Shiping Wang

List of Publications by Year
in descending order

99 papers	10,022 citations	39113 52 h-index	40945 97 g-index
101 all docs	101 docs citations	101 times ranked	9272 citing authors

#	Article	IF	Citations
1	An MKP-MAPK protein phosphorylation cascade controls vascular immunity in plants. Science Advances, 2022, 8, eabg8723.	4.7	35
2	OsMAPK6 phosphorylates a zinc finger protein OsLIC to promote downstream <i>OsWRKY30</i> for rice resistance to bacterial blight and leaf streak. Journal of Integrative Plant Biology, 2022, 64, 1116-1130.	4.1	10
3	miR395-regulated sulfate metabolism exploits pathogen sensitivity to sulfate to boost immunity in rice. Molecular Plant, 2022, 15, 671-688.	3.9	31
4	Pathogen-inducible OsMPKK10.2-OsMPK6 cascade phosphorylates the Raf-like kinase OsEDR1 and inhibits its scaffold function to promote rice disease resistance. Molecular Plant, 2021, 14, 620-632.	3.9	39
5	Two VQ Proteins are Substrates of the OsMPKK6-OsMPK4 Cascade in Rice Defense Against Bacterial Blight. Rice, 2021, 14, 39.	1.7	22
6	OsVQ1 links rice immunity and flowering via interaction with a mitogen-activated protein kinase OsMPK6. Plant Cell Reports, 2021, 40, 1989-1999.	2.8	7
7	The rice Rafâ€like MAPKKK OsILA1 confers broadâ€spectrum resistance to bacterial blight by suppressing the OsMAPKK4â€"OsMAPK6 cascade. Journal of Integrative Plant Biology, 2021, 63, 1815-1842.	4.1	16
8	Knock out of transcription factor <i>WRKY53</i> thickens sclerenchyma cell walls, confers bacterial blight resistance. Plant Physiology, 2021, 187, 1746-1761.	2.3	42
9	OsWRKY53 Promotes Abscisic Acid Accumulation to Accelerate Leaf Senescence and Inhibit Seed Germination by Downregulating Abscisic Acid Catabolic Genes in Rice. Frontiers in Plant Science, 2021, 12, 816156.	1.7	15
10	ARGONAUTE2 Enhances Grain Length and Salt Tolerance by Activating <i>BIG GRAIN3</i> to Modulate Cytokinin Distribution in Rice. Plant Cell, 2020, 32, 2292-2306.	3.1	91
11	Multiple Alleles Encoding Atypical NLRs with Unique Central Tandem Repeats in Rice Confer Resistance to Xanthomonas oryzae pv. oryzae. Plant Communications, 2020, 1, 100088.	3.6	28
12	The versatile functions of OsALDH2B1 provide a genic basis for growthâ€"defense trade-offs in rice. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 3867-3873.	3.3	52
13	An update on molecular mechanism of disease resistance genes and their application for genetic improvement of rice. Molecular Breeding, 2019, 39, 1.	1.0	18
14	Jasmonic Acid-Involved OsEDS1 Signaling in Rice-Bacteria Interactions. Rice, 2019, 12, 25.	1.7	25
15	Overexpression a â€œfruit-weight 2.2-likeâ€•gene OsFWL5 improves rice resistance. Rice, 2019, 12, 51.	1.7	5
16	The host basal transcription factor IIA subunits coordinate for facilitating infection of TALEs-carrying bacterial pathogens in rice. Plant Science, 2019, 284, 48-56.	1.7	8
17	Hd3a and OsFD1 negatively regulate rice resistance to Xanthomonas oryzae pv. oryzae and Xanthomonas oryzae pv. oryzicola. Biochemical and Biophysical Research Communications, 2019, 513, 775-780.	1.0	10
18	The group I GH3 family genes encoding JA-Ile synthetase act as positive regulator in the resistance of rice to Xanthomonas oryzae pv. oryzae. Biochemical and Biophysical Research Communications, 2019, 508, 1062-1066.	1.0	19

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19	TALEâ€carrying bacterial pathogens trap host nuclear import receptors for facilitation of infection of rice. Molecular Plant Pathology, 2019, 20, 519-532.	2.0	31
20	Exploring the mechanism and efficient use of a durable gene-mediated resistance to bacterial blight disease in rice. Molecular Breeding, 2018, 38, 1.	1.0	14
21	Xanthomonas TAL effectors hijack host basal transcription factor IIA Î± and Î³ subunits for invasion. Biochemical and Biophysical Research Communications, 2018, 496, 608-613.	1.0	11
22	Dominant and Recessive Major R Genes Lead to Different Types of Host Cell Death During Resistance to Xanthomonas oryzae in Rice. Frontiers in Plant Science, 2018, 9, 1711.	1.7	13
23	A Cytosolic Triosephosphate Isomerase Is a Key Component in XA3/XA26-Mediated Resistance. Plant Physiology, 2018, 178, 923-935.	2.3	28
24	Improvement of multiple agronomic traits by a disease resistance gene via cell wall reinforcement. Nature Plants, 2017, 3, 17009.	4.7	179
25	Characterization of a disease susceptibility locus for exploring an efficient way to improve rice resistance against bacterial blight. Science China Life Sciences, 2017, 60, 298-306.	2.3	21
26	uORF-mediated translation allows engineered plant disease resistance without fitness costs. Nature, 2017, 545, 491-494.	13.7	300
27	MAPK kinase 10.2 promotes disease resistance and drought tolerance by activating different MAPKs in rice. Plant Journal, 2017, 92, 557-570.	2.8	122
28	Advances in understanding broadâ€spectrum resistance to pathogens in rice. Plant Journal, 2017, 90, 738-748.	2.8	85
29	A Conserved Basal Transcription Factor Is Required for the Function of Diverse TAL Effectors in Multiple Plant Hosts. Frontiers in Plant Science, 2017, 8, 1919.	1.7	23
30	Two Different Transcripts of a LAMMER Kinase Gene Play Opposite Roles in Disease Resistance. Plant Physiology, 2016, 172, 1959-1972.	2.3	12
31	Transposon-derived small RNA is responsible for modified function of WRKY45 locus. Nature Plants, 2016, 2, 16016.	4.7	79
32	A host basal transcription factor is a key component for infection of rice by TALE-carrying bacteria. ELife, 2016, 5, .	2.8	108
33	Small RNAs and Gene Network in a Durable Disease Resistance Geneâ€"Mediated Defense Responses in Rice. PLoS ONE, 2015, 10, e0137360.	1.1	20
34	Transcriptome-based analysis of mitogen-activated protein kinase cascades in the rice response to Xanthomonas oryzae infection. Rice, 2015, 8, 4.	1.7	36
35	The WRKY45-2 WRKY13 WRKY42 Transcriptional Regulatory Cascade Is Required for Rice Resistance to Fungal Pathogen Â. Plant Physiology, 2015, 167, 1087-1099.	2.3	126
36	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.	3.3	165

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37	Multiple phytohormones and phytoalexins are involved in disease resistance to <i>Magnaporthe oryzae</i> invaded from roots in rice. Physiologia Plantarum, 2014, 152, 486-500.	2.6	93
38	Rice <scp>O</scp>s<i><scp>PAD</scp>4</i> functions differently from <scp>A</scp>rabidopsis <scp>A</scp>t<i><scp>PAD</scp>4</i> in hostâ€pathogen interactions. Plant Journal, 2014, 78, 619-631.	2.8	54
39	Comprehensive analysis of VQ motif-containing gene expression in rice defense responses to three pathogens. Plant Cell Reports, 2014, 33, 1493-1505.	2.8	46
40	Rice <i>MtN3/saliva/SWEET</i> gene family: Evolution, expression profiling, and sugar transport. Journal of Integrative Plant Biology, 2014, 56, 559-570.	4.1	71
41	WRKY-Type Transcription Factors: a Significant Factor in Rice-Pathogen Interactions. Scientia Sinica Vitae, 2014, 44, 784-793.	0.1	12
42	Rice versus Xanthomonas oryzae pv. oryzae: a unique pathosystem. Current Opinion in Plant Biology, 2013, 16, 188-195.	3.5	158
43	Rice MtN3/Saliva/SWEET Family Genes and Their Homologs in Cellular Organisms. Molecular Plant, 2013, 6, 665-674.	3.9	186
44	Rice WRKY13 Regulates Cross Talk between Abiotic and Biotic Stress Signaling Pathways by Selective Binding to Different cis-Elements Â Â Â. Plant Physiology, 2013, 163, 1868-1882.	2.3	106
45	Disease Resistance. , 2013, , 161-175.		8
46	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, 6467-6480.	2.4	291
47	A CCCH-Type Zinc Finger Nucleic Acid-Binding Protein Quantitatively Confers Resistance against Rice Bacterial Blight Disease. Plant Physiology, 2012, 158, 876-889.	2.3	122
48	Toward an understanding of the molecular basis of quantitative disease resistance in rice. Journal of Biotechnology, 2012, 159, 283-290.	1.9	41
49	A convenient method for simultaneous quantification of multiple phytohormones and metabolites: application in study of rice-bacterium interaction. Plant Methods, 2012, 8, 2.	1.9	199
50	Pathogen-Responsive cis-Elements. , 2012, , 363-378.		2
51	OsWRKY45 alleles play different roles in abscisic acid signalling and salt stress tolerance but similar roles in drought and cold tolerance in rice. Journal of Experimental Botany, 2011, 62, 4863-4874.	2.4	228
52	Manipulating Broad-Spectrum Disease Resistance by Suppressing Pathogen-Induced Auxin Accumulation in Rice Â Â Â. Plant Physiology, 2011, 155, 589-602.	2.3	220
53	Insights into Auxin Signaling in Plant?Pathogen Interactions. Frontiers in Plant Science, 2011, 2, 74.	1.7	194
54	OsEDR1 negatively regulates rice bacterial resistance via activation of ethylene biosynthesis. Plant, Cell and Environment, 2011, 34, 179-191.	2.8	117

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55	A paralog of the MtN3/saliva family recessively confers raceâ€specific resistance to <i>Xanthomonas oryzae</i> in rice. Plant, Cell and Environment, 2011, 34, 1958-1969.	2.8	213
56	A pair of orthologs of a leucine-rich repeat receptor kinase-like disease resistance gene family regulates rice response to raised temperature. BMC Plant Biology, 2011, 11, 160.	1.6	11
57	Molecular and functional analyses of COPT/Ctr-type copper transporter-like gene family in rice. BMC Plant Biology, 2011, 11, 69.	1.6	146
58	Characterization of Xanthomonas oryzae-Responsive cis-Acting Element in the Promoter of Rice Race-Specific Susceptibility Gene Xa13. Molecular Plant, 2011, 4, 300-309.	3.9	56
59	Rice <i>GH3</i> gene family. Plant Signaling and Behavior, 2011, 6, 570-574.	1.2	56
60	Identification of genes contributing to quantitative disease resistance in rice. Science China Life Sciences, 2010, 53, 1263-1273.	2.3	17
61	Transcriptomic analysis of rice responses to low phosphorus stress. Science Bulletin, 2010, 55, 251-258.	1.7	25
62	Broad-spectrum and durability: understanding of quantitative disease resistance. Current Opinion in Plant Biology, 2010, 13, 181-185.	3.5	273
63	Promoter elements of rice susceptibility genes are bound and activated by specific TAL effectors from the bacterial blight pathogen, <i>Xanthomonas oryzae</i> pv<i>. oryzae</i>. New Phytologist, 2010, 187, 1048-1057.	3.5	169
64	Opposite functions of a rice mitogen-activated protein kinase during the process of resistance against Xanthomonas oryzae. Plant Journal, 2010, 64, no-no.	2.8	94
65	The Bacterial Pathogen <i>Xanthomonas oryzae</i> Overcomes Rice Defenses by Regulating Host Copper Redistribution Â. Plant Cell, 2010, 22, 3164-3176.	3.1	214
66	Modulating plant hormones by enzyme action. Plant Signaling and Behavior, 2010, 5, 1607-1612.	1.2	78
67	A Rice Gene of De Novo Origin Negatively Regulates Pathogen-Induced Defense Response. PLoS ONE, 2009, 4, e4603.	1.1	114
68	A Pair of Allelic WRKY Genes Play Opposite Roles in Rice-Bacteria Interactions Â Â Â. Plant Physiology, 2009, 151, 936-948.	2.3	251
69	Pathogen-Induced Expressional Loss of Function is the Key Factor in Race-Specific Bacterial Resistance Conferred by a Recessive R Gene xa13 in Rice. Plant and Cell Physiology, 2009, 50, 947-955.	1.5	90
70	Exploring transcriptional signalling mediated by OsWRKY13, a potential regulator of multiple physiological processes in rice. BMC Plant Biology, 2009, 9, 74.	1.6	68
71	Dissection of the factors affecting development-controlled and race-specific disease resistance conferred by leucine-rich repeat receptor kinase-type R genes in rice. Theoretical and Applied Genetics, 2009, 119, 231-239.	1.8	38
72	Molecular analyses of the rice tubby-like protein gene family and their response to bacterial infection. Plant Cell Reports, 2009, 28, 113-121.	2.8	31

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73	Multiple gene loci affecting genetic background-controlled disease resistance conferred by R gene Xa3/Xa26 in rice. Theoretical and Applied Genetics, 2009, 120, 127-138.	1.8	25
74	Identification of novel pathogenâ€responsive <i>cis</i>â€elements and their binding proteins in the promoter of <i>OsWRKY13</i>, a gene regulating rice disease resistance. Plant, Cell and Environment, 2008, 31, 86-96.	2.8	110
75	Fine genetic mapping of xa24, a recessive gene for resistance against Xanthomonas oryzae pv. oryzae in rice. Theoretical and Applied Genetics, 2008, 118, 185-191.	1.8	21
76	Activation of the Indole-3-Acetic Acidâ€“Amido Synthetase GH3-8 Suppresses Expansin Expression and Promotes Salicylate- and Jasmonate-Independent Basal Immunity in Rice. Plant Cell, 2008, 20, 228-240.	3.1	513
77	Rice Gene Network Inferred from Expression Profiling of Plants Overexpressing OsWRKY13, a Positive Regulator of Disease Resistance. Molecular Plant, 2008, 1, 538-551.	3.9	52
78	Rice Gene Network Inferred from Expression Profiling of Plants Overexpressing OsWRKY13, a Positive Regulator of Disease Resistance. Molecular Plant, 2008, 1, 538-551.	3.9	131
79	OsWRKY13 Mediates Rice Disease Resistance by Regulating Defense-Related Genes in Salicylate- and Jasmonate-Dependent Signaling. Molecular Plant-Microbe Interactions, 2007, 20, 492-499.	1.4	409
80	The Expression Pattern of a Rice Disease Resistance Gene <i>Xa3/Xa26</i> Is Differentially Regulated by the Genetic Backgrounds and Developmental Stages That Influence Its Function. Genetics, 2007, 177, 523-533.	1.2	133
81	Expressional and Biochemical Characterization of Rice Disease Resistance Gene Xa3/Xa26 Family. Journal of Integrative Plant Biology, 2007, 49, 852-862.	4.1	7
82	Functional analysis of Xa3/Xa26 family members in rice resistance to Xanthomonas oryzae pv. oryzae. Theoretical and Applied Genetics, 2007, 115, 887-895.	1.8	41
83	Mitogen-activated protein kinase OsMPK6 negatively regulates rice disease resistance to bacterial pathogens. Planta, 2007, 226, 953-960.	1.6	100
84	Dual Function of Rice OsDR8 Gene in Disease Resistance and Thiamine Accumulation. Plant Molecular Biology, 2006, 60, 437-449.	2.0	92
85	Expression Profiles of 10,422 Genes at Early Stage of Low Nitrogen Stress in Rice Assayed using a cDNA Microarray. Plant Molecular Biology, 2006, 60, 617-631.	2.0	167
86	Heterosis and polymorphisms of gene expression in an elite rice hybrid as revealed by a microarray analysis of 9198 unique ESTs. Plant Molecular Biology, 2006, 62, 579-591.	2.0	104
87	A tissue culture system for different germplasms of indica rice. Plant Cell Reports, 2006, 25, 392-402.	2.8	113
88	Targeting xa13, a recessive gene for bacterial blight resistance in rice. Theoretical and Applied Genetics, 2006, 112, 455-461.	1.8	178
89	Xa3, conferring resistance for rice bacterial blight and encoding a receptor kinase-like protein, is the same as Xa26. Theoretical and Applied Genetics, 2006, 113, 1347-1355.	1.8	161
90	RMD: a rice mutant database for functional analysis of the rice genome. Nucleic Acids Research, 2006, 34, D745-D748.	6.5	200

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91	Promoter mutations of an essential gene for pollen development result in disease resistance in rice. Genes and Development, 2006, 20, 1250-1255.	2.7	457
92	Point Mutations with Positive Selection Were a Major Force during the Evolution of a Receptor-Kinase Resistance Gene Family of Rice. Plant Physiology, 2006, 140, 998-1008.	2.3	45
93	Features of the expressed sequences revealed by a large-scale analysis of ESTs from a normalized cDNA library of the elite indica rice cultivar Minghui 63. Plant Journal, 2005, 42, 772-780.	2.8	39
94	Xa26, a gene conferring resistance toXanthomonas oryzaepv.oryzaein rice, encodes an LRR receptor kinase-like protein. Plant Journal, 2004, 37, 517-527.	2.8	446
95	Construction and characterization of a normalized whole-life-cycle cDNA library of rice. Science Bulletin, 2003, 48, 229-235.	1.7	1
96	Development of enhancer trap lines for functional analysis of the rice genome. Plant Journal, 2003, 35, 418-427.	2.8	237
97	Comparative analyses of genomic locations and race specificities of loci for quantitative resistance to Pyricularia grisea in rice and barley. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 2544-2549.	3.3	122
98	New Gene for Bacterial Blight Resistance in Rice Located on Chromosome 12 Identified from Minghui 63, an Elite Restorer Line. Phytopathology, 2002, 92, 750-754.	1.1	133
99	The defense-responsive genes showing enhanced and repressed expression after pathogen infection in rice (Oryza sativa L.). Science in China Series C: Life Sciences, 2002, 45, 449.	1.3	35