

Lizhong Xiong

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107
papers

12,886
citations

57
h-index

111
g-index

111
ext. papers

16,238
ext. citations

7.6
avg, IF

6.65
L-index

#	Paper	IF	Citations
107	Overexpressing a NAM, ATAF, and CUC (NAC) transcription factor enhances drought resistance and salt tolerance in rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 12987-92	11.5	1133
106	Disease resistance and abiotic stress tolerance in rice are inversely modulated by an abscisic acid-inducible mitogen-activated protein kinase. <i>Plant Cell</i> , 2003 , 15, 745-59	11.6	624
105	A novel integrated method for large-scale detection, identification, and quantification of widely targeted metabolites: application in the study of rice metabolomics. <i>Molecular Plant</i> , 2013 , 6, 1769-80	14.4	532
104	General mechanisms of drought response and their application in drought resistance improvement in plants. <i>Cellular and Molecular Life Sciences</i> , 2015 , 72, 673-89	10.3	481
103	Characterization of transcription factor gene SNAC2 conferring cold and salt tolerance in rice. <i>Plant Molecular Biology</i> , 2008 , 67, 169-81	4.6	479
102	Characterization of OsZIP23 as a key player of the basic leucine zipper transcription factor family for conferring abscisic acid sensitivity and salinity and drought tolerance in rice. <i>Plant Physiology</i> , 2008 , 148, 1938-52	6.6	451
101	Genomic organization, differential expression, and interaction of SQUAMOSA promoter-binding-like transcription factors and microRNA156 in rice. <i>Plant Physiology</i> , 2006 , 142, 280-93	6.6	442
100	Genetic engineering and breeding of drought-resistant crops. <i>Annual Review of Plant Biology</i> , 2014 , 65, 715-41	30.7	387
99	Over-expression of a LEA gene in rice improves drought resistance under the field conditions. <i>Theoretical and Applied Genetics</i> , 2007 , 115, 35-46	6	384
98	Characterization of stress-responsive CIPK genes in rice for stress tolerance improvement. <i>Plant Physiology</i> , 2007 , 144, 1416-28	6.6	339
97	Systematic sequence analysis and identification of tissue-specific or stress-responsive genes of NAC transcription factor family in rice. <i>Molecular Genetics and Genomics</i> , 2008 , 280, 547-63	3.1	328
96	Combining high-throughput phenotyping and genome-wide association studies to reveal natural genetic variation in rice. <i>Nature Communications</i> , 2014 , 5, 5087	17.4	316
95	Genetic basis of drought resistance at reproductive stage in rice: separation of drought tolerance from drought avoidance. <i>Genetics</i> , 2006 , 172, 1213-28	4	292
94	Endogenous auxin and jasmonic acid levels are differentially modulated by abiotic stresses in rice. <i>Frontiers in Plant Science</i> , 2013 , 4, 397	6.2	261
93	A Raf-like MAPKKK gene DSM1 mediates drought resistance through reactive oxygen species scavenging in rice. <i>Plant Physiology</i> , 2010 , 152, 876-90	6.6	258
92	Identification and expression profiling analysis of TIFY family genes involved in stress and phytohormone responses in rice. <i>Plant Molecular Biology</i> , 2009 , 71, 291-305	4.6	243
91	A stress-responsive NAC transcription factor SNAC3 confers heat and drought tolerance through modulation of reactive oxygen species in rice. <i>Journal of Experimental Botany</i> , 2015 , 66, 6803-17	7	227

90	Global genome expression analysis of rice in response to drought and high-salinity stresses in shoot, flag leaf, and panicle. <i>Plant Molecular Biology</i> , 2007 , 63, 591-608	4.6	227
89	Constitutive activation of transcription factor OsbZIP46 improves drought tolerance in rice. <i>Plant Physiology</i> , 2012 , 158, 1755-68	6.6	224
88	Conserved miR164-targeted NAC genes negatively regulate drought resistance in rice. <i>Journal of Experimental Botany</i> , 2014 , 65, 2119-35	7	207
87	Characterization of the beta-carotene hydroxylase gene DSM2 conferring drought and oxidative stress resistance by increasing xanthophylls and abscisic acid synthesis in rice. <i>Plant Physiology</i> , 2010 , 154, 1304-18	6.6	203
86	A GH3 family member, OsGH3-2, modulates auxin and abscisic acid levels and differentially affects drought and cold tolerance in rice. <i>Journal of Experimental Botany</i> , 2012 , 63, 6467-80	7	201
85	Genetic mapping of the rice ionome in leaves and grain: identification of QTLs for 17 elements including arsenic, cadmium, iron and selenium. <i>Plant and Soil</i> , 2010 , 329, 139-153	4.2	198
84	Crop Phenomics and High-Throughput Phenotyping: Past Decades, Current Challenges, and Future Perspectives. <i>Molecular Plant</i> , 2020 , 13, 187-214	14.4	188
83	Plant phenomics and high-throughput phenotyping: accelerating rice functional genomics using multidisciplinary technologies. <i>Current Opinion in Plant Biology</i> , 2013 , 16, 180-7	9.9	174
82	RMD: a rice mutant database for functional analysis of the rice genome. <i>Nucleic Acids Research</i> , 2006 , 34, D745-8	20.1	171
81	Gradual increase of miR156 regulates temporal expression changes of numerous genes during leaf development in rice. <i>Plant Physiology</i> , 2012 , 158, 1382-94	6.6	162
80	Feedback Regulation of ABA Signaling and Biosynthesis by a bZIP Transcription Factor Targets Drought-Resistance-Related Genes. <i>Plant Physiology</i> , 2016 , 171, 2810-25	6.6	136
79	High-Throughput Phenotyping and QTL Mapping Reveals the Genetic Architecture of Maize Plant Growth. <i>Plant Physiology</i> , 2017 , 173, 1554-1564	6.6	133
78	Genome-wide profiling of histone H3K4-tri-methylation and gene expression in rice under drought stress. <i>Plant Molecular Biology</i> , 2013 , 81, 175-88	4.6	130
77	The SNAC1-targeted gene OsSRO1c modulates stomatal closure and oxidative stress tolerance by regulating hydrogen peroxide in rice. <i>Journal of Experimental Botany</i> , 2013 , 64, 569-83	7	127
76	Characterization of Glossy1-homologous genes in rice involved in leaf wax accumulation and drought resistance. <i>Plant Molecular Biology</i> , 2009 , 70, 443-56	4.6	119
75	A homolog of human ski-interacting protein in rice positively regulates cell viability and stress tolerance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 6410-5	11.5	117
74	Comprehensive expression profiling analysis of OsIAA gene family in developmental processes and in response to phytohormone and stress treatments. <i>Planta</i> , 2009 , 229, 577-91	4.7	117
73	Breeding signatures of rice improvement revealed by a genomic variation map from a large germplasm collection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E5411-9	11.5	116

72	Characterization of OsIAA1 gene, a member of rice Aux/IAA family involved in auxin and brassinosteroid hormone responses and plant morphogenesis. <i>Plant Molecular Biology</i> , 2009 , 70, 297-304	4.6	96
71	OsJAZ9 acts as a transcriptional regulator in jasmonate signaling and modulates salt stress tolerance in rice. <i>Plant Science</i> , 2015 , 232, 1-12	5.3	95
70	A STRESS-RESPONSIVE NAC1-regulated protein phosphatase gene rice protein phosphatase18 modulates drought and oxidative stress tolerance through abscisic acid-independent reactive oxygen species scavenging in rice. <i>Plant Physiology</i> , 2014 , 166, 2100-14	6.6	95
69	Increased leaf angle1, a Raf-like MAPKKK that interacts with a nuclear protein family, regulates mechanical tissue formation in the Lamina joint of rice. <i>Plant Cell</i> , 2011 , 23, 4334-47	11.6	95
68	Carotenoid deficiency impairs ABA and IAA biosynthesis and differentially affects drought and cold tolerance in rice. <i>Plant Molecular Biology</i> , 2013 , 83, 475-88	4.6	94
67	An ornithine ̢-aminotransferase gene OsOAT confers drought and oxidative stress tolerance in rice. <i>Plant Science</i> , 2012 , 197, 59-69	5.3	94
66	Characterization of a stress responsive proteinase inhibitor gene with positive effect in improving drought resistance in rice. <i>Planta</i> , 2007 , 226, 73-85	4.7	89
65	Genetic analysis for drought resistance of rice at reproductive stage in field with different types of soil. <i>Theoretical and Applied Genetics</i> , 2005 , 111, 1127-36	6	89
64	Panicle-SEG: a robust image segmentation method for rice panicles in the field based on deep learning and superpixel optimization. <i>Plant Methods</i> , 2017 , 13, 104	5.8	85
63	Mutant resources for the functional analysis of the rice genome. <i>Molecular Plant</i> , 2013 , 6, 596-604	14.4	84
62	Genetic mechanisms conferring adaptation to submergence and drought in rice: simple or complex?. <i>Current Opinion in Plant Biology</i> , 2013 , 16, 196-204	9.9	79
61	MODD Mediates Deactivation and Degradation of OsZIP46 to Negatively Regulate ABA Signaling and Drought Resistance in Rice. <i>Plant Cell</i> , 2016 , 28, 2161-2177	11.6	78
60	Global expression profiling of rice microRNAs by one-tube stem-loop reverse transcription quantitative PCR revealed important roles of microRNAs in abiotic stress responses. <i>Molecular Genetics and Genomics</i> , 2010 , 284, 477-88	3.1	77
59	New insights into the genetic basis of natural chilling and cold shock tolerance in rice by genome-wide association analysis. <i>Plant, Cell and Environment</i> , 2016 , 39, 556-70	8.4	75
58	Genome-Wide Association Studies of Image Traits Reveal Genetic Architecture of Drought Resistance in Rice. <i>Molecular Plant</i> , 2018 , 11, 789-805	14.4	72
57	Putative megaenzyme DWA1 plays essential roles in drought resistance by regulating stress-induced wax deposition in rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 17790-5	11.5	72
56	A structural view of the conserved domain of rice stress-responsive NAC1. <i>Protein and Cell</i> , 2011 , 2, 55-63	3.2	71
55	Evaluation of near-isogenic lines for drought resistance QTL and fine mapping of a locus affecting flag leaf width, spikelet number, and root volume in rice. <i>Theoretical and Applied Genetics</i> , 2011 , 123, 815-26	6	69

54	The OsMYB30 Transcription Factor Suppresses Cold Tolerance by Interacting with a JAZ Protein and Suppressing β Amylase Expression. <i>Plant Physiology</i> , 2017 , 173, 1475-1491	6.6	68
53	Genetic control of the root system in rice under normal and drought stress conditions by genome-wide association study. <i>PLoS Genetics</i> , 2017 , 13, e1006889	6	68
52	OsJAZ1 Attenuates Drought Resistance by Regulating JA and ABA Signaling in Rice. <i>Frontiers in Plant Science</i> , 2017 , 8, 2108	6.2	68
51	Systematic analysis of GT factor family of rice reveals a novel subfamily involved in stress responses. <i>Molecular Genetics and Genomics</i> , 2010 , 283, 157-69	3.1	57
50	Genome-wide association study of rice (<i>Oryza sativa</i> L.) leaf traits with a high-throughput leaf scorer. <i>Journal of Experimental Botany</i> , 2015 , 66, 5605-15	7	55
49	Integrative Regulation of Drought Escape through ABA-Dependent and -Independent Pathways in Rice. <i>Molecular Plant</i> , 2018 , 11, 584-597	14.4	52
48	A homolog of ETHYLENE OVERPRODUCER, OsETOL1, differentially modulates drought and submergence tolerance in rice. <i>Plant Journal</i> , 2014 , 78, 834-49	6.9	49
47	Genome-wide identification of BURP domain-containing genes in rice reveals a gene family with diverse structures and responses to abiotic stresses. <i>Planta</i> , 2009 , 230, 149-63	4.7	49
46	Identification of a cluster of PR4-like genes involved in stress responses in rice. <i>Journal of Plant Physiology</i> , 2011 , 168, 2212-24	3.6	48
45	Characterization of an inositol 1,3,4-trisphosphate 5/6-kinase gene that is essential for drought and salt stress responses in rice. <i>Plant Molecular Biology</i> , 2011 , 77, 547-63	4.6	48
44	Ghd2, a CONSTANS-like gene, confers drought sensitivity through regulation of senescence in rice. <i>Journal of Experimental Botany</i> , 2016 , 67, 5785-5798	7	46
43	Characterization of a purine permease family gene OsPUP7 involved in growth and development control in rice. <i>Journal of Integrative Plant Biology</i> , 2013 , 55, 1119-35	8.3	45
42	A high-throughput stereo-imaging system for quantifying rape leaf traits during the seedling stage. <i>Plant Methods</i> , 2017 , 13, 7	5.8	40
41	Translational repression by a miniature inverted-repeat transposable element in the 3' untranslated region. <i>Nature Communications</i> , 2017 , 8, 14651	17.4	38
40	Combining high-throughput micro-CT-RGB phenotyping and genome-wide association study to dissect the genetic architecture of tiller growth in rice. <i>Journal of Experimental Botany</i> , 2019 , 70, 545-567	7	35
39	Co-overexpression of the Constitutively Active Form of OsbZIP46 and ABA-Activated Protein Kinase SAPK6 Improves Drought and Temperature Stress Resistance in Rice. <i>Frontiers in Plant Science</i> , 2017 , 8, 1102	6.2	32
38	Insight into differential responses of upland and paddy rice to drought stress by comparative expression profiling analysis. <i>International Journal of Molecular Sciences</i> , 2013 , 14, 5214-38	6.3	31
37	A special member of the rice SRO family, OsSRO1c, mediates responses to multiple abiotic stresses through interaction with various transcription factors. <i>Plant Molecular Biology</i> , 2014 , 84, 693-705	4.6	29

36	Establishment of a patterned GAL4-VP16 transactivation system for discovering gene function in rice. <i>Plant Journal</i> , 2006 , 46, 1059-72	6.9	29
35	Novel Digital Features Discriminate Between Drought Resistant and Drought Sensitive Rice Under Controlled and Field Conditions. <i>Frontiers in Plant Science</i> , 2018 , 9, 492	6.2	25
34	GID1 modulates stomatal response and submergence tolerance involving abscisic acid and gibberellic acid signaling in rice. <i>Journal of Integrative Plant Biology</i> , 2015 , 57, 954-68	8.3	23
33	Reversible Histone H2B Monoubiquitination Fine-Tunes Abscisic Acid Signaling and Drought Response in Rice. <i>Molecular Plant</i> , 2019 , 12, 263-277	14.4	22
32	Rice panicle length measuring system based on dual-camera imaging. <i>Computers and Electronics in Agriculture</i> , 2013 , 98, 158-165	6.5	22
31	An integrated hyperspectral imaging and genome-wide association analysis platform provides spectral and genetic insights into the natural variation in rice. <i>Scientific Reports</i> , 2017 , 7, 4401	4.9	22
30	Genome-Wide Identification of SNAC1-Targeted Genes Involved in Drought Response in Rice. <i>Frontiers in Plant Science</i> , 2019 , 10, 982	6.2	21
29	Comprehensive sequence and expression profile analysis of PEX11 gene family in rice. <i>Gene</i> , 2008 , 412, 59-70	3.8	19
28	Functional analysis of the HD-Zip transcription factor genes Oshox12 and Oshox14 in rice. <i>PLoS ONE</i> , 2018 , 13, e0199248	3.7	15
27	Is Required for Formation of the Stigma and Style in Rice. <i>Plant Physiology</i> , 2019 , 180, 926-936	6.6	14
26	Systematic analysis of NPK1-like genes in rice reveals a stress-inducible gene cluster co-localized with a quantitative trait locus of drought resistance. <i>Molecular Genetics and Genomics</i> , 2008 , 280, 535-46 ^{3.1}		14
25	High-throughput phenotyping accelerates the dissection of the dynamic genetic architecture of plant growth and yield improvement in rapeseed. <i>Plant Biotechnology Journal</i> , 2020 , 18, 2345-2353	11.6	13
24	A hyperspectral imaging system for an accurate prediction of the above-ground biomass of individual rice plants. <i>Review of Scientific Instruments</i> , 2013 , 84, 095107	1.7	13
23	BIG regulates stomatal immunity and jasmonate production in Arabidopsis. <i>New Phytologist</i> , 2019 , 222, 335-348	9.8	12
22	and Redundantly Shape Rice Tiller Angle by Reducing Expression and Auxin Content. <i>Plant Physiology</i> , 2020 , 184, 1424-1437	6.6	11
21	OsARID3, an AT-rich Interaction Domain-containing protein, is required for shoot meristem development in rice. <i>Plant Journal</i> , 2015 , 83, 806-17	6.9	10
20	Systematic identification of X1-homologous genes reveals a family involved in stress responses in rice. <i>Plant Molecular Biology</i> , 2009 , 71, 483-96	4.6	10
19	Synergistic regulation of drought-responsive genes by transcription factor OsbZIP23 and histone modification in rice. <i>Journal of Integrative Plant Biology</i> , 2020 , 62, 723-729	8.3	10

18	Nondestructive 3D Image Analysis Pipeline to Extract Rice Grain Traits Using X-Ray Computed Tomography. <i>Plant Phenomics</i> , 2020 , 2020, 3414926	7	9
17	Using high-throughput multiple optical phenotyping to decipher the genetic architecture of maize drought tolerance. <i>Genome Biology</i> , 2021 , 22, 185	18.3	9
16	A lamin-like protein OsNMCP1 regulates drought resistance and root growth through chromatin accessibility modulation by interacting with a chromatin remodeller OsSWI3C in rice. <i>New Phytologist</i> , 2020 , 227, 65-83	9.8	8
15	Natural variation in the sequence of SNAC1 and its expression level polymorphism in rice Germplasms under drought stress. <i>Journal of Genetics and Genomics</i> , 2014 , 41, 609-12	4	6
14	Systematic identification and expression analysis of BREVIS RADIX-like homologous genes in rice. <i>Plant Science</i> , 2010 , 178, 183-191	5.3	6
13	A deep learning-integrated micro-CT image analysis pipeline for quantifying rice lodging resistance-related traits. <i>Plant Communications</i> , 2021 , 2, 100165	9	6
12	Combining UAV-RGB high-throughput field phenotyping and genome-wide association study to reveal genetic variation of rice germplasms in dynamic response to drought stress. <i>New Phytologist</i> , 2021 , 232, 440-455	9.8	5
11	Detecting quantitative trait loci for water use efficiency in rice using a recombinant inbred line population. <i>Science Bulletin</i> , 2011 , 56, 1481-1487		4
10	OsTMF attenuates cold tolerance by affecting cell wall properties in rice. <i>New Phytologist</i> , 2020 , 227, 498-512	9.8	3
9	Directional upgrading of brown planthopper resistance in an elite rice cultivar by precise introgression of two resistance genes using genomics-based breeding. <i>Plant Science</i> , 2019 , 288, 110211	5.3	3
8	Genetic Improvement of Drought Resistance in Rice 2015 , 73-102		3
7	A nondestructive method for estimating the total green leaf area of individual rice plants using multi-angle color images. <i>Journal of Innovative Optical Health Sciences</i> , 2015 , 08, 1550002	1.2	3
6	A FLASH pipeline for arrayed CRISPR library construction and the gene function discovery of rice receptor-like kinases. <i>Molecular Plant</i> , 2021 ,	14.4	3
5	Genetic analyses of lodging resistance and yield provide insights into post-Green-Revolution breeding in rice. <i>Plant Biotechnology Journal</i> , 2021 , 19, 814-829	11.6	3
4	Abiotic Stress Resistance 2013 , 193-215		1
3	A MITE variation-associated heat-inducible isoform of a heat-shock factor confers heat tolerance through regulation of JASMONATE ZIM-DOMAIN genes in rice.. <i>New Phytologist</i> , 2022 ,	9.8	1
2	Improvement of Stress Tolerance in Crops by Genetic Manipulation of ABA Metabolism, Signaling, and Regulation 2014 , 447-465		
1	Genome-wide association study revealed genetic variations of ABA sensitivity controlled by multiple stress-related genes in rice. <i>Stress Biology</i> , 2021 , 1, 1		

