

Jianlong Xu

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/776733/publications.pdf>

Version: 2024-02-01

98
papers

4,098
citations

147566

31
h-index

143772

57
g-index

104
all docs

104
docs citations

104
times ranked

3936
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.	4.1	19
2	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
3	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
4	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
5	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
6	Genetic Bases of Flow- and Sink-Related Traits in Rice Revealed by Genome-Wide Association Study. <i>Agronomy</i> , 2022, 12, 776.	1.3	1
7	Genome-wide selection and introgression of Chinese rice varieties during breeding. <i>Journal of Genetics and Genomics</i> , 2022, 49, 492-501.	1.7	6
8	Long-read sequencing of 111 rice genomes reveals significantly larger pan-genomes. <i>Genome Research</i> , 2022, , .	2.4	21
9	Genetic Dissection of Rice Ratoon Ability Using an Introgression Line Population and Substitution Mapping of a Pleiotropic Quantitative Trait Locus qRA5. <i>Plants</i> , 2022, 11, 1134.	1.6	2
10	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
11	The divergence of brassinosteroid sensitivity between rice subspecies involves natural variation conferring altered internal auto-binding of OsBSK2. <i>Journal of Integrative Plant Biology</i> , 2022, 64, 1614-1630.	4.1	6
12	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. <i>Crop Journal</i> , 2021, 9, 400-411.	2.3	1
13	Silicon and selenium fertilizer management improved productivity and aroma of fragrant rice. <i>Crop Science</i> , 2021, 61, 936-946.	0.8	6
14	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
15	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
16	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
17	Identification of Structure-Controlling Rice Biosynthesis Enzymes. <i>Biomacromolecules</i> , 2021, 22, 2148-2159.	2.6	10
18	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

#	ARTICLE	IF	CITATIONS
19	Genetic dissection of heterosis of indicaâ€“japonica by introgression line, recombinant inbred line and their testcross populations. <i>Scientific Reports</i> , 2021, 11, 10265.	1.6	5
20	The landscape of geneâ€“CDSâ€“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	Breeding by design for future rice: Genes and genome technologies. <i>Crop Journal</i> , 2021, 9, 491-496.	2.3	9
22	Breeding by selective introgression: Theory, practices, and lessons learned from rice. <i>Crop Journal</i> , 2021, 9, 646-657.	2.3	17
23	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
24	Molecular mechanisms of salinity tolerance in rice. <i>Crop Journal</i> , 2021, 9, 506-520.	2.3	91
25	Molecular Dissection of the Gene OsGA2ox8 Conferring Osmotic Stress Tolerance in Rice. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9107.	1.8	11
26	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
27	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
28	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
29	New insights into amylose and amylopectin biosynthesis in rice endosperm. <i>Carbohydrate Polymers</i> , 2020, 230, 115656.	5.1	45
30	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
31	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
32	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
33	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
34	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
35	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
36	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

#	ARTICLE	IF	CITATIONS
37	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
38	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
39	Chloroplast development at low temperature requires the pseudouridine synthase gene TCD3 in rice. <i>Scientific Reports</i> , 2020, 10, 8518.	1.6	14
40	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
41	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
42	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
43	Genomic variation in 3,010 diverse accessions of Asian cultivated rice. <i>Nature</i> , 2018, 557, 43-49.	13.7	1,091
44	Novel sequences, structural variations and gene presence variations of Asian cultivated rice. <i>Scientific Data</i> , 2018, 5, 180079.	2.4	14
45	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
46	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
47	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
48	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
49	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
50	Joint Exploration of Favorable Haplotypes for Mineral Concentrations in Milled Grains of Rice (<i>Oryza</i>) Tj ETQq0 0 0 rBT /Overlock 10 Tf 5	1.7	34
51	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
52	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
53	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
54	Genome-wide association mapping of aluminum toxicity tolerance and fine mapping of a candidate gene for <i>Nrat1</i> in rice. <i>PLoS ONE</i> , 2018, 13, e0198589.	1.1	24

#	ARTICLE	IF	CITATIONS
55	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
56	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
57	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
58	Recurrent selection breeding by dominant male sterility for multiple abiotic stresses tolerant rice cultivars. <i>Euphytica</i> , 2017, 213, 268.	0.6	21
59	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
60	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
61	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
62	Harnessing the hidden genetic diversity for improving multiple abiotic stress tolerance in rice (<i>Oryza</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 19	1.1	74
63	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
64	Scanning QTLs for Grain Shape using Two Sets of Introgression Lines in Rice. <i>International Journal of Agriculture and Biology</i> , 2017, 19, 509-516.	0.2	3
65	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
66	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
67	The Rice Pentatricopeptide Repeat Gene TCD10 is Needed for Chloroplast Development under Cold Stress. <i>Rice</i> , 2016, 9, 67.	1.7	62
68	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
69	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
70	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
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	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

#	ARTICLE	IF	CITATIONS
73	Relationship of Rice Grain Amylose, Gelatinization Temperature and Pasting Properties for Breeding Better Eating and Cooking Quality of Rice Varieties. PLoS ONE, 2016, 11, e0168483.	1.1	66
74	Identification of salt tolerance-improving quantitative trait loci alleles from a salt-tolerant susceptible rice breeding line by introgression breeding. Plant Breeding, 2015, 134, 653-660.	1.0	21
75	Genome-Wide Responses to Selection and Genetic Networks Underlying Submergence Tolerance in Rice. Plant Genome, 2015, 8, eplantgenome2014.10.0066.	1.6	12
76	Examining Two Sets of Introgression Lines in Rice (<i>Oryza sativa</i> L.) Reveals Favorable Alleles that Improve Grain Zn and Fe Concentrations. PLoS ONE, 2015, 10, e0131846.	1.1	61
77	Identification and Fine Mapping of a Stably Expressed QTL for Cold Tolerance at the Booting Stage Using an Interconnected Breeding Population in Rice. PLoS ONE, 2015, 10, e0145704.	1.1	91
78	Rice functional genomics and breeding database (RFGB)-3K-rice SNP and InDel sub-database. Chinese Science Bulletin, 2015, 60, 367-371.	0.4	31
79	The rice ALS3 encoding a novel pentatricopeptide repeat protein is required for chloroplast development and seedling growth. Rice, 2015, 8, 17.	1.7	27
80	Detecting major QTL associated with resistance to bacterial blight using a set of rice reciprocal introgression lines with high density SNP markers. Plant Breeding, 2015, 134, 286-292.	1.0	12
81	<i>Xa39</i> , a novel dominant gene conferring broad-spectrum resistance to <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> in rice. Plant Pathology, 2015, 64, 568-575.	1.2	61
82	SS1 (NAL1)- and SS2-Mediated Genetic Networks Underlying Source-Sink and Yield Traits in Rice (<i>Oryza</i>) Tj ETQq0 0 0 rgBT /Overlock 10	1.1	20
83	Genome-Wide Association Study of Grain Appearance and Milling Quality in a Worldwide Collection of Indica Rice Germplasm. PLoS ONE, 2015, 10, e0145577.	1.1	67
84	Metabolic Profiling and Physiological Analysis of a Novel Rice Introgression Line with Broad Leaf Size. PLoS ONE, 2015, 10, e0145646.	1.1	6
85	Biomass accumulation and partitioning of newly developed Green Super Rice (GSR) cultivars under drought stress during the reproductive stage. Field Crops Research, 2014, 162, 30-38.	2.3	34
86	The rice <i>OsV4</i> encoding a novel pentatricopeptide repeat protein is required for chloroplast development during the early leaf stage under cold stress. Journal of Integrative Plant Biology, 2014, 56, 400-410.	4.1	72
87	Highly efficient genotyping of rice biparental populations by GoldenGate assays based on parental resequencing. Theoretical and Applied Genetics, 2014, 127, 297-307.	1.8	13
88	Genetic background effects on QTL and QTL \times environment interaction for yield and its component traits as revealed by reciprocal introgression lines in rice. Crop Journal, 2014, 2, 345-357.	2.3	42
89	Advanced Backcross QTL Analysis for the Whole Plant Growth Duration Salt Tolerance in Rice (<i>Oryza</i>) Tj ETQq1 1 0,784314 rgBT /Overlock 19	1.7	19
90	Drought-tolerance QTLs commonly detected in two sets of reciprocal introgression lines in rice. Crop and Pasture Science, 2014, 65, 171.	0.7	21

#	ARTICLE	IF	CITATIONS
91	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
92	Simultaneous improvement in cold tolerance and yield of temperate japonica rice (<i>Oryza sativa</i> L.) by introgression breeding. <i>Plant Breeding</i> , 2013, 132, 604-612.	1.0	23
93	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
94	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
95	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
96	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
97	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
98	Genetic architecture of seed glycerolipids in Asian cultivated rice. <i>Plant, Cell and Environment</i> , 0, , .	2.8	9