

Zi-chao Li

List of Publications by Year in descending order

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89
papers

5,407
citations

117625

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91884

69
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93
all docs

93
docs citations

93
times ranked

5433
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic variation in 3,010 diverse accessions of Asian cultivated rice. <i>Nature</i> , 2018, 557, 43-49.	27.8	1,091
2	Natural Variation in OsPRR37 Regulates Heading Date and Contributes to Rice Cultivation at a Wide Range of Latitudes. <i>Molecular Plant</i> , 2013, 6, 1877-1888.	8.3	298
3	Overexpression of OsMYB48-1, a Novel MYB-Related Transcription Factor, Enhances Drought and Salinity Tolerance in Rice. <i>PLoS ONE</i> , 2014, 9, e92913.	2.5	287
4	A core collection and mini core collection of <i>Oryza sativa</i> L. in China. <i>Theoretical and Applied Genetics</i> , 2011, 122, 49-61.	3.6	197
5	Natural variation in CTB4a enhances rice adaptation to cold habitats. <i>Nature Communications</i> , 2017, 8, 14788.	12.8	192
6	<i>OsASR5</i> enhances drought tolerance through a stomatal closure pathway associated with ABA and H ₂ O ₂ signalling in rice. <i>Plant Biotechnology Journal</i> , 2017, 15, 183-196.	8.3	174
7	Variation of a major facilitator superfamily gene contributes to differential cadmium accumulation between rice subspecies. <i>Nature Communications</i> , 2019, 10, 2562.	12.8	155
8	QTL mapping of root traits in a doubled haploid population from a cross between upland and lowland japonica rice in three environments. <i>Theoretical and Applied Genetics</i> , 2005, 110, 1244-1252.	3.6	148
9	OsMIOX, a myo-inositol oxygenase gene, improves drought tolerance through scavenging of reactive oxygen species in rice (<i>Oryza sativa</i> L.). <i>Plant Science</i> , 2012, 196, 143-151.	3.6	136
10	Natural Variation in <i>OsLG3</i> Increases Drought Tolerance in Rice by Inducing ROS Scavenging. <i>Plant Physiology</i> , 2018, 178, 451-467.	4.8	121
11	Mapping QTLs of root morphological traits at different growth stages in rice. <i>Genetica</i> , 2008, 133, 187-200.	1.1	117
12	The C ¹ A gene system regulates hull pigmentation and reveals evolution of anthocyanin biosynthesis pathway in rice. <i>Journal of Experimental Botany</i> , 2018, 69, 1485-1498.	4.8	114
13	Genetic Analysis of Cold Tolerance at the Germination and Booting Stages in Rice by Association Mapping. <i>PLoS ONE</i> , 2015, 10, e0120590.	2.5	109
14	Alternative splicing of <i>OsLG3b</i> controls grain length and yield in japonica rice. <i>Plant Biotechnology Journal</i> , 2018, 16, 1667-1678.	8.3	109
15	Root and shoot traits responses to phosphorus deficiency and QTL analysis at seedling stage using introgression lines of rice. <i>Journal of Genetics and Genomics</i> , 2009, 36, 173-183.	3.9	102
16	OsLG3 contributing to rice grain length and yield was mined by Ho-LAMap. <i>BMC Biology</i> , 2017, 15, 28.	3.8	100
17	Identification and mapping of quantitative trait loci for cold tolerance at the booting stage in a japonica rice near-isogenic line. <i>Plant Science</i> , 2008, 174, 340-347.	3.6	99
18	A super pan-genomic landscape of rice. <i>Cell Research</i> , 2022, 32, 878-896.	12.0	99

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19	Fine mapping a QTL qCTB7 for cold tolerance at the booting stage on rice chromosome 7 using a near-isogenic line. <i>Theoretical and Applied Genetics</i> , 2010, 121, 895-905.	3.6	79
20	OsERF71 confers drought tolerance via modulating ABA signaling and proline biosynthesis. <i>Plant Science</i> , 2018, 270, 131-139.	3.6	78
21	Genetic structure and differentiation of <i>Oryza sativa</i> L. in China revealed by microsatellites. <i>Theoretical and Applied Genetics</i> , 2009, 119, 1105-1117.	3.6	76
22	Comparison of gene expression between upland and lowland rice cultivars under water stress using cDNA microarray. <i>Theoretical and Applied Genetics</i> , 2007, 115, 1109-1126.	3.6	66
23	Genetic basis and identification of candidate genes for salt tolerance in rice by GWAS. <i>Scientific Reports</i> , 2020, 10, 9958.	3.3	64
24	Characterization of Transcription Factor Gene OsDRAP1 Conferring Drought Tolerance in Rice. <i>Frontiers in Plant Science</i> , 2018, 9, 94.	3.6	63
25	Gnp4/LAX2, a RAWUL protein, interferes with the OsIAA3-OsARF25 interaction to regulate grain length via the auxin signaling pathway in rice. <i>Journal of Experimental Botany</i> , 2018, 69, 4723-4737.	4.8	62
26	Loci and natural alleles underlying robust roots and adaptive domestication of upland ecotype rice in aerobic conditions. <i>PLoS Genetics</i> , 2018, 14, e1007521.	3.5	61
27	Genetic Architecture and Candidate Genes for Deep-Sowing Tolerance in Rice Revealed by Non-syn GWAS. <i>Frontiers in Plant Science</i> , 2018, 9, 332.	3.6	49
28	Natural variation in <i>early flowering1</i> contributes to early flowering in <i>japonica</i> rice under long days. <i>Plant, Cell and Environment</i> , 2014, 37, 101-112.	5.7	46
29	An improved 2b-RAD approach (I2b-RAD) offering genotyping tested by a rice (<i>Oryza sativa</i> L.) F2 population. <i>BMC Genomics</i> , 2014, 15, 956.	2.8	44
30	Evaluation of Genetic Diversity of Rice Landraces (<i>Oryza sativa</i> L.) in Yunnan, China. <i>Breeding Science</i> , 2007, 57, 91-99.	1.9	43
31	Genetic structure and phylogeography of rice landraces in Yunnan, China, revealed by SSR. <i>Genome</i> , 2007, 50, 72-83.	2.0	40
32	Genetic diversity of rice cultivars (<i>Oryza sativa</i> L.) in China and the temporal trends in recent fifty years. <i>Science Bulletin</i> , 2006, 51, 681-688.	1.7	39
33	Domestication and geographic origin of <i>Oryza sativa</i> in China: insights from multilocus analysis of nucleotide variation of <i>O. sativa</i> and <i>O. rufipogon</i> . <i>Molecular Ecology</i> , 2012, 21, 5073-5087.	3.9	39
34	QTL mapping and QTL-environment interaction analysis of multi-seed pod in cultivated peanut (<i>Arachis tj</i> BT /Ov	5.2	39
35	New alleles for chlorophyll content and stay-green traits revealed by a genome wide association study in rice (<i>Oryza sativa</i>). <i>Scientific Reports</i> , 2019, 9, 2541.	3.3	34
36	QTLs of cold tolerance-related traits at the booting stage for NIL-RILs in rice revealed by SSR. <i>Genes and Genomics</i> , 2009, 31, 143-154.	1.4	33

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37	Rice functional genomics and breeding database (RFGB)-3K-rice SNP and InDel sub-database. Chinese Science Bulletin, 2015, 60, 367-371.	0.7	31
38	Stepwise selection of natural variations at <i>CTB2</i> and <i>CTB4a</i> improves cold adaptation during domestication of <i>japonica</i> rice. New Phytologist, 2021, 231, 1056-1072.	7.3	30
39	Title is missing!. Genetic Resources and Crop Evolution, 2002, 49, 67-74.	1.6	29
40	Genetic control of panicle architecture in rice. Crop Journal, 2021, 9, 590-597.	5.2	29
41	Genomics-based plant germplasm research (GPGR). Crop Journal, 2017, 5, 166-174.	5.2	28
42	Fine mapping of QTL qCTB10-2 that confers cold tolerance at the booting stage in rice. Theoretical and Applied Genetics, 2018, 131, 157-166.	3.6	28
43	Genetic Basis Underlying Correlations Among Growth Duration and Yield Traits Revealed by GWAS in Rice (<i>Oryza sativa</i> L.). Frontiers in Plant Science, 2018, 9, 650.	3.6	28
44	Natural alleles of <i>GLA</i> for grain length and awn development were differently domesticated in rice subspecies <i>japonica</i> and <i>indica</i> . Plant Biotechnology Journal, 2019, 17, 1547-1559.	8.3	27
45	Genetic analysis of roots and shoots in rice seedling by association mapping. Genes and Genomics, 2019, 41, 95-105.	1.4	27
46	Differentiation, evolution and utilization of natural alleles for cold adaptability at the reproductive stage in rice. Plant Biotechnology Journal, 2020, 18, 2491-2503.	8.3	27
47	Fine mapping of the awn gene on chromosome 4 in rice by association and linkage analyses. Science Bulletin, 2011, 56, 835-839.	1.7	26
48	Analysis of Gene Expression Profile Induced by Water Stress in Upland Rice (<i>Oryza sativa</i> L. var.) Tj ETQq0 0 0 rgBT /Overlock 10 T Biology, 2007, 49, 1455-1463.	8.5	23
49	Genetic structure and diversity of <i>Oryza sativa</i> L. in Guizhou, China. Science Bulletin, 2007, 52, 343-351.	1.7	23
50	Quantitative Trait Loci for Mercury Tolerance in Rice Seedlings. Rice Science, 2013, 20, 238-242.	3.9	23
51	Simple Sequence Repeat Analysis of Genetic Diversity in Primary Core Collection of Peach (<i>Prunus</i>) Tj ETQq1 1 0,784314 rgBT /Overlock 10 T	8.5	22
52	GNP6, a novel allele of MOC1, regulates panicle and tiller development in rice. Crop Journal, 2021, 9, 57-67.	5.2	22
53	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.	3.9	21
54	Characterization and identification of cold tolerant near-isogenic lines in rice. Breeding Science, 2012, 62, 196-201.	1.9	21

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55	Rice SPL10 positively regulates trichome development through expression of <i>HL6</i> and auxin-related genes. <i>Journal of Integrative Plant Biology</i> , 2021, 63, 1521-1537.	8.5	21
56	QTL mapping of the root traits and their correlation analysis with drought resistance using DH lines from paddy and upland rice cross. <i>Science Bulletin</i> , 2003, 48, 2718-2724.	1.7	20
57	OsADR3 increases drought stress tolerance by inducing antioxidant defense mechanisms and regulating OsGPX1 in rice (<i>Oryza sativa</i> L.). <i>Crop Journal</i> , 2021, 9, 1003-1017.	5.2	19
58	<i>RGN1</i> controls grain number and shapes panicle architecture in rice. <i>Plant Biotechnology Journal</i> , 2022, 20, 158-167.	8.3	19
59	QTL Mapping and Q \times E Interactions of Grain Cooking and Nutrient Qualities in Rice Under Upland and Lowland Environments. <i>Journal of Genetics and Genomics</i> , 2007, 34, 420-428.	3.9	18
60	Localization of QTL for basal root thickness in japonica rice and effect of marker-assisted selection for a major QTL. <i>Euphytica</i> , 2008, 164, 729-737.	1.2	17
61	Fine Mapping and Cloning of the Grain Number Per-Panicle Gene (<i>Gnp4</i>) on Chromosome 4 in Rice (<i>Oryza sativa</i> L.). <i>Agricultural Sciences in China</i> , 2011, 10, 1825-1833.	0.6	17
62	Fine Mapping of qTGW3-1, a QTL for 1000-Grain Weight on Chromosome 3 in Rice. <i>Journal of Integrative Agriculture</i> , 2012, 11, 879-887.	3.5	15
63	Cold-adaptive evolution at the reproductive stage in <i>Geng</i> / <i>japonica</i> subspecies reveals the role of <i>OsMAPK3</i> and <i>OsLEA9</i> . <i>Plant Journal</i> , 2022, 111, 1032-1051.	5.7	13
64	QTL Mapping and Correlations Between Leaf Water Potential and Drought Resistance in Rice Under Upland and Lowland Environments. <i>Acta Agronomica Sinica</i> , 2008, 34, 198-206.	0.3	12
65	Yield Trait Variation and QTL Mapping in a DH Population of Rice Under Phosphorus Deficiency. <i>Acta Agronomica Sinica</i> , 2008, 34, 1137-1142.	0.3	12
66	Genetic structure and eco-geographical differentiation of cultivated Hsien rice (<i>Oryza sativa</i> L. subsp.) Tj ETQq0 0 0,rgBT /Overlock 10 T	1.7	12
67	Genetic architecture of flag leaf length and width in rice (<i>Oryza sativa</i> L.) revealed by association mapping. <i>Genes and Genomics</i> , 2017, 39, 341-352.	1.4	12
68	Genetic architecture to cause dynamic change in tiller and panicle numbers revealed by genome-wide association study and transcriptome profile in rice. <i>Plant Journal</i> , 2020, 104, 1603-1616.	5.7	12
69	Comparative transcriptional profiling under drought stress between upland and lowland rice (<i>Oryza</i>) Tj ETQq1 1 0.784314 rgBT /Overbo	9.0	11
70	Nucleotide diversity, natural variation, and evolution of Flexible culm-1 and Strong culm-2 lodging resistance genes in rice. <i>Genome</i> , 2016, 59, 473-483.	2.0	11
71	Identification of main effect and epistatic QTLs controlling initial flowering date in cultivated peanut (<i>Arachis hypogaea</i> L.). <i>Journal of Integrative Agriculture</i> , 2020, 19, 2383-2393.	3.5	11
72	Assessing indica-japonica differentiation of improved rice varieties using microsatellite markers. <i>Journal of Genetics and Genomics</i> , 2009, 36, 305-312.	3.9	10

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73	Genome-Wide Identification of MDH Family Genes and Their Association with Salt Tolerance in Rice. <i>Plants</i> , 2022, 11, 1498.	3.5	10
74	Identification and Validation of Aerobic Adaptation QTLs in Upland Rice. <i>Life</i> , 2020, 10, 65.	2.4	7
75	Geographical genetic diversity and divergence of common wild rice (<i>O. rufipogon</i> Griff.) in China. <i>Science Bulletin</i> , 2008, 53, 3559-3566.	9.0	6
76	Genetic Structure and Eco-Geographical Differentiation of Cultivated Keng Rice (<i>Oryza sativa</i> L. subsp.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	3.5	6
77	High-density genetic map development and QTL mapping for concentration degree of floret flowering date in cultivated peanut (<i>Arachis hypogaea</i> L.). <i>Molecular Breeding</i> , 2020, 40, 1.	2.1	6
78	OsNBL1, a Multi-Organelle Localized Protein, Plays Essential Roles in Rice Senescence, Disease Resistance, and Salt Tolerance. <i>Rice</i> , 2021, 14, 10.	4.0	4
79	Genetic basis and network underlying synergistic roots and shoots biomass accumulation revealed by genome-wide association studies in rice. <i>Scientific Reports</i> , 2021, 11, 13769.	3.3	4
80	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
81	Correlation analysis and QTL mapping of osmotic potential in japonica rice under upland and lowland conditions. <i>Canadian Journal of Plant Science</i> , 2013, 93, 785-792.	0.9	3
82	Identifying natural genotypes of grain number per panicle in rice (<i>Oryza sativa</i> L.) by association mapping. <i>Genes and Genomics</i> , 2019, 41, 283-295.	1.4	3
83	Fine Mapping of Two Additive Effect Genes for Awn Development in Rice (<i>Oryza sativa</i> L.). <i>PLoS ONE</i> , 2016, 11, e0160792.	2.5	3
84	Dissection of genetic architecture for tiller angle in rice (<i>Oryza sativa</i> L.) by multiple genome-wide association analyses. <i>PeerJ</i> , 0, 10, e12674.	2.0	3
85	Effects of TaMTL-Edited Mutations on Grain Phenotype and Storage Component Composition in Wheat. <i>Agriculture (Switzerland)</i> , 2022, 12, 587.	3.1	3
86	Correlation between allele sizes of microsatellites and phenotypic variations in rice landraces. <i>Frontiers of Agriculture in China</i> , 2009, 3, 130-139.	0.2	2
87	Comparison and rapid prediction of lignocellulose and organic elements of a wide variety of rice straw based on near infrared spectroscopy. <i>International Journal of Agricultural and Biological Engineering</i> , 2019, 12, 166-172.	0.6	2
88	Mapping of three QTLs for seed setting and analysis on the candidate gene for qSS-1 in rice (<i>Oryza</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	3.5	1
89	Transcriptome and metabolome profiling of unheading in F1 hybrid rice. <i>Journal of Integrative Agriculture</i> , 2020, 19, 2367-2382.	3.5	1