genome and tea quality. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E4151-E4158.	3.3	730
31	Rice Functional Genomics Research: Past Decade and Future. <i>Molecular Plant</i> , 2018, 11, 359-380.	3.9	113
32	A defensin-like protein drives cadmium efflux and allocation in rice. <i>Nature Communications</i> , 2018, 9, 645.	5.8	263
33	Genome-Wide Association Mapping of Complex Traits in Rice. , 2018, , 497-510.		3
34	Sequence divergence between spelt and common wheat. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1125-1132.	1.8	7
35	Genomes of 13 domesticated and wild rice relatives highlight genetic conservation, turnover and innovation across the genus <i>Oryza</i> . <i>Nature Genetics</i> , 2018, 50, 285-296.	9.4	413
36	Shortened Basal Internodes Encodes a Gibberellin 2-Oxidase and Contributes to Lodging Resistance in Rice. <i>Molecular Plant</i> , 2018, 11, 288-299.	3.9	85

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37	Pan-genome analysis highlights the extent of genomic variation in cultivated and wild rice. <i>Nature Genetics</i> , 2018, 50, 278-284.	9.4	453
38	FAIR: A Call to Make Published Data More Findable, Accessible, Interoperable, and Reusable. <i>Molecular Plant</i> , 2018, 11, 1105-1108.	3.9	31
39	Genomic insights into divergence and dual domestication of cultivated allotetraploid cottons. <i>Genome Biology</i> , 2017, 18, 33.	3.8	128
40	A natural tandem array alleviates epigenetic repression of IPA1 and leads to superior yielding rice. <i>Nature Communications</i> , 2017, 8, 14789.	5.8	149
41	Dissecting the Genetic Basis of Grain Shape and Chalkiness Traits in Hybrid Rice Using Multiple Collaborative Populations. <i>Molecular Plant</i> , 2017, 10, 1353-1356.	3.9	38
42	Gene duplication confers enhanced expression of 27-kDa $\beta$ -zein for endosperm modification in quality protein maize. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 4964-4969.	3.3	67
43	Genomic architecture of heterosis for yield traits in rice. <i>Nature</i> , 2016, 537, 629-633.	13.7	336
44	Genomics: Decoding the ancestors of peanut. <i>Nature Plants</i> , 2016, 2, 16042.	4.7	3
45	How can rice genetics benefit from rice-domestication study?. <i>National Science Review</i> , 2016, 3, 278-280.	4.6	6
46	Rice domestication occurred through single origin and multiple introgressions. <i>Nature Plants</i> , 2016, 2, 15207.	4.7	40
47	OryzaGenome: Genome Diversity Database of Wild <i>Oryza</i> Species. <i>Plant and Cell Physiology</i> , 2016, 57, e1-e1.	1.5	34
48	OsSPL13 controls grain size in cultivated rice. <i>Nature Genetics</i> , 2016, 48, 447-456.	9.4	662
49	Fine mapping of a large-effect QTL conferring Fusarium crown rot resistance on the long arm of chromosome 3B in hexaploid wheat. <i>BMC Genomics</i> , 2015, 16, 850.	1.2	40
50	Comparative Population Genomics Reveals Strong Divergence and Infrequent Introgression between Asian and African Rice. <i>Molecular Plant</i> , 2015, 8, 958-960.	3.9	18
51	Genomic analysis of hybrid rice varieties reveals numerous superior alleles that contribute to heterosis. <i>Nature Communications</i> , 2015, 6, 6258.	5.8	292
52	Rapid turnover of antimicrobial-type cysteine-rich protein genes in closely related <i>Oryza</i> genomes. <i>Molecular Genetics and Genomics</i> , 2015, 290, 1753-1770.	1.0	6
53	The draft genome of the grass carp ( <i>Ctenopharyngodon idellus</i> ) provides insights into its evolution and vegetarian adaptation. <i>Nature Genetics</i> , 2015, 47, 625-631.	9.4	352
54	Natural alleles of a proteasome $\beta$ 2 subunit gene contribute to thermotolerance and adaptation of African rice. <i>Nature Genetics</i> , 2015, 47, 827-833.	9.4	265

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55	An-2 Encodes a Cytokinin Synthesis Enzyme that Regulates Awn Length and Grain Production in Rice. <i>Molecular Plant</i> , 2015, 8, 1635-1650.	3.9	116
56	Genetic discovery for oil production and quality in sesame. <i>Nature Communications</i> , 2015, 6, 8609.	5.8	183
57	RiTE database: a resource database for genus-wide rice genomics and evolutionary biology. <i>BMC Genomics</i> , 2015, 16, 538.	1.2	86
58	Transcriptome-wide investigation of circular RNAs in rice. <i>Rna</i> , 2015, 21, 2076-2087.	1.6	362
59	Natural Variations and Genome-Wide Association Studies in Crop Plants. <i>Annual Review of Plant Biology</i> , 2014, 65, 531-551.	8.6	567
60	A two-locus interaction causes interspecific hybrid weakness in rice. <i>Nature Communications</i> , 2014, 5, 3357.	5.8	88
61	Transcriptome and Allele Specificity Associated with a 3BL Locus for Fusarium Crown Rot Resistance in Bread Wheat. <i>PLoS ONE</i> , 2014, 9, e113309.	1.1	42
62	Sequencing-based genome-wide association study in rice. <i>Current Opinion in Plant Biology</i> , 2013, 16, 133-138.	3.5	107
63	The rice OsLTP6 gene promoter directs anther-specific expression by a combination of positive and negative regulatory elements. <i>Planta</i> , 2013, 238, 845-857.	1.6	24
64	Resequencing rice genomes: an emerging new era of rice genomics. <i>Trends in Genetics</i> , 2013, 29, 225-232.	2.9	108
65	Identification of QTLs associated with tissue culture response through sequencing-based genotyping of RILs derived from 93-11 A— Nipponbare in rice ( <i>Oryza sativa</i> ). <i>Plant Cell Reports</i> , 2013, 32, 103-116.	2.8	24
66	The draft genome of the fast-growing non-timber forest species moso bamboo ( <i>Phyllostachys</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 302	9.4	483
67	A haplotype map of genomic variations and genome-wide association studies of agronomic traits in foxtail millet ( <i>Setaria italica</i> ). <i>Nature Genetics</i> , 2013, 45, 957-961.	9.4	411
68	An-1 Encodes a Basic Helix-Loop-Helix Protein That Regulates Awn Development, Grain Size, and Grain Number in Rice. <i>Plant Cell</i> , 2013, 25, 3360-3376.	3.1	226
69	Natural Variation and Sequencing-Based Genetics Studies. , 2013, , 27-34.		0
70	Genetic Control of Seed Shattering in Rice by the APETALA2 Transcription Factor SHATTERING ABORTION1. <i>Plant Cell</i> , 2012, 24, 1034-1048.	3.1	217
71	Identification of QTLs for eight agronomically important traits using an ultra-high-density map based on SNPs generated from high-throughput sequencing in sorghum under contrasting photoperiods. <i>Journal of Experimental Botany</i> , 2012, 63, 5451-5462.	2.4	156
72	Variability and adaptability of <i>Miscanthus</i> species evaluated for energy crop domestication. <i>GCB Bioenergy</i> , 2012, 4, 49-60.	2.5	107

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73	A map of rice genome variation reveals the origin of cultivated rice. <i>Nature</i> , 2012, 490, 497-501.	13.7	1,428
74	A Pyramid Breeding of Eight Grain-yield Related Quantitative Trait Loci Based on Marker-assistant and Phenotype Selection in Rice ( <i>Oryza sativa</i> L.). <i>Journal of Genetics and Genomics</i> , 2012, 39, 335-350.	1.7	35
75	Genome-wide association study of flowering time and grain yield traits in a worldwide collection of rice germplasm. <i>Nature Genetics</i> , 2012, 44, 32-39.	9.4	1,030
76	A WUSCHEL-like homeobox gene, OsWOX3B responses to NUDA/GL-1 locus in rice. <i>Rice</i> , 2012, 5, 30.	1.7	40
77	Development and high-throughput genotyping of substitution lines carrying the chromosome segments of indica 9311 in the background of japonica Nipponbare. <i>Journal of Genetics and Genomics</i> , 2011, 38, 603-611.	1.7	42
78	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
79	Genetic Control of a Transition from Black to Straw-White Seed Hull in Rice Domestication. <i>Plant Physiology</i> , 2011, 155, 1301-1311.	2.3	155
80	Genomic structure and evolution of the Pi2/9 locus in wild rice species. <i>Theoretical and Applied Genetics</i> , 2010, 121, 295-309.	1.8	25
81	SEG-Map: A Novel Software for Genotype Calling and Genetic Map Construction from Next-generation Sequencing. <i>Rice</i> , 2010, 3, 98-102.	1.7	40
82	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
83	Genome-wide characterization of the biggest grass, bamboo, based on 10,608 putative full-length cDNA sequences. <i>BMC Plant Biology</i> , 2010, 10, 116.	1.6	81
84	Genome-wide association studies of 14 agronomic traits in rice landraces. <i>Nature Genetics</i> , 2010, 42, 961-967.	9.4	1,978
85	Parent-independent genotyping for constructing an ultrahigh-density linkage map based on population sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 10578-10583.	3.3	299
86	High throughput DNA sequencing: The new sequencing revolution. <i>Plant Science</i> , 2010, 179, 407-422.	1.7	76
87	Function annotation of the rice transcriptome at single-nucleotide resolution by RNA-seq. <i>Genome Research</i> , 2010, 20, 1238-1249.	2.4	307
88	Identification and characterization of <i>Bph14</i> , a gene conferring resistance to brown planthopper in rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 22163-22168.	3.3	437
89	High-throughput genotyping by whole-genome resequencing. <i>Genome Research</i> , 2009, 19, 1068-1076.	2.4	812
90	Identification of OsbZIP72 as a positive regulator of ABA response and drought tolerance in rice. <i>Planta</i> , 2009, 229, 605-615.	1.6	319

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91	Dwarf 88, a novel putative esterase gene affecting architecture of rice plant. <i>Plant Molecular Biology</i> , 2009, 71, 265-276.	2.0	143
92	Identification of a novel tillering dwarf mutant and fine mapping of the TDDL(T) gene in rice ( <i>Oryza</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	4.3	5
93	Overexpression of a NAC transcription factor enhances rice drought and salt tolerance. <i>Biochemical and Biophysical Research Communications</i> , 2009, 379, 985-989.	1.0	425
94	Evolutionary and expression study of the aldehyde dehydrogenase (ALDH) gene superfamily in rice ( <i>Oryza sativa</i> ). <i>Gene</i> , 2009, 431, 86-94.	1.0	69
95	Evolutionary conservation of neighbouring gene pairs in plants. <i>Gene</i> , 2009, 437, 71-79.	1.0	16
96	Genome-wide survey and expression profiling of heat shock proteins and heat shock factors revealed overlapped and stress specific response under abiotic stresses in rice. <i>Plant Science</i> , 2009, 176, 583-590.	1.7	290
97	Analysis of collinear regions of <i>Oryza</i> AA and CC genomes. <i>Journal of Genetics and Genomics</i> , 2009, 36, 667-677.	1.7	6
98	RICD: A rice indicacDNA database resource for rice functional genomics. <i>BMC Plant Biology</i> , 2008, 8, 118.	1.6	24
99	Rice 2020: A Call For An International Coordinated Effort In Rice Functional Genomics. <i>Molecular Plant</i> , 2008, 1, 715-719.	3.9	104
100	Collection and Comparative Analysis of 1888 Full-length cDNAs from Wild Rice <i>Oryza rufipogon</i> Griff. W1943. <i>DNA Research</i> , 2008, 15, 285-295.	1.5	34
101	Independent Losses of Function in a Polyphenol Oxidase in Rice: Differentiation in Grain Discoloration between Subspecies and the Role of Positive Selection under Domestication. <i>Plant Cell</i> , 2008, 20, 2946-2959.	3.1	80
102	Rice Genome Research: Current Status and Future Perspectives. <i>Plant Genome</i> , 2008, 1, .	1.6	7
103	Genome-Wide Analysis of Transposon Insertion Polymorphisms Reveals Intraspecific Variation in Cultivated Rice $\hat{A}$ . <i>Plant Physiology</i> , 2008, 148, 25-40.	2.3	88
104	The Rice Annotation Project Database (RAP-DB): 2008 update. <i>Nucleic Acids Research</i> , 2007, 36, D1028-D1033.	6.5	295
105	Curated genome annotation of <i>Oryza sativa</i> ssp. japonica and comparative genome analysis with <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , 2007, 17, 175-183.	2.4	218
106	Rice functional genomics research in China. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2007, 362, 1009-1021.	1.8	28
107	Genome-wide analysis of the auxin response factors (ARF) gene family in rice ( <i>Oryza sativa</i> ). <i>Gene</i> , 2007, 394, 13-24.	1.0	371
108	Rice Genome Sequence: The Foundation for Understanding the Genetic Systems. , 2007, , 5-20.		3

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109	Non-random distribution of T-DNA insertions at various levels of the genome hierarchy as revealed by analyzing 13,804 T-DNA flanking sequences from an enhancer-trap mutant library. <i>Plant Journal</i> , 2007, 49, 947-959.	2.8	107
110	A collection of 10,096 indica rice full-length cDNAs reveals highly expressed sequence divergence between <i>Oryza sativa indica</i> and <i>japonica</i> subspecies. <i>Plant Molecular Biology</i> , 2007, 65, 403-415.	2.0	55
111	Differentiation of a Miniature Inverted Transposable Element (MITE) System in Asian Rice Cultivars and Its Inference for a Diphyletic Origin of Two Subspecies of Asian Cultivated Rice. <i>Journal of Integrative Plant Biology</i> , 2006, 48, 260-267.	4.1	10
112	QTLs and candidate genes for chlorate resistance in rice ( <i>Oryzasativa</i> L.). <i>Euphytica</i> , 2006, 152, 141-148.	0.6	14
113	GS3, a major QTL for grain length and weight and minor QTL for grain width and thickness in rice, encodes a putative transmembrane protein. <i>Theoretical and Applied Genetics</i> , 2006, 112, 1164-1171.	1.8	1,252
114	Sequence analysis of mRNA polyadenylation signals of rice genes. <i>Science Bulletin</i> , 2006, 51, 1069-1077.	1.7	12
115	The Broad-Spectrum Blast Resistance Gene Pi9 Encodes a Nucleotide-Binding Site-“Leucine-Rich Repeat Protein and Is a Member of a Multigene Family in Rice. <i>Genetics</i> , 2006, 172, 1901-1914.	1.2	479
116	Isolation and annotation of 10828 putative full length cDNAs from indica rice. <i>Science in China Series C: Life Sciences</i> , 2005, 48, 445.	1.3	17
117	Features of the expressed sequences revealed by a large-scale analysis of ESTs from a normalized cDNA library of the elite indica rice cultivar Minghui 63. <i>Plant Journal</i> , 2005, 42, 772-780.	2.8	39
118	The <i>Oryza</i> Map Alignment Project: The Golden Path to Unlocking the Genetic Potential of Wild Rice Species. <i>Plant Molecular Biology</i> , 2005, 59, 53-62.	2.0	143
119	Microarray Analysis Reveals Similarities and Variations in Genetic Programs Controlling Pollination/Fertilization and Stress Responses in Rice ( <i>Oryza sativa</i> L.). <i>Plant Molecular Biology</i> , 2005, 59, 151-164.	2.0	61
120	A Pilot Study of Transcription Unit Analysis in Rice Using Oligonucleotide Tiling-path Microarray. <i>Plant Molecular Biology</i> , 2005, 59, 137-149.	2.0	17
121	A Tiling Microarray Expression Analysis of Rice Chromosome 4 Suggests a Chromosome-Level Regulation of Transcription. <i>Plant Cell</i> , 2005, 17, 1641-1657.	3.1	56
122	Dampable Waves along Nucleic Acid Sequences Mediating Nucleotides' Interactions. <i>DNA Sequence</i> , 2004, 15, 135-139.	0.7	0
123	Structural features of the rice chromosome 4 centromere. <i>Nucleic Acids Research</i> , 2004, 32, 2023-2030.	6.5	95
124	Isolation of a single rice chromosome by optical micromanipulation. <i>Journal of Optics</i> , 2004, 6, 89-93.	1.5	8
125	Monitoring of Gene Expression Profiles and Isolation of Candidate Genes Involved in Pollination and Fertilization in Rice ( <i>Oryza Sativa</i> L.) with a 10K cDNA Microarray. <i>Plant Molecular Biology</i> , 2004, 54, 471-487.	2.0	66
126	Sequence variations of simple sequence repeats on chromosome-4 in two subspecies of the Asian cultivated rice. <i>Theoretical and Applied Genetics</i> , 2004, 108, 392-400.	1.8	22



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127	Transcript abundance of <i>rml1</i> , encoding a putative GT1-like factor in rice, is up-regulated by <i>Magnaporthe grisea</i> and down-regulated by light. <i>Gene</i> , 2004, 324, 105-115.	1.0	34
128	Preparation of single rice chromosome for construction of a DNA library using a laser microbeam trap. <i>Journal of Biotechnology</i> , 2004, 109, 217-226.	1.9	28
129	Structural and transcriptional analysis of <i>S</i> -locus F-box genes in <i>Antirrhinum</i> . <i>Sexual Plant Reproduction</i> , 2003, 16, 165-177.	2.2	70
130	Genome-wide intraspecific DNA-sequence variations in rice. <i>Current Opinion in Plant Biology</i> , 2003, 6, 134-138.	3.5	99
131	Control of tillering in rice. <i>Nature</i> , 2003, 422, 618-621.	13.7	988
132	BRITTLE CULM1, Which Encodes a COBRA-Like Protein, Affects the Mechanical Properties of Rice Plants. <i>Plant Cell</i> , 2003, 15, 2020-2031.	3.1	369
133	A Fine Physical Map of the Rice Chromosome 4. <i>Genome Research</i> , 2002, 12, 817-823.	2.4	64
134	Sequence and analysis of rice chromosome 4. <i>Nature</i> , 2002, 420, 316-320.	13.7	471
135	Dentinogenesis imperfecta 1 with or without progressive hearing loss is associated with distinct mutations in <i>DSPP</i> . <i>Nature Genetics</i> , 2001, 27, 201-204.	9.4	302
136	Cutting the Gordian knot of plant genetics: retrieval of missing heritability in tomato. <i>Science China Life Sciences</i> , 0, , .	2.3	0