

Yuqing He

List of Publications by Year in descending order

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58
papers

3,748
citations

218677

26
h-index

149698

56
g-index

64
all docs

64
docs citations

64
times ranked

3492
citing authors

#	ARTICLE	IF	CITATIONS
1	Natural variation in GS5 plays an important role in regulating grain size and yield in rice. <i>Nature Genetics</i> , 2011, 43, 1266-1269.	21.4	821
2	Field performance of transgenic elite commercial hybrid rice expressing <i>Bacillus thuringiensis</i> δ -endotoxin. <i>Nature Biotechnology</i> , 2000, 18, 1101-1104.	17.5	412
3	Chalk5 encodes a vacuolar H ⁺ -translocating pyrophosphatase influencing grain chalkiness in rice. <i>Nature Genetics</i> , 2014, 46, 398-404.	21.4	281
4	A High-Density SNP Genotyping Array for Rice Biology and Molecular Breeding. <i>Molecular Plant</i> , 2014, 7, 541-553.	8.3	251
5	OsAAP6 functions as an important regulator of grain protein content and nutritional quality in rice. <i>Nature Communications</i> , 2014, 5, 4847.	12.8	214
6	Breeding signatures of rice improvement revealed by a genomic variation map from a large germplasm collection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E5411-9.	7.1	165
7	GL3.3, a Novel QTL Encoding a GSK3/SHAGGY-like Kinase, Epistatically Interacts with GS3 to Produce Extra-long Grains in Rice. <i>Molecular Plant</i> , 2018, 11, 754-756.	8.3	113
8	Recent progress on the genetics and molecular breeding of brown planthopper resistance in rice. <i>Rice</i> , 2016, 9, 30.	4.0	105
9	BAC and RNA sequencing reveal the brown planthopper resistance gene BPH15 in a recombination cold spot that mediates a unique defense mechanism. <i>BMC Genomics</i> , 2014, 15, 674.	2.8	86
10	Rice grain quality—traditional traits for high quality rice and health-plus substances. <i>Molecular Breeding</i> , 2020, 40, 1.	2.1	78
11	Pyramiding and evaluation of the brown planthopper resistance genes Bph14 and Bph15 in hybrid rice. <i>Molecular Breeding</i> , 2012, 29, 61-69.	2.1	70
12	Natural variation and artificial selection in four genes determine grain shape in rice. <i>New Phytologist</i> , 2013, 200, 1269-1280.	7.3	70
13	The QTL controlling amino acid content in grains of rice (<i>Oryza sativa</i>) are co-localized with the regions involved in the amino acid metabolism pathway. <i>Molecular Breeding</i> , 2007, 21, 127-137.	2.1	69
14	Genome-wide Association Analyses Reveal the Genetic Basis of Stigma Exsertion in Rice. <i>Molecular Plant</i> , 2017, 10, 634-644.	8.3	66
15	Improving blast resistance of Jin 23B and its hybrid rice by marker-assisted gene pyramiding. <i>Molecular Breeding</i> , 2012, 30, 1679-1688.	2.1	65
16	Pyramiding and evaluation of three dominant brown planthopper resistance genes in the elite <i>indica</i> rice 9311 and its hybrids. <i>Pest Management Science</i> , 2013, 69, 802-808.	3.4	61
17	Identification and analysis of brown planthopper-responsive microRNAs in resistant and susceptible rice plants. <i>Scientific Reports</i> , 2017, 7, 8712.	3.3	58
18	Genetic Basis of Variation in Rice Seed Storage Protein (Albumin, Globulin, Prolamin, and Glutelin) Content Revealed by Genome-Wide Association Analysis. <i>Frontiers in Plant Science</i> , 2018, 9, 612.	3.6	53

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19	Comparative mapping of chalkiness components in rice using five populations across two environments. <i>BMC Genetics</i> , 2014, 15, 49.	2.7	51
20	How rice organs are colored: The genetic basis of anthocyanin biosynthesis in rice. <i>Crop Journal</i> , 2021, 9, 598-608.	5.2	44
21	The origin of <i>Wx^{la}</i> provides new insights into the improvement of grain quality in rice. <i>Journal of Integrative Plant Biology</i> , 2021, 63, 878-888.	8.5	43
22	Natural variation in <i>WHITE-CORE RATE 1</i> regulates redox homeostasis in rice endosperm to affect grain quality. <i>Plant Cell</i> , 2022, 34, 1912-1932.	6.6	41
23	Fine mapping and pyramiding of brown planthopper resistance genes <i>QBph3</i> and <i>QBph4</i> in an introgression line from wild rice <i>O. officinalis</i> . <i>Molecular Breeding</i> , 2015, 35, 1.	2.1	38
24	Development and evaluation of improved lines with broad-spectrum resistance to rice blast using nine resistance genes. <i>Rice</i> , 2019, 12, 29.	4.0	34
25	Genetic Architecture of Natural Variation in Rice Nonphotochemical Quenching Capacity Revealed by Genome-Wide Association Study. <i>Frontiers in Plant Science</i> , 2017, 8, 1773.	3.6	33
26	Analysis of quantitative trait loci affecting chlorophyll content of rice leaves in a double haploid population and two backcross populations. <i>Gene</i> , 2014, 536, 287-295.	2.2	30
27	Genetic mapping and validation of quantitative trait loci for stigma exertion rate in rice. <i>Molecular Breeding</i> , 2014, 34, 2131-2138.	2.1	28
28	Evaluation and breeding application of six brown planthopper resistance genes in rice maintainer line Jin 23B. <i>Rice</i> , 2018, 11, 22.	4.0	28
29	Genome-wide association analyses reveal the genetic basis of combining ability in rice. <i>Plant Biotechnology Journal</i> , 2019, 17, 2211-2222.	8.3	26
30	Analysis of minor quantitative trait loci for eating and cooking quality traits in rice using a recombinant inbred line population derived from two indica cultivars with similar amylose content. <i>Molecular Breeding</i> , 2014, 34, 2151-2163.	2.1	22
31	Identification of quantitative trait loci for grain size and the contributions of major grain-size QTLs to grain weight in rice. <i>Molecular Breeding</i> , 2013, 31, 451-461.	2.1	20
32	QTLs identification of crude fat content in brown rice and its genetic basis analysis using DH and two backcross populations. <i>Euphytica</i> , 2009, 169, 197-205.	1.2	18
33	Genetic architecture and key genes controlling the diversity of oil composition in rice grains. <i>Molecular Plant</i> , 2021, 14, 456-469.	8.3	18
34	Genetic mapping and confirmation of quantitative trait loci for grain chalkiness in rice. <i>Molecular Breeding</i> , 2016, 36, 1.	2.1	17
35	Genetic loci simultaneously controlling lignin monomers and biomass digestibility of rice straw. <i>Scientific Reports</i> , 2018, 8, 3636.	3.3	17
36	Identification of a Novel Semi-Dominant Spotted-Leaf Mutant with Enhanced Resistance to <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> in Rice. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3766.	4.1	17

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37	QTL analysis on rice grain appearance quality, as exemplifying the typical events of transgenic or backcrossing breeding. <i>Breeding Science</i> , 2014, 64, 231-239.	1.9	16
38	Gene diagnosis and targeted breeding for blast-resistant Kongyu 131 without changing regional adaptability. <i>Journal of Genetics and Genomics</i> , 2018, 45, 539-547.	3.9	16
39	Dissecting combining ability effect in a rice NCII-III population provides insights into heterosis in indica-japonica cross. <i>Rice</i> , 2017, 10, 39.	4.0	15
40	Identification of Blast Resistance QTLs Based on Two Advanced Backcross Populations in Rice. <i>Rice</i> , 2020, 13, 31.	4.0	14
41	Genetic dissection of large grain shape in rice cultivar "Nanyangzhan"™ and validation of a grain thickness QTL (qGT3.1) and a grain length QTL (qGL3.4). <i>Molecular Breeding</i> , 2017, 37, 1.	2.1	13
42	The coordination of OsbZIP72 and OsMYBS2 with reverse roles regulates the transcription of <i>OsPsbS1</i> in rice. <i>New Phytologist</i> , 2021, 229, 370-387.	7.3	12
43	Mapping and verification of grain shape QTLs based on high-throughput SNP markers in rice. <i>Molecular Breeding</i> , 2019, 39, 1.	2.1	10
44	Rice appearance quality. , 2019, , 371-383.		10
45	Genome-Wide Association Studies Reveal the Genetic Basis of Fertility Restoration of CMS-WA and CMS-HL in xian/indica and aus Accessions of Rice (<i>Oryza sativa</i> L.). <i>Rice</i> , 2020, 13, 11.	4.0	10
46	FLOURY ENDOSPERM19 encoding a class I glutamine amidotransferase affects grain quality in rice. <i>Molecular Breeding</i> , 2021, 41, 1.	2.1	10
47	Mapping and verification of grain shape QTLs based on an advanced backcross population in rice. <i>PLoS ONE</i> , 2017, 12, e0187553.	2.5	9
48	Integrated NIRS and QTL assays reveal minor mannose and galactose as contrast lignocellulose factors for biomass enzymatic saccharification in rice. <i>Biotechnology for Biofuels</i> , 2021, 14, 144.	6.2	8
49	Mapping of minor quantitative trait loci (QTLs) conferring fertility restoration of wild abortive cytoplasmic male sterility and QTLs conferring stigma exertion in rice. <i>Plant Breeding</i> , 2014, 133, 722-727.	1.9	7
50	Genome-wide association study of flowering time reveals complex genetic heterogeneity and epistatic interactions in rice. <i>Gene</i> , 2021, 770, 145353.	2.2	6
51	qFC6, a major gene for crude fat content and quality in rice. <i>Theoretical and Applied Genetics</i> , 2022, 135, 2675-2685.	3.6	5
52	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.	2.1	3
53	Ghd7 is a negative regulator of zinc concentration in brown rice. <i>Molecular Breeding</i> , 2020, 40, 1.	2.1	3
54	Fine mapping of qWCR7, a grain chalkiness QTL in rice. <i>Molecular Breeding</i> , 2021, 41, 1.	2.1	3

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55	Genomics-Based Breeding Technology. , 2013, , 329-348.		3
56	Fine Mapping of qWCR4, a Rice Chalkiness QTL Affecting Yield and Quality. Agronomy, 2022, 12, 706.	3.0	3
57	Mapping and evaluating quantitative trait loci for blast resistance under natural infection conditions using an advanced backcross population in rice. Euphytica, 2015, 204, 121-133.	1.2	2
58	Genetic dissection of vitamin E content in rice (<i>Oryza sativa</i>) grains using recombinant inbred lines derived from a cross between 'Zhenshan97B' and 'Nanyangzhan'. Plant Breeding, 2019, 138, 820-829.	1.9	2