

Guanjun Gao

List of Publications by Year in descending order

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Version: 2024-02-01

22
papers

820
citations

623734

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22
all docs

22
docs citations

22
times ranked

952
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	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
3	Genome-wide Association Analyses Reveal the Genetic Basis of Stigma Exsertion in Rice. <i>Molecular Plant</i> , 2017, 10, 634-644.	8.3	66
4	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
5	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
6	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
7	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
8	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
9	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
10	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
11	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
12	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
13	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
14	Genetic mapping and confirmation of quantitative trait loci for grain chalkiness in rice. <i>Molecular Breeding</i> , 2016, 36, 1.	2.1	17
15	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
16	Identification of Blast Resistance QTLs Based on Two Advanced Backcross Populations in Rice. <i>Rice</i> , 2020, 13, 31.	4.0	14
17	FLOURY ENDOSPERM19 encoding a class I glutamine amidotransferase affects grain quality in rice. <i>Molecular Breeding</i> , 2021, 41, 1.	2.1	10
18	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

#	ARTICLE	IF	CITATIONS
19	Development and evaluation of improved lines based on an elite rice variety 9311 for overcoming hybrid sterility in rice. <i>Molecular Breeding</i> , 2020, 40, 1.	2.1	3
20	Fine mapping of qWCR7, a grain chalkiness QTL in rice. <i>Molecular Breeding</i> , 2021, 41, 1.	2.1	3
21	Fine Mapping of qWCR4, a Rice Chalkiness QTL Affecting Yield and Quality. <i>Agronomy</i> , 2022, 12, 706.	3.0	3
22	Mapping and evaluating quantitative trait loci for blast resistance under natural infection conditions using an advanced backcross population in rice. <i>Euphytica</i> , 2015, 204, 121-133.	1.2	2