

Shaokui Wang

List of Publications by Year in descending order

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Version: 2024-02-01

32
papers

2,156
citations

516561

16
h-index

434063

31
g-index

35
all docs

35
docs citations

35
times ranked

2007
citing authors

#	ARTICLE	IF	CITATIONS
1	Natural variations in grain length 10 (GL10) regulate rice grain size. <i>Journal of Genetics and Genomics</i> , 2022, 49, 405-413.	1.7	27
2	Dynamic analysis of QTLs on plant height with single segment substitution lines in rice. <i>Scientific Reports</i> , 2022, 12, 5465.	1.6	5
3	Methylesterification of cell-wall pectin controls the diurnal flower-opening times in rice. <i>Molecular Plant</i> , 2022, 15, 956-972.	3.9	22
4	Development of Wide-Compatible Indica Lines by Pyramiding Multiple Neutral Alleles of Indicaâ€“Japonica Hybrid Sterility Loci. <i>Frontiers in Plant Science</i> , 2022, 13, 890568.	1.7	4
5	Dissection of closely linked QTLs controlling stigma exertion rate in rice by substitution mapping. <i>Theoretical and Applied Genetics</i> , 2021, 134, 1253-1262.	1.8	16
6	Mapping QTLs controlling low-temperature germinability in rice by using single segment substitution lines derived from 4 AA-genome species of wild rice. <i>Euphytica</i> , 2021, 217, 1.	0.6	2
7	Fine mapping of two grain chalkiness QTLs sensitive to high temperature in rice. <i>Rice</i> , 2021, 14, 33.	1.7	30
8	GW10, a member of P450 subfamily regulates grain size and grain number in rice. <i>Theoretical and Applied Genetics</i> , 2021, 134, 3941-3950.	1.8	20
9	Functional mapping of tillering QTLs using the Wangâ€“Lanâ€“Ding model and a SSSL population. <i>Molecular Genetics and Genomics</i> , 2021, 296, 1279-1286.	1.0	2
10	Natural allelic variation in a modulator of auxin homeostasis improves grain yield and nitrogen use efficiency in rice. <i>Plant Cell</i> , 2021, 33, 566-580.	3.1	53
11	Substitution Mapping of Two Closely Linked QTLs on Chromosome 8 Controlling Grain Chalkiness in Rice. <i>Rice</i> , 2021, 14, 85.	1.7	17
12	The Wild Rice Locus CTS-12 Mediates ABA-Dependent Stomatal Opening Modulation to Limit Water Loss Under Severe Chilling Stress. <i>Frontiers in Plant Science</i> , 2020, 11, 575699.	1.7	7
13	Weighted gene coexpression network analysis-based identification of key modules and hub genes associated with drought sensitivity in rice. <i>BMC Plant Biology</i> , 2020, 20, 478.	1.6	18
14	The Molecular Regulatory Pathways and Metabolic Adaptation in the Seed Germination and Early Seedling Growth of Rice in Response to Low O ₂ Stress. <i>Plants</i> , 2020, 9, 1363.	1.6	21
15	Unconditional and conditional analysis of epistasis between tillering QTLs based on single segment substitution lines in rice. <i>Scientific Reports</i> , 2020, 10, 15912.	1.6	8
16	Substitution Mapping of the Major Quantitative Trait Loci Controlling Stigma Exsertion Rate from <i>Oryza glumaepatula</i> . <i>Rice</i> , 2020, 13, 37.	1.7	24
17	Chloroplastsâ€” Beyond Energy Capture and Carbon Fixation: Tuning of Photosynthesis in Response to Chilling Stress. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5046.	1.8	52
18	Breeding by design of CMS lines on the platform of SSSL library in rice. <i>Molecular Breeding</i> , 2019, 39, 1.	1.0	15

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19	Analysis of Epistasis among QTLs on Heading Date based on Single Segment Substitution Lines in Rice. Scientific Reports, 2018, 8, 3059.	1.6	20
20	<scp>QTL</scp> epistatic analysis for yield components with singleâ€segment substitution lines in rice. Plant Breeding, 2018, 137, 346-354.	1.0	16
21	Analysis of QTLs on heading date based on single segment substitution lines in rice (<i>Oryza Sativa</i> L.). Scientific Reports, 2018, 8, 13232.	1.6	18
22	Genome-wide transcriptome profiling provides insights into panicle development of rice (<i>Oryza sativa</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.6	13
23	Substitution mapping of QTLs controlling seed dormancy using single segment substitution lines derived from multiple cultivated rice donors in seven cropping seasons. Theoretical and Applied Genetics, 2017, 130, 1191-1205.	1.8	31
24	Development and trait evaluation of chromosome single-segment substitution lines of <i>O. meridionalis</i> in the background of <i>O. sativa</i> . Euphytica, 2017, 213, 1.	0.6	25
25	Development of a platform for breeding by design of CMS restorer lines based on an SSSL library in rice (<i>Oryza sativa</i> L.). Breeding Science, 2016, 66, 768-775.	0.9	24
26	Overcoming inter-subspecific hybrid sterility in rice by developing indica-compatible japonica lines. Scientific Reports, 2016, 6, 26878.	1.6	47
27	Detection and characterization of epistasis between QTLs on plant height in rice using single segment substitution lines. Breeding Science, 2015, 65, 192-200.	0.9	19
28	The OsSPL16-GW7 regulatory module determines grain shape and simultaneously improves rice yield and grain quality. Nature Genetics, 2015, 47, 949-954.	9.4	555
29	Development of a platform for breeding by design of CMS lines based on an SSSL library in rice (<i>Oryza</i>) Tj ETQq1 1 0,784314 rgBT /Over	0.6	19
30	Control of grain size, shape and quality by OsSPL16 in rice. Nature Genetics, 2012, 44, 950-954.	9.4	1,004
31	Reconstruction of the High Stigma Exsertion Rate Trait in Rice by Pyramiding Multiple QTLs. Frontiers in Plant Science, 0, 13, .	1.7	9
32	Fine Mapping of Two Major Quantitative Trait Loci for Rice Chalkiness With High Temperature-Enhanced Additive Effects. Frontiers in Plant Science, 0, 13, .	1.7	5