Lizhong Xiong

List of Publications by Year in Descending Order

Source: https://exaly.com/author-pdf/7415337/lizhong-xiong-publications-by-year.pdf
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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	A MITE variation-associated heat-inducible isoform of a heat-shock factor confers heat tolerance through regulation of JASMONATE ZIM-DOMAIN genes in rice.. *New Phytologist*, **2022**,	9.8	1
106	Genome-wide association study revealed genetic variations of ABA sensitivity controlled by multiple stress-related genes in rice. *Stress Biology*, **2021**, 1, 1		
105	A FLASH pipeline for arrayed CRISPR library construction and the gene function discovery of rice receptor-like kinases. *Molecular Plant*, **2021**,	14.4	3
104	A deep learning-integrated micro-CT image analysis pipeline for quantifying rice lodging resistance-related traits. *Plant Communications*, **2021**, 2, 100165	9	6
103	Using high-throughput multiple optical phenotyping to decipher the genetic architecture of maize drought tolerance. *Genome Biology*, **2021**, 22, 185	18.3	9
102	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. *New Phytologist*, **2021**, 232, 440-455	9.8	5
101	Genetic analyses of lodging resistance and yield provide insights into post-Green-Revolution breeding in rice. *Plant Biotechnology Journal*, **2021**, 19, 814-829	11.6	3
100	High-throughput phenotyping accelerates the dissection of the dynamic genetic architecture of plant growth and yield improvement in rapeseed. *Plant Biotechnology Journal*, **2020**, 18, 2345-2353	11.6	13
99	OsTMF attenuates cold tolerance by affecting cell wall properties in rice. *New Phytologist*, **2020**, 227, 498-512	9.8	3
98	A lamin-like protein OsNMCP1 regulates drought resistance and root growth through chromatin accessibility modulation by interacting with a chromatin remodeller OsSWI3C in rice. *New Phytologist*, **2020**, 227, 65-83	9.8	8
97	Crop Phenomics and High-Throughput Phenotyping: Past Decades, Current Challenges, and Future Perspectives. *Molecular Plant*, **2020**, 13, 187-214	14.4	188
96	Nondestructive 3D Image Analysis Pipeline to Extract Rice Grain Traits Using X-Ray Computed Tomography. *Plant Phenomics*, **2020**, 2020, 3414926	7	9
95	and Redundantly Shape Rice Tiller Angle by Reducing Expression and Auxin Content. *Plant Physiology*, **2020**, 184, 1424-1437	6.6	11
94	Synergistic regulation of drought-responsive genes by transcription factor OsbZIP23 and histone modification in rice. *Journal of Integrative Plant Biology*, **2020**, 62, 723-729	8.3	10
93	Reversible Histone H2B Monoubiquitination Fine-Tunes Abscisic Acid Signaling and Drought Response in Rice. *Molecular Plant*, **2019**, 12, 263-277	14.4	22
92	Is Required for Formation of the Stigma and Style in Rice. *Plant Physiology*, **2019**, 180, 926-936	6.6	14
91	Directional upgrading of brown planthopper resistance in an elite rice cultivar by precise introgression of two resistance genes using genomics-based breeding. *Plant Science*, **2019**, 288, 110211	5.3	3

90	Genome-Wide Identification of SNAC1-Targeted Genes Involved in Drought Response in Rice. *Frontiers in Plant Science*, **2019**, 10, 982	6.2	21
89	BIG regulates stomatal immunity and jasmonate production in Arabidopsis. *New Phytologist*, **2019**, 222, 335-348	9.8	12
88	Combining high-throughput micro-CT-RGB phenotyping and genome-wide association study to dissect the genetic architecture of tiller growth in rice. *Journal of Experimental Botany*, **2019**, 70, 545-561	7	35
87	Genome-Wide Association Studies of Image Traits Reveal Genetic Architecture of Drought Resistance in Rice. *Molecular Plant*, **2018**, 11, 789-805	14.4	72
86	Integrative Regulation of Drought Escape through ABA-Dependent and -Independent Pathways in□Rice. *Molecular Plant*, **2018**, 11, 584-597	14.4	52
85	Novel Digital Features Discriminate Between Drought Resistant and Drought Sensitive Rice Under Controlled and Field Conditions. *Frontiers in Plant Science*, **2018**, 9, 492	6.2	25
84	Functional analysis of the HD-Zip transcription factor genes Oshox12 and Oshox14 in rice. *PLoS ONE*, **2018**, 13, e0199248	3.7	15
83	The OsMYB30 Transcription Factor Suppresses Cold Tolerance by Interacting with a JAZ Protein and Suppressing □Amylase Expression. *Plant Physiology*, **2017**, 173, 1475-1491	6.6	68
82	High-Throughput Phenotyping and QTL Mapping Reveals the Genetic Architecture of Maize Plant Growth. *Plant Physiology*, **2017**, 173, 1554-1564	6.6	133
81	Translational repression by a miniature inverted-repeat transposable element in the 3S untranslated region. *Nature Communications*, **2017**, 8, 14651	17.4	38
80	A high-throughput stereo-imaging system for quantifying rape leaf traits during the seedling stage. *Plant Methods*, **2017**, 13, 7	5.8	40
79	Genetic control of the root system in rice under normal and drought stress conditions by genome-wide association study. *PLoS Genetics*, **2017**, 13, e1006889	6	68
78	An integrated hyperspectral imaging and genome-wide association analysis platform provides spectral and genetic insights into the natural variation in rice. *Scientific Reports*, **2017**, 7, 4401	4.9	22
77	Panicle-SEG: a robust image segmentation method for rice panicles in the field based on deep learning and superpixel optimization. *Plant Methods*, **2017**, 13, 104	5.8	85
76	Co-overexpression of the Constitutively Active Form of OsbZIP46 and ABA-Activated Protein Kinase SAPK6 Improves Drought and Temperature Stress Resistance in Rice. *Frontiers in Plant Science*, **2017**, 8, 1102	6.2	32
75	OsJAZ1 Attenuates Drought Resistance by Regulating JA and ABA Signaling in Rice. *Frontiers in Plant Science*, **2017**, 8, 2108	6.2	68
74	Ghd2, a CONSTANS-like gene, confers drought sensitivity through regulation of senescence in rice. *Journal of Experimental Botany*, **2016**, 67, 5785-5798	7	46
73	Feedback Regulation of ABA Signaling and Biosynthesis by a bZIP Transcription Factor Targets Drought-Resistance-Related Genes. *Plant Physiology*, **2016**, 171, 2810-25	6.6	136

72	New insights into the genetic basis of natural chilling and cold shock tolerance in rice by genome-wide association analysis. *Plant, Cell and Environment*, **2016**, 39, 556-70	8.4	75
71	MODD Mediates Deactivation and Degradation of OsbZIP46 to Negatively Regulate ABA Signaling and Drought Resistance in Rice. *Plant Cell*, **2016**, 28, 2161-2177	11.6	78
70	Genome-wide association study of rice (Oryza sativa L.) leaf traits with a high-throughput leaf scorer. *Journal of Experimental Botany*, **2015**, 66, 5605-15	7	55
69	A stress-responsive NAC transcription factor SNAC3 confers heat and drought tolerance through modulation of reactive oxygen species in rice. *Journal of Experimental Botany*, **2015**, 66, 6803-17	7	227
68	Breeding signatures of rice improvement revealed by a genomic variation map from a large germplasm collection. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, E5411-9	11.5	116
67	GID1 modulates stomatal response and submergence tolerance involving abscisic acid and gibberellic acid signaling in rice. *Journal of Integrative Plant Biology*, **2015**, 57, 954-68	8.3	23
66	General mechanisms of drought response and their application in drought resistance improvement in plants. *Cellular and Molecular Life Sciences*, **2015**, 72, 673-89	10.3	481
65	OsARID3, an AT-rich Interaction Domain-containing protein, is required for shoot meristem development in rice. *Plant Journal*, **2015**, 83, 806-17	6.9	10
64	Genetic Improvement of Drought Resistance in Rice **2015**, 73-102		3
63	OsJAZ9 acts as a transcriptional regulator in jasmonate signaling and modulates salt stress tolerance in rice. *Plant Science*, **2015**, 232, 1-12	5.3	95
62	A nondestructive method for estimating the total green leaf area of individual rice plants using multi-angle color images. *Journal of Innovative Optical Health Sciences*, **2015**, 08, 1550002	1.2	3
61	A homolog of ETHYLENE OVERPRODUCER, OsETOL1, differentially modulates drought and submergence tolerance in rice. *Plant Journal*, **2014**, 78, 834-49	6.9	49
60	Genetic engineering and breeding of drought-resistant crops. *Annual Review of Plant Biology*, **2014**, 65, 715-41	30.7	387
59	Combining high-throughput phenotyping and genome-wide association studies to reveal natural genetic variation in rice. *Nature Communications*, **2014**, 5, 5087	17.4	316
58	Conserved miR164-targeted NAC genes negatively regulate drought resistance in rice. *Journal of Experimental Botany*, **2014**, 65, 2119-35	7	207
57	Improvement of Stress Tolerance in Crops by Genetic Manipulation of ABA Metabolism, Signaling, and Regulation **2014**, 447-465		
56	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. *Plant Physiology*, **2014**, 166, 2100-14	6.6	95
55	Natural variation in the sequence of SNAC1 and its expression level polymorphism in rice Germplasms under drought stress. *Journal of Genetics and Genomics*, **2014**, 41, 609-12	4	6

54	A special member of the rice SRO family, OsSRO1c, mediates responses to multiple abiotic stresses through interaction with various transcription factors. *Plant Molecular Biology*, **2014**, 84, 693-705	4.6	29
53	Carotenoid deficiency impairs ABA and IAA biosynthesis and differentially affects drought and cold tolerance in rice. *Plant Molecular Biology*, **2013**, 83, 475-88	4.6	94
52	Characterization of a purine permease family gene OsPUP7 involved in growth and development control in rice. *Journal of Integrative Plant Biology*, **2013**, 55, 1119-35	8.3	45
51	Mutant resources for the functional analysis of the rice genome. *Molecular Plant*, **2013**, 6, 596-604	14.4	84
50	Rice panicle length measuring system based on dual-camera imaging. *Computers and Electronics in Agriculture*, **2013**, 98, 158-165	6.5	22
49	Genome-wide profiling of histone H3K4-tri-methylation and gene expression in rice under drought stress. *Plant Molecular Biology*, **2013**, 81, 175-88	4.6	130
48	The SNAC1-targeted gene OsSRO1c modulates stomatal closure and oxidative stress tolerance by regulating hydrogen peroxide in rice. *Journal of Experimental Botany*, **2013**, 64, 569-83	7	127
47	Plant phenomics and high-throughput phenotyping: accelerating rice functional genomics using multidisciplinary technologies. *Current Opinion in Plant Biology*, **2013**, 16, 180-7	9.9	174
46	Genetic mechanisms conferring adaptation to submergence and drought in rice: simple or complex?. *Current Opinion in Plant Biology*, **2013**, 16, 196-204	9.9	79
45	Insight into differential responses of upland and paddy rice to drought stress by comparative expression profiling analysis. *International Journal of Molecular Sciences*, **2013**, 14, 5214-38	6.3	31
44	Endogenous auxin and jasmonic acid levels are differentially modulated by abiotic stresses in rice. *Frontiers in Plant Science*, **2013**, 4, 397	6.2	261
43	A hyperspectral imaging system for an accurate prediction of the above-ground biomass of individual rice plants. *Review of Scientific Instruments*, **2013**, 84, 095107	1.7	13
42	Putative megaenzyme DWA1 plays essential roles in drought resistance by regulating stress-induced wax deposition in rice. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 17790-5	11.5	72
41	A novel integrated method for large-scale detection, identification, and quantification of widely targeted metabolites: application in the study of rice metabolomics. *Molecular Plant*, **2013**, 6, 1769-80	14.4	532
40	Abiotic Stress Resistance **2013**, 193-215		1
39	An ornithine □-aminotransferase gene OsOAT confers drought and oxidative stress tolerance in rice. *Plant Science*, **2012**, 197, 59-69	5.3	94
38	A GH3 family member, OsGH3-2, modulates auxin and abscisic acid levels and differentially affects drought and cold tolerance in rice. *Journal of Experimental Botany*, **2012**, 63, 6467-80	7	201
37	Constitutive activation of transcription factor OsbZIP46 improves drought tolerance in rice. *Plant Physiology*, **2012**, 158, 1755-68	6.6	224

36	Gradual increase of miR156 regulates temporal expression changes of numerous genes during leaf development in rice. *Plant Physiology*, **2012**, 158, 1382-94	6.6	162
35	Identification of a cluster of PR4-like genes involved in stress responses in rice. *Journal of Plant Physiology*, **2011**, 168, 2212-24	3.6	48
34	Characterization of an inositol 1,3,4-trisphosphate 5/6-kinase gene that is essential for drought and salt stress responses in rice. *Plant Molecular Biology*, **2011**, 77, 547-63	4.6	48
33	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. *Theoretical and Applied Genetics*, **2011**, 123, 815-26	6	69
32	A structural view of the conserved domain of rice stress-responsive NAC1. *Protein and Cell*, **2011**, 2, 55-63	7.2	71
31	Detecting quantitative trait loci for water use efficiency in rice using a recombinant inbred line population. *Science Bulletin*, **2011**, 56, 1481-1487		4
30	Increased leaf angle1, a Raf-like MAPKKK that interacts with a nuclear protein family, regulates mechanical tissue formation in the Lamina joint of rice. *Plant Cell*, **2011**, 23, 4334-47	11.6	95
29	A Raf-like MAPKKK gene DSM1 mediates drought resistance through reactive oxygen species scavenging in rice. *Plant Physiology*, **2010**, 152, 876-90	6.6	258
28	Characterization of the beta-carotene hydroxylase gene DSM2 conferring drought and oxidative stress resistance by increasing xanthophylls and abscisic acid synthesis in rice. *Plant Physiology*, **2010**, 154, 1304-18	6.6	203
27	Systematic identification and expression analysis of BREVIS RADIX-like homologous genes in rice. *Plant Science*, **2010**, 178, 183-191	5.3	6
26	Systematic analysis of GT factor family of rice reveals a novel subfamily involved in stress responses. *Molecular Genetics and Genomics*, **2010**, 283, 157-69	3.1	57
25	Global expression profiling of rice microRNAs by one-tube stem-loop reverse transcription quantitative PCR revealed important roles of microRNAs in abiotic stress responses. *Molecular Genetics and Genomics*, **2010**, 284, 477-88	3.1	77
24	Genetic mapping of the rice ionome in leaves and grain: identification of QTLs for 17 elements including arsenic, cadmium, iron and selenium. *Plant and Soil*, **2010**, 329, 139-153	4.2	198
23	A homolog of human ski-interacting protein in rice positively regulates cell viability and stress tolerance. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 6410-5	11.5	117
22	Comprehensive expression profiling analysis of OsIAA gene family in developmental processes and in response to phytohormone and stress treatments. *Planta*, **2009**, 229, 577-91	4.7	117
21	Genome-wide identification of BURP domain-containing genes in rice reveals a gene family with diverse structures and responses to abiotic stresses. *Planta*, **2009**, 230, 149-63	4.7	49
20	Characterization of OsIAA1 gene, a member of rice Aux/IAA family involved in auxin and brassinosteroid hormone responses and plant morphogenesis. *Plant Molecular Biology*, **2009**, 70, 297-309	4.6	96
19	Characterization of Glossy1-homologous genes in rice involved in leaf wax accumulation and drought resistance. *Plant Molecular Biology*, **2009**, 70, 443-56	4.6	119

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18	Identification and expression profiling analysis of TIFY family genes involved in stress and phytohormone responses in rice. *Plant Molecular Biology*, **2009**, 71, 291-305	4.6	243
17	Systematic identification of X1-homologous genes reveals a family involved in stress responses in rice. *Plant Molecular Biology*, **2009**, 71, 483-96	4.6	10
16	Comprehensive sequence and expression profile analysis of PEX11 gene family in rice. *Gene*, **2008**, 412, 59-70	3.8	19
15	Characterization of OsbZIP23 as a key player of the basic leucine zipper transcription factor family for conferring abscisic acid sensitivity and salinity and drought tolerance in rice. *Plant Physiology*, **2008**, 148, 1938-52	6.6	451
14	Characterization of transcription factor gene SNAC2 conferring cold and salt tolerance in rice. *Plant Molecular Biology*, **2008**, 67, 169-81	4.6	479
13	Systematic analysis of NPK1-like genes in rice reveals a stress-inducible gene cluster co-localized with a quantitative trait locus of drought resistance. *Molecular Genetics and Genomics*, **2008**, 280, 535-46	3.1	14
12	Systematic sequence analysis and identification of tissue-specific or stress-responsive genes of NAC transcription factor family in rice. *Molecular Genetics and Genomics*, **2008**, 280, 547-63	3.1	328
11	Over-expression of a LEA gene in rice improves drought resistance under the field conditions. *Theoretical and Applied Genetics*, **2007**, 115, 35-46	6	384
10	Global genome expression analysis of rice in response to drought and high-salinity stresses in shoot, flag leaf, and panicle. *Plant Molecular Biology*, **2007**, 63, 591-608	4.6	227
9	Characterization of a stress responsive proteinase inhibitor gene with positive effect in improving drought resistance in rice. *Planta*, **2007**, 226, 73-85	4.7	89
8	Characterization of stress-responsive CIPK genes in rice for stress tolerance improvement. *Plant Physiology*, **2007**, 144, 1416-28	6.6	339
7	RMD: a rice mutant database for functional analysis of the rice genome. *Nucleic Acids Research*, **2006**, 34, D745-8	20.1	171
6	Genomic organization, differential expression, and interaction of SQUAMOSA promoter-binding-like transcription factors and microRNA156 in rice. *Plant Physiology*, **2006**, 142, 280-93	6.6	442
5	Genetic basis of drought resistance at reproductive stage in rice: separation of drought tolerance from drought avoidance. *Genetics*, **2006**, 172, 1213-28	4	292
4	Overexpressing a NAM, ATAF, and CUC (NAC) transcription factor enhances drought resistance and salt tolerance in rice. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 12987-92	11.5	1133
3	Establishment of a patterned GAL4-VP16 transactivation system for discovering gene function in rice. *Plant Journal*, **2006**, 46, 1059-72	6.9	29
2	Genetic analysis for drought resistance of rice at reproductive stage in field with different types of soil. *Theoretical and Applied Genetics*, **2005**, 111, 1127-36	6	89
1	Disease resistance and abiotic stress tolerance in rice are inversely modulated by an abscisic acid-inducible mitogen-activated protein kinase. *Plant Cell*, **2003**, 15, 745-59	11.6	624