

Jianlong Xu

List of Publications by Year in descending order

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98
papers

4,098
citations

147566

31
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143772

57
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104
all docs

104
docs citations

104
times ranked

3936
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic variation in 3,010 diverse accessions of Asian cultivated rice. <i>Nature</i> , 2018, 557, 43-49.	13.7	1,091
2	A natural tandem array alleviates epigenetic repression of IPA1 and leads to superior yielding rice. <i>Nature Communications</i> , 2017, 8, 14789.	5.8	149
3	Ca ²⁺ sensor-mediated ROS scavenging suppresses rice immunity and is exploited by a fungal effector. <i>Cell</i> , 2021, 184, 5391-5404.e17.	13.5	117
4	Identification of genes for salt tolerance and yield-related traits in rice plants grown hydroponically and under saline field conditions by genome-wide association study. <i>Rice</i> , 2019, 12, 88.	1.7	105
5	Complex molecular mechanisms underlying seedling salt tolerance in rice revealed by comparative transcriptome and metabolomic profiling. <i>Journal of Experimental Botany</i> , 2016, 67, 405-419.	2.4	104
6	Identification and Fine Mapping of a Stably Expressed QTL for Cold Tolerance at the Booting Stage Using an Interconnected Breeding Population in Rice. <i>PLoS ONE</i> , 2015, 10, e0145704.	1.1	91
7	Molecular mechanisms of salinity tolerance in rice. <i>Crop Journal</i> , 2021, 9, 506-520.	2.3	91
8	Identification of salt-tolerant QTLs with strong genetic background effect using two sets of reciprocal introgression lines in rice. <i>Genome</i> , 2012, 55, 45-55.	0.9	80
9	Harnessing the hidden genetic diversity for improving multiple abiotic stress tolerance in rice (<i>Oryza</i>) Tj ETQq1 1 0.784314 rgBT /Ove 1.1 74	1.1	74
10	The rice <i>OsV4</i> encoding a novel pentatricopeptide repeat protein is required for chloroplast development during the early leaf stage under cold stress. <i>Journal of Integrative Plant Biology</i> , 2014, 56, 400-410.	4.1	72
11	Genome-Wide Association Study of Grain Appearance and Milling Quality in a Worldwide Collection of Indica Rice Germplasm. <i>PLoS ONE</i> , 2015, 10, e0145577.	1.1	67
12	Relationship of Rice Grain Amylose, Gelatinization Temperature and Pasting Properties for Breeding Better Eating and Cooking Quality of Rice Varieties. <i>PLoS ONE</i> , 2016, 11, e0168483.	1.1	66
13	Dissection of genetic overlap of salt tolerance QTLs at the seedling and tillering stages using backcross introgression lines in rice. <i>Science in China Series C: Life Sciences</i> , 2008, 51, 583-591.	1.3	65
14	The Rice Pentatricopeptide Repeat Gene TCD10 is Needed for Chloroplast Development under Cold Stress. <i>Rice</i> , 2016, 9, 67.	1.7	62
15	Examining Two Sets of Introgression Lines in Rice (<i>Oryza sativa</i> L.) Reveals Favorable Alleles that Improve Grain Zn and Fe Concentrations. <i>PLoS ONE</i> , 2015, 10, e0131846.	1.1	61
16	<i>Xa39</i> , a novel dominant gene conferring broad-spectrum resistance to <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> in rice. <i>Plant Pathology</i> , 2015, 64, 568-575.	1.2	61
17	Loci and natural alleles underlying robust roots and adaptive domestication of upland ecotype rice in aerobic conditions. <i>PLoS Genetics</i> , 2018, 14, e1007521.	1.5	61
18	Genome-wide and gene-based association mapping for rice eating and cooking characteristics and protein content. <i>Scientific Reports</i> , 2017, 7, 17203.	1.6	60

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19	QTL mapping and candidate gene analysis of ferrous iron and zinc toxicity tolerance at seedling stage in rice by genome-wide association study. <i>BMC Genomics</i> , 2017, 18, 828.	1.2	58
20	The landscape of geneâ€CDSâ€C haplotype diversity in rice: Properties, population organization, footprints of domestication and breeding, and implications for genetic improvement. <i>Molecular Plant</i> , 2021, 14, 787-804.	3.9	58
21	New Candidate Genes Affecting Rice Grain Appearance and Milling Quality Detected by Genome-Wide and Gene-Based Association Analyses. <i>Frontiers in Plant Science</i> , 2016, 7, 1998.	1.7	55
22	Integrated Analysis of the Transcriptome and Metabolome Revealed the Molecular Mechanisms Underlying the Enhanced Salt Tolerance of Rice Due to the Application of Exogenous Melatonin. <i>Frontiers in Plant Science</i> , 2020, 11, 618680.	1.7	48
23	Simultaneous Improvement and Genetic Dissection of Salt Tolerance of Rice (<i>Oryza sativa</i> L.) by Designed QTL Pyramiding. <i>Frontiers in Plant Science</i> , 2017, 8, 1275.	1.7	45
24	QTL mapping and candidate gene analysis of peduncle vascular bundle related traits in rice by genome-wide association study. <i>Rice</i> , 2018, 11, 13.	1.7	45
25	New insights into amylose and amylopectin biosynthesis in rice endosperm. <i>Carbohydrate Polymers</i> , 2020, 230, 115656.	5.1	45
26	From Green Super Rice to green agriculture: Reaping the promise of functional genomics research. <i>Molecular Plant</i> , 2022, 15, 9-26.	3.9	44
27	Genetic background effects on QTL and QTL \times environment interaction for yield and its component traits as revealed by reciprocal introgression lines in rice. <i>Crop Journal</i> , 2014, 2, 345-357.	2.3	42
28	The Rice TCM5 Gene Encoding a Novel Deg Protease Protein is Essential for Chloroplast Development under High Temperatures. <i>Rice</i> , 2016, 9, 13.	1.7	42
29	Examining two sets of introgression lines reveals background-independent and stably expressed QTL that improve grain appearance quality in rice (<i>Oryza sativa</i> L.). <i>Theoretical and Applied Genetics</i> , 2017, 130, 951-967.	1.8	35
30	Biomass accumulation and partitioning of newly developed Green Super Rice (GSR) cultivars under drought stress during the reproductive stage. <i>Field Crops Research</i> , 2014, 162, 30-38.	2.3	34
31	Joint Exploration of Favorable Haplotypes for Mineral Concentrations in Milled Grains of Rice (<i>Oryza</i>) Tj ETQq1 1 0.784314 rgBT /Over	1.7	34
32	Genetic Dissection and Simultaneous Improvement of Drought and Low Nitrogen Tolerances by Designed QTL Pyramiding in Rice. <i>Frontiers in Plant Science</i> , 2018, 9, 306.	1.7	33
33	Rice functional genomics and breeding database (RFGB)-3K-rice SNP and InDel sub-database. <i>Chinese Science Bulletin</i> , 2015, 60, 367-371.	0.4	31
34	Background-independent Quantitative Trait Loci for Drought Tolerance Identified Using Advanced Backcross Introgression Lines in Rice. <i>Crop Science</i> , 2013, 53, 430-441.	0.8	29
35	Exploiting the Genomic Diversity of Rice (<i>Oryza sativa</i> L.): SNP-Typing in 11 Early-Backcross Introgression-Breeding Populations. <i>Frontiers in Plant Science</i> , 2018, 9, 849.	1.7	28
36	The rice ALS3 encoding a novel pentatricopeptide repeat protein is required for chloroplast development and seedling growth. <i>Rice</i> , 2015, 8, 17.	1.7	27

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37	QTL and QTL networks for cold tolerance at the reproductive stage detected using selective introgression in rice. <i>PLoS ONE</i> , 2018, 13, e0200846.	1.1	27
38	Comparative transcriptome and metabolome profiling reveal molecular mechanisms underlying OsDRAP1-mediated salt tolerance in rice. <i>Scientific Reports</i> , 2021, 11, 5166.	1.6	27
39	Genome-wide association analysis identifies resistance loci for bacterial blight in a diverse collection of indica rice germplasm. <i>PLoS ONE</i> , 2017, 12, e0174598.	1.1	27
40	Alterations in stomatal response to fluctuating light increase biomass and yield of rice under drought conditions. <i>Plant Journal</i> , 2020, 104, 1334-1347.	2.8	26
41	Joint Mapping and Allele Mining of the Rolled Leaf Trait in Rice (<i>Oryza sativa</i> L.). <i>PLoS ONE</i> , 2016, 11, e0158246.	1.1	24
42	Genome-wide association mapping of aluminum toxicity tolerance and fine mapping of a candidate gene for Nrat1 in rice. <i>PLoS ONE</i> , 2018, 13, e0198589.	1.1	24
43	Characterizing the metabolites related to rice salt tolerance with introgression lines exhibiting contrasting performances in response to saline conditions. <i>Plant Growth Regulation</i> , 2020, 92, 157-167.	1.8	24
44	Selection efficiencies for improving drought/salt tolerances and yield using introgression breeding in rice (<i>Oryza sativa</i> L.). <i>Crop Journal</i> , 2013, 1, 134-142.	2.3	23
45	Simultaneous improvement in cold tolerance and yield of temperate <i>japonica</i> rice (<i>Oryza sativa</i> L.) by introgression breeding. <i>Plant Breeding</i> , 2013, 132, 604-612.	1.0	23
46	Developing green super rice varieties with high nutrient use efficiency by phenotypic selection under varied nutrient conditions. <i>Crop Journal</i> , 2019, 7, 368-377.	2.3	22
47	Genetic bases of source-, sink-, and yield-related traits revealed by genome-wide association study in Xian rice. <i>Crop Journal</i> , 2020, 8, 119-131.	2.3	22
48	Novel loci for field resistance to black-streaked dwarf and stripe viruses identified in a set of reciprocal introgression lines of rice (<i>Oryza sativa</i> L.). <i>Molecular Breeding</i> , 2012, 29, 925-938.	1.0	21
49	Drought-tolerance QTLs commonly detected in two sets of reciprocal introgression lines in rice. <i>Crop and Pasture Science</i> , 2014, 65, 171.	0.7	21
50	Identification of salt tolerance-improving quantitative trait loci alleles from a salt-susceptible rice breeding line by introgression breeding. <i>Plant Breeding</i> , 2015, 134, 653-660.	1.0	21
51	Recurrent selection breeding by dominant male sterility for multiple abiotic stresses tolerant rice cultivars. <i>Euphytica</i> , 2017, 213, 268.	0.6	21
52	Natural Sequence Variations and Combinations of GNP1 and NAL1 Determine the Grain Number per Panicle in Rice. <i>Rice</i> , 2020, 13, 14.	1.7	21
53	Reciprocal adaptation of rice and <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> cross-species 2D GWAS reveals the underlying genetics. <i>Plant Cell</i> , 2021, 33, 2538-2561.	3.1	21
54	Long-read sequencing of 111 rice genomes reveals significantly larger pan-genomes. <i>Genome Research</i> , 2022, . .	2.4	21

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55	SS1 (NAL1)- and SS2-Mediated Genetic Networks Underlying Source-Sink and Yield Traits in Rice (<i>Oryza</i>) Tj ETQq1 1 0.784314.rgBT /Ov	1.1	20
56	Advanced Backcross QTL Analysis for the Whole Plant Growth Duration Salt Tolerance in Rice (<i>Oryza</i>) Tj ETQq0 0 0.rgBT /Overlock 10 Tf	1.7	19
57	Simultaneous Improvement and Genetic Dissection of Drought Tolerance Using Selected Breeding Populations of Rice. <i>Frontiers in Plant Science</i> , 2018, 9, 320.	1.7	19
58	<i>RGN1</i> controls grain number and shapes panicle architecture in rice. <i>Plant Biotechnology Journal</i> , 2022, 20, 158-167.	4.1	19
59	Impact of Pre-Anthesis Drought Stress on Physiology, Yield-Related Traits, and Drought-Responsive Genes in Green Super Rice. <i>Frontiers in Genetics</i> , 2022, 13, 832542.	1.1	18
60	Breeding by selective introgression: Theory, practices, and lessons learned from rice. <i>Crop Journal</i> , 2021, 9, 646-657.	2.3	17
61	Combining Limited Multiple Environment Trials Data with Crop Modeling to Identify Widely Adaptable Rice Varieties. <i>PLoS ONE</i> , 2016, 11, e0164456.	1.1	16
62	Rice <i>TSV3</i> Encoding Obg-Like GTPase Protein Is Essential for Chloroplast Development During the Early Leaf Stage Under Cold Stress. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 253-263.	0.8	15
63	Novel sequences, structural variations and gene presence variations of Asian cultivated rice. <i>Scientific Data</i> , 2018, 5, 180079.	2.4	14
64	Pleiotropic Effect of GNP1 Underlying Grain Number per Panicle on Sink, Source and Flow in Rice. <i>Frontiers in Plant Science</i> , 2020, 11, 933.	1.7	14
65	Chloroplast development at low temperature requires the pseudouridine synthase gene TCD3 in rice. <i>Scientific Reports</i> , 2020, 10, 8518.	1.6	14
66	Highly efficient genotyping of rice biparental populations by GoldenGate assays based on parental resequencing. <i>Theoretical and Applied Genetics</i> , 2014, 127, 297-307.	1.8	13
67	Identification and allele mining of new candidate genes underlying rice grain weight and grain shape by genome-wide association study. <i>BMC Genomics</i> , 2021, 22, 602.	1.2	13
68	Genome-wide Responses to Selection and Genetic Networks Underlying Submergence Tolerance in Rice. <i>Plant Genome</i> , 2015, 8, eplantgenome2014.10.0066.	1.6	12
69	Detecting major <sc>QTL</sc> associated with resistance to bacterial blight using a set of rice reciprocal introgression lines with high density <sc>SNP</sc> markers. <i>Plant Breeding</i> , 2015, 134, 286-292.	1.0	12
70	QTL underlying iron and zinc toxicity tolerances at seedling stage revealed by two sets of reciprocal introgression populations of rice (<i>Oryza sativa</i> L.). <i>Crop Journal</i> , 2016, 4, 280-289.	2.3	12
71	Overlap between Signaling Pathways Responsive to <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> Infection and Drought Stress in Rice Introgression Line Revealed by RNA-Seq. <i>Journal of Plant Growth Regulation</i> , 2016, 35, 345-356.	2.8	12
72	Rapid prediction of head rice yield and grain shape for genome-wide association study in indica rice. <i>Journal of Cereal Science</i> , 2020, 96, 103091.	1.8	12

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73	Genetic Bases of the Stomata-Related Traits Revealed by a Genome-Wide Association Analysis in Rice (<i>Oryza sativa</i> L.). <i>Frontiers in Genetics</i> , 2020, 11, 611.	1.1	12
74	Construction and integration of genetic linkage maps from three multi-parent advanced generation inter-cross populations in rice. <i>Rice</i> , 2020, 13, 13.	1.7	12
75	Identification of Candidate Genes for Salinity and Anaerobic Tolerance at the Germination Stage in Rice by Genome-Wide Association Analyses. <i>Frontiers in Genetics</i> , 2022, 13, 822516.	1.1	12
76	Genome-Wide Association Study on Resistance to Rice Black-Streaked Dwarf Disease Caused by Rice black-streaked dwarf virus. <i>Plant Disease</i> , 2021, 105, 607-615.	0.7	11
77	Molecular Dissection of the Gene <i>OsGA2ox8</i> Conferring Osmotic Stress Tolerance in Rice. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9107.	1.8	11
78	Global N6-Methyladenosine Profiling Revealed the Tissue-Specific Epitranscriptomic Regulation of Rice Responses to Salt Stress. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2091.	1.8	11
79	Genetic dissection of rice appearance quality and cooked rice elongation by genome-wide association study. <i>Crop Journal</i> , 2021, 9, 1470-1480.	2.3	10
80	Identification of Structure-controlling Rice Biosynthesis Enzymes. <i>Biomacromolecules</i> , 2021, 22, 2148-2159.	2.6	10
81	Identification of Stably Expressed Quantitative Trait Loci for Grain Yield and Protein Content Using Recombinant Inbred Line and Reciprocal Introgression Line Populations in Rice. <i>Crop Science</i> , 2013, 53, 1437-1446.	0.8	9
82	Rice <i>TCM1</i> Encoding a Component of the TAC Complex is Required for Chloroplast Development under Cold Stress. <i>Plant Genome</i> , 2018, 11, 160065.	1.6	9
83	Breeding by design for future rice: Genes and genome technologies. <i>Crop Journal</i> , 2021, 9, 491-496.	2.3	9
84	Genetic architecture of seed glycerolipids in Asian cultivated rice. <i>Plant, Cell and Environment</i> , 0, , .	2.8	9
85	Characterization of Salt-Induced Epigenetic Segregation by Genome-Wide Loss of Heterozygosity and its Association with Salt Tolerance in Rice (<i>Oryza sativa</i> L.). <i>Frontiers in Plant Science</i> , 2017, 8, 977.	1.7	8
86	Transcriptome and genome sequencing elucidates the molecular basis for the high yield and good quality of the hybrid rice variety Chuanyou6203. <i>Scientific Reports</i> , 2020, 10, 19935.	1.6	7
87	QTL Mapping and Favorable Allele Mining of Nitrogen Deficiency Tolerance Using an Interconnected Breeding Population in Rice. <i>Frontiers in Genetics</i> , 2021, 12, 616428.	1.1	7
88	Genetic mechanism of heterosis for rice milling and appearance quality in an elite rice hybrid. <i>Crop Journal</i> , 2022, 10, 1705-1716.	2.3	7
89	Identify QTLs and candidate genes underlying source-, sink-, and grain yield-related traits in rice by integrated analysis of bi-parental and natural populations. <i>PLoS ONE</i> , 2020, 15, e0237774.	1.1	6
90	Silicon and selenium fertilizer management improved productivity and aroma of fragrant rice. <i>Crop Science</i> , 2021, 61, 936-946.	0.8	6

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91	Metabolic Profiling and Physiological Analysis of a Novel Rice Introgression Line with Broad Leaf Size. PLoS ONE, 2015, 10, e0145646.	1.1	6
92	Genome-wide selection and introgression of Chinese rice varieties during breeding. Journal of Genetics and Genomics, 2022, 49, 492-501.	1.7	6
93	The divergence of brassinosteroid sensitivity between rice subspecies involves natural variation conferring altered internal auto-binding of OsBSK2. Journal of Integrative Plant Biology, 2022, 64, 1614-1630.	4.1	6
94	Genetic dissection of heterosis of indica-japonica by introgression line, recombinant inbred line and their testcross populations. Scientific Reports, 2021, 11, 10265.	1.6	5
95	Scanning QTLs for Grain Shape using Two Sets of Introgression Lines in Rice. International Journal of Agriculture and Biology, 2017, 19, 509-516.	0.2	3
96	Genetic Dissection of Rice Ratooning Ability Using an Introgression Line Population and Substitution Mapping of a Pleiotropic Quantitative Trait Locus qRA5. Plants, 2022, 11, 1134.	1.6	2
97	Dominant early heading without yield drag in a sister-line BC breeding progeny DEH_229 is controlled by multiple genetic factors with main-effect loci. Crop Journal, 2021, 9, 400-411.	2.3	1
98	Genetic Bases of Flow- and Sink-Related Traits in Rice Revealed by Genome-Wide Association Study. Agronomy, 2022, 12, 776.	1.3	1