

Zi-chao Li

List of Publications by Year in descending order

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Version: 2024-02-01

89
papers

5,407
citations

117625

34
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91884

69
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93
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93
docs citations

93
times ranked

5433
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | <i>RGN1</i> controls grain number and shapes panicle architecture in rice. <i>Plant Biotechnology Journal</i> , 2022, 20, 158-167. | 8.3 | 19 |
| 2 | Effects of TaMTL-Edited Mutations on Grain Phenotype and Storage Component Composition in Wheat. <i>Agriculture (Switzerland)</i> , 2022, 12, 587. | 3.1 | 3 |
| 3 | Genome-Wide Identification of MDH Family Genes and Their Association with Salt Tolerance in Rice. <i>Plants</i> , 2022, 11, 1498. | 3.5 | 10 |
| 4 | Cold-adaptive evolution at the reproductive stage in <i>Gengjaponica</i> subspecies reveals the role of <i>OsMAPK3</i> and <i>OsLEA9</i> . <i>Plant Journal</i> , 2022, 111, 1032-1051. | 5.7 | 13 |
| 5 | A super pan-genomic landscape of rice. <i>Cell Research</i> , 2022, 32, 878-896. | 12.0 | 99 |
| 6 | GNP6, a novel allele of MOC1, regulates panicle and tiller development in rice. <i>Crop Journal</i> , 2021, 9, 57-67. | 5.2 | 22 |
| 7 | <i>OsADR3</i> increases drought stress tolerance by inducing antioxidant defense mechanisms and regulating <i>OsGPX1</i> in rice (<i>Oryza sativa</i> L.). <i>Crop Journal</i> , 2021, 9, 1003-1017. | 5.2 | 19 |
| 8 | <i>OsNBL1</i> , 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 |
| 9 | Genetic control of panicle architecture in rice. <i>Crop Journal</i> , 2021, 9, 590-597. | 5.2 | 29 |
| 10 | Stepwise selection of natural variations at <i>CTB2</i> and <i>CTB4a</i> improves cold adaptation during domestication of <i>japonica</i> rice. <i>New Phytologist</i> , 2021, 231, 1056-1072. | 7.3 | 30 |
| 11 | 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 |
| 12 | Rice <i>SPL10</i> 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 |
| 13 | 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 |
| 14 | Transcriptome and metabolome profiling of unheading in F1 hybrid rice. <i>Journal of Integrative Agriculture</i> , 2020, 19, 2367-2382. | 3.5 | 1 |
| 15 | 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 |
| 16 | Identification and Validation of Aerobic Adaptation QTLs in Upland Rice. <i>Life</i> , 2020, 10, 65. | 2.4 | 7 |
| 17 | Differentiation, evolution and utilization of natural alleles for cold adaptability at the reproductive stage in rice. <i>Plant Biotechnology Journal</i> , 2020, 18, 2491-2503. | 8.3 | 27 |
| 18 | Genetic basis and identification of candidate genes for salt tolerance in rice by GWAS. <i>Scientific Reports</i> , 2020, 10, 9958. | 3.3 | 64 |

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|----|--|------|-----------|
| 19 | 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 |
| 20 | 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> . <i>Plant Biotechnology Journal</i> , 2019, 17, 1547-1559. | 8.3 | 27 |
| 21 | 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 |
| 22 | 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 |
| 23 | 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 |
| 24 | QTL mapping and QTL × environment interaction analysis of multi-seed pod in cultivated peanut (<i>Arachis</i>) TjEJQq000rgBT/Ove | 5.2 | 39 |
| 25 | Genetic analysis of roots and shoots in rice seedling by association mapping. <i>Genes and Genomics</i> , 2019, 41, 95-105. | 1.4 | 27 |
| 26 | 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 |
| 27 | Alternative splicing of <i>OsLGS3</i> controls grain length and yield in <i>japonica</i> rice. <i>Plant Biotechnology Journal</i> , 2018, 16, 1667-1678. | 8.3 | 109 |
| 28 | Genomic variation in 3,010 diverse accessions of Asian cultivated rice. <i>Nature</i> , 2018, 557, 43-49. | 27.8 | 1,091 |
| 29 | <i>OsERF71</i> confers drought tolerance via modulating ABA signaling and proline biosynthesis. <i>Plant Science</i> , 2018, 270, 131-139. | 3.6 | 78 |
| 30 | The <i>Sâ€‘A</i> 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 |
| 31 | Fine mapping of QTL <i>qCTB10-2</i> that confers cold tolerance at the booting stage in rice. <i>Theoretical and Applied Genetics</i> , 2018, 131, 157-166. | 3.6 | 28 |
| 32 | <i>Gnp4/LAX2</i> , a RAWL protein, interferes with the <i>OsIAA3</i> – <i>OsARF25</i> 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 |
| 33 | Characterization of Transcription Factor Gene <i>OsDRAP1</i> Conferring Drought Tolerance in Rice. <i>Frontiers in Plant Science</i> , 2018, 9, 94. | 3.6 | 63 |
| 34 | 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 |
| 35 | Genetic Basis Underlying Correlations Among Growth Duration and Yield Traits Revealed by GWAS in Rice (<i>Oryza sativa</i> L.). <i>Frontiers in Plant Science</i> , 2018, 9, 650. | 3.6 | 28 |
| 36 | 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 |

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|----|---|------|-----------|
| 37 | 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 |
| 38 | Genomics-based plant germplasm research (GPGR). <i>Crop Journal</i> , 2017, 5, 166-174. | 5.2 | 28 |
| 39 | Natural variation in CTB4a enhances rice adaptation to cold habitats. <i>Nature Communications</i> , 2017, 8, 14788. | 12.8 | 192 |
| 40 | OsLG3 contributing to rice grain length and yield was mined by Ho-LAMap. <i>BMC Biology</i> , 2017, 15, 28. | 3.8 | 100 |
| 41 | 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 |
| 42 | <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 |
| 43 | Mapping of three QTLs for seed setting and analysis on the candidate gene for qSS-1 in rice (<i>Oryza</i>) Tj ETQq1 1 0.784314 rgBT /Overl | 3.5 | 1 |
| 44 | 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 |
| 45 | 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 |
| 46 | 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 |
| 47 | Rice functional genomics and breeding database (RFGB)-3K-rice SNP and InDel sub-database. <i>Chinese Science Bulletin</i> , 2015, 60, 367-371. | 0.7 | 31 |
| 48 | 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 |
| 49 | Natural variation in <i>E</i> contributes to early flowering in japonica rice under long days. <i>Plant, Cell and Environment</i> , 2014, 37, 101-112. | 5.7 | 46 |
| 50 | 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 |
| 51 | Genetic structure and eco-geographical differentiation of cultivated Hsien rice (<i>Oryza sativa</i> L. subsp.) Tj ETQq1 1 0.784314 rgBT /Overl | 1.7 | 12 |
| 52 | 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 |
| 53 | Quantitative Trait Loci for Mercury Tolerance in Rice Seedlings. <i>Rice Science</i> , 2013, 20, 238-242. | 3.9 | 23 |
| 54 | 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 |

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|----|--|-----|-----------|
| 55 | Characterization and identification of cold tolerant near-isogenic lines in rice. <i>Breeding Science</i> , 2012, 62, 196-201. | 1.9 | 21 |
| 56 | Domestication and geographic origin of <i>Oryza sativa</i> in China: insights from multilocus analysis of nucleotide variation of <i>Oryza sativa</i> and <i>Oryza rufipogon</i> . <i>Molecular Ecology</i> , 2012, 21, 5073-5087. | 3.9 | 39 |
| 57 | Fine Mapping of qTCW3-1, a QTL for 1000-Grain Weight on Chromosome 3 in Rice. <i>Journal of Integrative Agriculture</i> , 2012, 11, 879-887. | 3.5 | 15 |
| 58 | Genetic Structure and Eco-Geographical Differentiation of Cultivated Keng Rice (<i>Oryza sativa</i> L. subsp.) Tj ETQq0 0 0 rgBT /Overlock 10 | 3.5 | 6 |
| 59 | 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 |
| 60 | Fine Mapping and Cloning of the Grain Number Per-Panicle Gene (Gnp4) on Chromosome 4 in Rice (<i>Oryza sativa</i> L.). <i>Agricultural Sciences in China</i> , 2011, 10, 1825-1833. | 0.6 | 17 |
| 61 | Development of upland rice introgression lines and identification of QTLs for basal root thickness under different water regimes. <i>Journal of Genetics and Genomics</i> , 2011, 38, 547-556. | 3.9 | 21 |
| 62 | 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 |
| 63 | Fine mapping of the awn gene on chromosome 4 in rice by association and linkage analyses. <i>Science Bulletin</i> , 2011, 56, 835-839. | 1.7 | 26 |
| 64 | 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 |
| 65 | 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 |
| 66 | Comparative transcriptional profiling under drought stress between upland and lowland rice (<i>Oryza</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 | 9.0 | 11 |
| 67 | 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 |
| 68 | 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 |
| 69 | 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 |
| 70 | 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 |
| 71 | 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 |
| 72 | 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 |

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|----|---|-----|-----------|
| 73 | Mapping QTLs of root morphological traits at different growth stages in rice. <i>Genetica</i> , 2008, 133, 187-200. | 1.1 | 117 |
| 74 | 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 |
| 75 | 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 |
| 76 | 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 |
| 77 | 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 |
| 78 | 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 |
| 79 | 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 |
| 80 | Genetic structure and phylogeography of rice landraces in Yunnan, China, revealed by SSR. <i>Genome</i> , 2007, 50, 72-83. | 2.0 | 40 |
| 81 | 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 |
| 82 | 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 <i>Biology</i> , 2007, 49, 1455-1463. | 8.5 | 23 |
| 83 | 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 |
| 84 | Genetic structure and diversity of <i>Oryza sativa</i> L. in Guizhou, China. <i>Science Bulletin</i> , 2007, 52, 343-351. | 1.7 | 23 |
| 85 | 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 |
| 86 | 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 |
| 87 | 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 |
| 88 | Title is missing!. <i>Genetic Resources and Crop Evolution</i> , 2002, 49, 67-74. | 1.6 | 29 |
| 89 | 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 |