

# Xianghua Li

## List of Publications by Year in descending order

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100  
papers

13,865  
citations

34100

52  
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32838

100  
g-index

102  
all docs

102  
docs citations

102  
times ranked

11110  
citing authors

#	ARTICLE	IF	CITATIONS
1	Natural variation in <i>Ghd7</i> is an important regulator of heading date and yield potential in rice. <i>Nature Genetics</i> , 2008, 40, 761-767.	21.4	1,666
2	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, 12987-12992.	7.1	1,371
3	Natural variation in <i>GS5</i> plays an important role in regulating grain size and yield in rice. <i>Nature Genetics</i> , 2011, 43, 1266-1269.	21.4	821
4	Activation of the Indole-3-Acetic Acid- <i>Amido Synthetase</i> GH3-8 Suppresses Expansin Expression and Promotes Salicylate- and Jasmonate-Independent Basal Immunity in Rice. <i>Plant Cell</i> , 2008, 20, 228-240.	6.6	513
5	<i>Xa26</i> , a gene conferring resistance to <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> in rice, encodes an LRR receptor kinase-like protein. <i>Plant Journal</i> , 2004, 37, 517-527.	5.7	446
6	<i>OsWRKY13</i> Mediates Rice Disease Resistance by Regulating Defense-Related Genes in Salicylate- and Jasmonate-Dependent Signaling. <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 492-499.	2.6	409
7	A stress-responsive NAC transcription factor <i>SNAC3</i> confers heat and drought tolerance through modulation of reactive oxygen species in rice. <i>Journal of Experimental Botany</i> , 2015, 66, 6803-6817.	4.8	353
8	A Raf-Like MAPKKK Gene <i>DSM1</i> Mediates Drought Resistance through Reactive Oxygen Species Scavenging in Rice. <i>Plant Physiology</i> , 2010, 152, 876-890.	4.8	340
9	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.	3.9	336
10	Constitutive Activation of Transcription Factor <i>OsZIP46</i> Improves Drought Tolerance in Rice. <i>Plant Physiology</i> , 2012, 158, 1755-1768.	4.8	305
11	<i>Chalk5</i> encodes a vacuolar H <sup>+</sup> -translocating pyrophosphatase influencing grain chalkiness in rice. <i>Nature Genetics</i> , 2014, 46, 398-404.	21.4	281
12	A Killer-Protector System Regulates Both Hybrid Sterility and Segregation Distortion in Rice. <i>Science</i> , 2012, 337, 1336-1340.	12.6	263
13	A triallelic system of <i>S5</i> is a major regulator of the reproductive barrier and compatibility of indica-japonica hybrids in rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 11436-11441.	7.1	257
14	A Pair of Allelic WRKY Genes Play Opposite Roles in Rice-Bacteria Interactions. <i>Plant Physiology</i> , 2009, 151, 936-948.	4.8	251
15	<i>PMS1T</i> , producing phased small-interfering RNAs, regulates photoperiod-sensitive male sterility in rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 15144-15149.	7.1	234
16	Coordinated regulation of vegetative and reproductive branching in rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 15504-15509.	7.1	218
17	The Bacterial Pathogen <i>Xanthomonas oryzae</i> Overcomes Rice Defenses by Regulating Host Copper Redistribution. <i>Plant Cell</i> , 2010, 22, 3164-3176.	6.6	214
18	<i>OsAAP6</i> functions as an important regulator of grain protein content and nutritional quality in rice. <i>Nature Communications</i> , 2014, 5, 4847.	12.8	214

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19	A paralog of the MtN3/saliva family recessively confers race-specific resistance to <i>Xanthomonas oryzae</i> in rice. <i>Plant, Cell and Environment</i> , 2011, 34, 1958-1969.	5.7	213
20	A convenient method for simultaneous quantification of multiple phytohormones and metabolites: application in study of rice-bacterium interaction. <i>Plant Methods</i> , 2012, 8, 2.	4.3	199
21	Grain Number, Plant Height, and Heading Date Is a Central Regulator of Growth, Development, and Stress Response. <i>Plant Physiology</i> , 2014, 164, 735-747.	4.8	198
22	A G-protein pathway determines grain size in rice. <i>Nature Communications</i> , 2018, 9, 851.	12.8	195
23	Development of insect-resistant transgenic indica rice with a synthetic cry1C* gene. <i>Molecular Breeding</i> , 2006, 18, 1-10.	2.1	192
24	Improvement of multiple agronomic traits by a disease resistance gene via cell wall reinforcement. <i>Nature Plants</i> , 2017, 3, 17009.	9.3	179
25	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.	7.1	165
26	Xa3, conferring resistance for rice bacterial blight and encoding a receptor kinase-like protein, is the same as Xa26. <i>Theoretical and Applied Genetics</i> , 2006, 113, 1347-1355.	3.6	161
27	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, 2100-2114.	4.8	142
28	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, 556-570.	5.7	141
29	MODD Mediates Deactivation and Degradation of OsbZIP46 to Negatively Regulate ABA Signaling and Drought Resistance in Rice. <i>Plant Cell</i> , 2016, 28, 2161-2177.	6.6	140
30	The OsMYB30 Transcription Factor Suppresses Cold Tolerance by Interacting with a JAZ Protein and Suppressing $\alpha$ -Amylase Expression. <i>Plant Physiology</i> , 2017, 173, 1475-1491.	4.8	136
31	The Expression Pattern of a Rice Disease Resistance Gene Xa3/Xa26 Is Differentially Regulated by the Genetic Backgrounds and Developmental Stages That Influence Its Function. <i>Genetics</i> , 2007, 177, 523-533.	2.9	133
32	Rice Gene Network Inferred from Expression Profiling of Plants Overexpressing OsWRKY13, a Positive Regulator of Disease Resistance. <i>Molecular Plant</i> , 2008, 1, 538-551.	8.3	131
33	The WRKY45-2 WRKY13 WRKY42 Transcriptional Regulatory Cascade Is Required for Rice Resistance to Fungal Pathogen. <i>Plant Physiology</i> , 2015, 167, 1087-1099.	4.8	126
34	A CCCH-Type Zinc Finger Nucleic Acid-Binding Protein Quantitatively Confers Resistance against Rice Bacterial Blight Disease. <i>Plant Physiology</i> , 2012, 158, 876-889.	4.8	122
35	MAPK kinase 10.2 promotes disease resistance and drought tolerance by activating different MAPKs in rice. <i>Plant Journal</i> , 2017, 92, 557-570.	5.7	122
36	Differential expression of GS5 regulates grain size in rice. <i>Journal of Experimental Botany</i> , 2015, 66, 2611-2623.	4.8	119

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37	OsEDR1 negatively regulates rice bacterial resistance via activation of ethylene biosynthesis. <i>Plant, Cell and Environment</i> , 2011, 34, 179-191.	5.7	117
38	A Rice Gene of De Novo Origin Negatively Regulates Pathogen-Induced Defense Response. <i>PLoS ONE</i> , 2009, 4, e4603.	2.5	114
39	Integrative Regulation of Drought Escape through ABA-Dependent and -Independent Pathways in Rice. <i>Molecular Plant</i> , 2018, 11, 584-597.	8.3	112
40	A host basal transcription factor is a key component for infection of rice by TALE-carrying bacteria. <i>ELife</i> , 2016, 5, .	6.0	108
41	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.	3.5	107
42	Rice WRKY13 Regulates Cross Talk between Abiotic and Biotic Stress Signaling Pathways by Selective Binding to Different cis-Elements. <i>Plant Physiology</i> , 2013, 163, 1868-1882.	4.8	106
43	Mitogen-activated protein kinase OsMPK6 negatively regulates rice disease resistance to bacterial pathogens. <i>Planta</i> , 2007, 226, 953-960.	3.2	100
44	Opposite functions of a rice mitogen-activated protein kinase during the process of resistance against <i>Xanthomonas oryzae</i> . <i>Plant Journal</i> , 2010, 64, no-no.	5.7	94
45	Dual Function of Rice OsDR8 Gene in Disease Resistance and Thiamine Accumulation. <i>Plant Molecular Biology</i> , 2006, 60, 437-449.	3.9	92
46	Pathogen-Induced Expressional Loss of Function is the Key Factor in Race-Specific Bacterial Resistance Conferred by a Recessive R Gene xa13 in Rice. <i>Plant and Cell Physiology</i> , 2009, 50, 947-955.	3.1	90
47	Overexpression of OsSWEET5 in Rice Causes Growth Retardation and Precocious Senescence. <i>PLoS ONE</i> , 2014, 9, e94210.	2.5	84
48	<i>Ghd2</i> , a <i>CONSTANS</i> -like gene, confers drought sensitivity through regulation of senescence in rice. <i>Journal of Experimental Botany</i> , 2016, 67, 5785-5798.	4.8	82
49	Transposon-derived small RNA is responsible for modified function of WRKY45 locus. <i>Nature Plants</i> , 2016, 2, 16016.	9.3	79
50	The QTL controlling amino acid content in grains of rice ( <i>Oryza sativa</i> ) are co-localized with the regions involved in the amino acid metabolism pathway. <i>Molecular Breeding</i> , 2007, 21, 127-137.	2.1	69
51	Genome-wide Association Analyses Reveal the Genetic Basis of Stigma Exsertion in Rice. <i>Molecular Plant</i> , 2017, 10, 634-644.	8.3	66
52	Translational repression by a miniature inverted-repeat transposable element in the 3' untranslated region. <i>Nature Communications</i> , 2017, 8, 14651.	12.8	65
53	The RING-Finger Ubiquitin Ligase HAF1 Mediates Heading date 1 Degradation during Photoperiodic Flowering in Rice. <i>Plant Cell</i> , 2015, 27, 2455-2468.	6.6	58
54	Rice <i>OsPAD4</i> functions differently from <i>Arabidopsis AtPAD4</i> in host-pathogen interactions. <i>Plant Journal</i> , 2014, 78, 619-631.	5.7	54

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55	Genetic Basis of Variation in Rice Seed Storage Protein (Albumin, Globulin, Prolamin, and Glutelin) Content Revealed by Genome-Wide Association Analysis. <i>Frontiers in Plant Science</i> , 2018, 9, 612.	3.6	53
56	Reversible Histone H2B Monoubiquitination Fine-Tunes Abscisic Acid Signaling and Drought Response in Rice. <i>Molecular Plant</i> , 2019, 12, 263-277.	8.3	53
57	<i>OsHOX1</i> and <i>OsHOX28</i> Redundantly Shape Rice Tiller Angle by Reducing <i>HSFA2D</i> Expression and Auxin Content. <i>Plant Physiology</i> , 2020, 184, 1424-1437.	4.8	44
58	The origin of <i>Wx<sup>la</sup></i> provides new insights into the improvement of grain quality in rice. <i>Journal of Integrative Plant Biology</i> , 2021, 63, 878-888.	8.5	43
59	Functional analysis of Xa3/Xa26 family members in rice resistance to <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> . <i>Theoretical and Applied Genetics</i> , 2007, 115, 887-895.	3.6	41
60	Natural variation in <i>WHITE-CORE RATE 1</i> regulates redox homeostasis in rice endosperm to affect grain quality. <i>Plant Cell</i> , 2022, 34, 1912-1932.	6.6	41
61	Dissection of the factors affecting development-controlled and race-specific disease resistance conferred by leucine-rich repeat receptor kinase-type R genes in rice. <i>Theoretical and Applied Genetics</i> , 2009, 119, 231-239.	3.6	38
62	Transcriptome-based analysis of mitogen-activated protein kinase cascades in the rice response to <i>Xanthomonas oryzae</i> infection. <i>Rice</i> , 2015, 8, 4.	4.0	36
63	Bract suppression regulated by the miR156/529-SPLs-NL1-PLA1 module is required for the transition from vegetative to reproductive branching in rice. <i>Molecular Plant</i> , 2021, 14, 1168-1184.	8.3	35
64	Three representative inter and intra-subspecific crosses reveal the genetic architecture of reproductive isolation in rice. <i>Plant Journal</i> , 2017, 92, 349-362.	5.7	33
65	Epistasis and complementary gene action adequately account for the genetic bases of transgressive segregation of kilo-grain weight in rice. <i>Euphytica</i> , 2011, 180, 261-271.	1.2	28
66	A Cytosolic Triosephosphate Isomerase Is a Key Component in XA3/XA26-Mediated Resistance. <i>Plant Physiology</i> , 2018, 178, 923-935.	4.8	28
67	Multiple Alleles Encoding Atypical NLRs with Unique Central Tandem Repeats in Rice Confer Resistance to <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> . <i>Plant Communications</i> , 2020, 1, 100088.	7.7	28
68	Transcriptomic analysis of rice responses to low phosphorus stress. <i>Science Bulletin</i> , 2010, 55, 251-258.	1.7	25
69	Jasmonic Acid-Involved OsEDS1 Signaling in Rice-Bacteria Interactions. <i>Rice</i> , 2019, 12, 25.	4.0	25
70	A Conserved Basal Transcription Factor Is Required for the Function of Diverse TAL Effectors in Multiple Plant Hosts. <i>Frontiers in Plant Science</i> , 2017, 8, 1919.	3.6	23
71	Processes Underlying a Reproductive Barrier in <i>indica</i> - <i>japonica</i> Rice Hybrids Revealed by Transcriptome Analysis. <i>Plant Physiology</i> , 2017, 174, 1683-1696.	4.8	22
72	Two VQ Proteins are Substrates of the OsMPKK6-OsMPK4 Cascade in Rice Defense Against Bacterial Blight. <i>Rice</i> , 2021, 14, 39.	4.0	22

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73	Characterization of a disease susceptibility locus for exploring an efficient way to improve rice resistance against bacterial blight. <i>Science China Life Sciences</i> , 2017, 60, 298-306.	4.9	21
74	Small RNAs and Gene Network in a Durable Disease Resistance Gene-Mediated Defense Responses in Rice. <i>PLoS ONE</i> , 2015, 10, e0137360.	2.5	20
75	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.	7.3	20
76	The group I GH3 family genes encoding JA-Ile synthetase act as positive regulator in the resistance of rice to <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> . <i>Biochemical and Biophysical Research Communications</i> , 2019, 508, 1062-1066.	2.1	19
77	Origination and Establishment of a Trigenic Reproductive Isolation System in Rice. <i>Molecular Plant</i> , 2016, 9, 1542-1545.	8.3	18
78	OsTMF attenuates cold tolerance by affecting cell wall properties in rice. <i>New Phytologist</i> , 2020, 227, 498-512.	7.3	18
79	Genetic architecture and key genes controlling the diversity of oil composition in rice grains. <i>Molecular Plant</i> , 2021, 14, 456-469.	8.3	18
80	Identification of genes contributing to quantitative disease resistance in rice. <i>Science China Life Sciences</i> , 2010, 53, 1263-1273.	4.9	17
81	The rice Raf-like MAPKKK OsILA1 confers broad-spectrum resistance to bacterial blight by suppressing the OsMAPKK4-OsMAPK6 cascade. <i>Journal of Integrative Plant Biology</i> , 2021, 63, 1815-1842.	8.5	16
82	Comparison of quantitative trait loci for 1,000-grain weight and spikelets per panicle across three connected rice populations. <i>Euphytica</i> , 2010, 175, 383-394.	1.2	15
83	OsARID3, an AT-rich Interaction Domain-containing protein, is required for shoot meristem development in rice. <i>Plant Journal</i> , 2015, 83, 806-817.	5.7	15
84	Exploring the mechanism and efficient use of a durable gene-mediated resistance to bacterial blight disease in rice. <i>Molecular Breeding</i> , 2018, 38, 1.	2.1	14
85	Dominant and Recessive Major R Genes Lead to Different Types of Host Cell Death During Resistance to <i>Xanthomonas oryzae</i> in Rice. <i>Frontiers in Plant Science</i> , 2018, 9, 1711.	3.6	13
86	A MITE variation-associated heat-inducible isoform of a heat shock factor confers heat tolerance through regulation of <i>JASMONATE ZIMEDOMAIN</i> genes in rice. <i>New Phytologist</i> , 2022, 234, 1315-1331.	7.3	13
87	Two Different Transcripts of a LAMMER Kinase Gene Play Opposite Roles in Disease Resistance. <i>Plant Physiology</i> , 2016, 172, 1959-1972.	4.8	12
88	Artificial Selection in Domestication and Breeding Prevents Speciation in Rice. <i>Molecular Plant</i> , 2020, 13, 650-657.	8.3	12
89	Hd3a and OsFD1 negatively regulate rice resistance to <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> and <i>Xanthomonas oryzae</i> pv. <i>oryzicola</i> . <i>Biochemical and Biophysical Research Communications</i> , 2019, 513, 775-780.	2.1	10
90	Autophagy-Like Cell Death Regulates Hydrogen Peroxide and Calcium Ion Distribution in Xa3/Xa26-Mediated Resistance to <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 194.	4.1	10

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91	Different Cell Wall-Degradation Ability Leads to Tissue-Specificity between <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> and <i>Xanthomonas oryzae</i> pv. <i>oryzicola</i> . <i>Pathogens</i> , 2020, 9, 187.	2.8	10
92	FLOURY ENDOSPERM19 encoding a class I glutamine amidotransferase affects grain quality in rice. <i>Molecular Breeding</i> , 2021, 41, 1.	2.1	10
93	The host basal transcription factor IIA subunits coordinate for facilitating infection of TALEs-carrying bacterial pathogens in rice. <i>Plant Science</i> , 2019, 284, 48-56.	3.6	8
94	Expressional and Biochemical Characterization of Rice Disease Resistance Gene Xa3/Xa26 Family. <i>Journal of Integrative Plant Biology</i> , 2007, 49, 852-862.	8.5	7
95	Up- and Down-regulated Expression of OsCPK25/26 Results in Increased Number of Stamens in Rice. <i>Plant Molecular Biology Reporter</i> , 2014, 32, 1114-1128.	1.8	7
96	OsVQ1 links rice immunity and flowering via interaction with a mitogen-activated protein kinase OsMPK6. <i>Plant Cell Reports</i> , 2021, 40, 1989-1999.	5.6	7
97	Overexpression of a fruit-weight 2.2-like gene OsFWL5 improves rice resistance. <i>Rice</i> , 2019, 12, 51.	4.0	5
98	Fine mapping of qWCR7, a grain chalkiness QTL in rice. <i>Molecular Breeding</i> , 2021, 41, 1.	2.1	3
99	Fine Mapping of qWCR4, a Rice Chalkiness QTL Affecting Yield and Quality. <i>Agronomy</i> , 2022, 12, 706.	3.0	3
100	Rapid genome evolution in Pms1 region of rice revealed by comparative sequence analysis. <i>Science Bulletin</i> , 2007, 52, 912-921.	1.7	2