

Guo-Liang Wang

List of Publications by Year in descending order

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Version: 2024-02-01

168
papers

12,488
citations

30551

56
h-index

32181

105
g-index

175
all docs

175
docs citations

175
times ranked

10403
citing authors

#	ARTICLE	IF	CITATIONS
1	VIGE: virus-induced genome editing for improving abiotic and biotic stress traits in plants. <i>Stress Biology</i> , 2022, 2, 1.	1.5	14
2	Ubiquitination of susceptibility proteins modulates rice broad-spectrum resistance. <i>Trends in Plant Science</i> , 2022, 27, 322-324.	4.3	2
3	Function of hydroxycinnamoyl transferases for the biosynthesis of phenolamides in rice resistance to <i>Magnaporthe oryzae</i> . <i>Journal of Genetics and Genomics</i> , 2022, , .	1.7	12
4	<i>Oryzae</i> pathotype of <i>Magnaporthe oryzae</i> can cause typical blast disease symptoms on both leaves and spikes of wheat under a growth room condition. <i>Phytopathology Research</i> , 2022, 4, .	0.9	4
5	The WRKY10-VOQ8 module safely and effectively regulates rice thermotolerance. <i>Plant, Cell and Environment</i> , 2022, 45, 2126-2144.	2.8	22
6	APIP5 functions as a transcription factor and an RNA-binding protein to modulate cell death and immunity in rice. <i>Nucleic Acids Research</i> , 2022, 50, 5064-5079.	6.5	16
7	Nuclear EPL-HAM complex is essential for the development of chloroplasts. <i>Journal of Genetics and Genomics</i> , 2022, 49, 1165-1168.	1.7	2
8	Mitochondrial functions in plant immunity. <i>Trends in Plant Science</i> , 2022, 27, 1063-1076.	4.3	18
9	Rice catalase OsCATC is degraded by E3 ligase APIP6 to negatively regulate immunity. <i>Plant Physiology</i> , 2022, 190, 1095-1099.	2.3	14
10	An ORFeome of rice E3 ubiquitin ligases for global analysis of the ubiquitination interactome. <i>Genome Biology</i> , 2022, 23, .	3.8	13
11	Two VOZ transcription factors link an E3 ligase and an NLR immune receptor to modulate immunity in rice. <i>Molecular Plant</i> , 2021, 14, 253-266.	3.9	43
12	Development of marker-free rice with stable and high resistance to rice black-streaked dwarf virus disease through RNA interference. <i>Plant Biotechnology Journal</i> , 2021, 19, 212-214.	4.1	10
13	In planta transcriptome analysis reveals tissue-specific expression of pathogenicity genes and microRNAs during rice- <i>Magnaporthe</i> interactions. <i>Genomics</i> , 2021, 113, 265-275.	1.3	5
14	An <i>Oryza</i> -specific hydroxycinnamoyl tyramine gene cluster contributes to enhanced disease resistance. <i>Science Bulletin</i> , 2021, 66, 2369-2380.	4.3	35
15	Comparative genome analyses of four rice-infecting <i>Rhizoctonia solani</i> isolates reveal extensive enrichment of homogalacturonan modification genes. <i>BMC Genomics</i> , 2021, 22, 242.	1.2	18
16	The rice RNase P protein subunit Rpp30 confers broad-spectrum resistance to fungal and bacterial pathogens. <i>Plant Biotechnology Journal</i> , 2021, 19, 1988-1999.	4.1	14
17	A monocot-specific hydroxycinnamoylputrescine gene cluster contributes to immunity and cell death in rice. <i>Science Bulletin</i> , 2021, 66, 2381-2393.	4.3	27
18	Integrated Strategies for Durable Rice Blast Resistance in Sub-Saharan Africa. <i>Plant Disease</i> , 2021, 105, 2749-2770.	0.7	15

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19	Engineering broad-spectrum disease-resistant rice by editing multiple susceptibility genes. <i>Journal of Integrative Plant Biology</i> , 2021, 63, 1639-1648.	4.1	27
20	Next Generation Rice Disease Research. <i>Rice</i> , 2021, 14, 84.	1.7	2
21	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
22	Multilayer regulatory landscape during pattern-triggered immunity in rice. <i>Plant Biotechnology Journal</i> , 2021, 19, 2629-2645.	4.1	21
23	Rapid Detection of Wheat Blast Pathogen <i>Magnaporthe oryzae</i> Triticum Pathotype Using Genome-Specific Primers and Cas12a-mediated Technology. <i>Engineering</i> , 2021, 7, 1326-1335.	3.2	26
24	Association Mapping and Functional Analysis of Rice Cold Tolerance QTLs at the Bud Burst Stage. <i>Rice</i> , 2021, 14, 98.	1.7	3
25	Genome-wide association study identifies an NLR gene that confers partial resistance to <i>Magnaporthe oryzae</i> in rice. <i>Plant Biotechnology Journal</i> , 2020, 18, 1376-1383.	4.1	35
26	A CRISPR/dCas9 toolkit for functional analysis of maize genes. <i>Plant Methods</i> , 2020, 16, 133.	1.9	21
27	Fine-Tuning of RBOH-Mediated ROS Signaling in Plant Immunity. <i>Trends in Plant Science</i> , 2020, 25, 1060-1062.	4.3	47
28	A fungal effector targets a heat shock-dynamin protein complex to modulate mitochondrial dynamics and reduce plant immunity. <i>Science Advances</i> , 2020, 6, .	4.7	39
29	Wheat blast: a new threat to food security. <i>Phytopathology Research</i> , 2020, 2, .	0.9	49
30	A fungal effector and a rice NLR protein have antagonistic effects on a Bowman-Birk trypsin inhibitor. <i>Plant Biotechnology Journal</i> , 2020, 18, 2354-2363.	4.1	39
31	Phenylalanine ammonia lyases mediate broad-spectrum resistance to pathogens and insect pests in plants. <i>Science Bulletin</i> , 2020, 65, 1425-1427.	4.3	15
32	Exploiting Broad-Spectrum Disease Resistance in Crops: From Molecular Dissection to Breeding. <i>Annual Review of Plant Biology</i> , 2020, 71, 575-603.	8.6	125
33	Quantitative proteomics analysis reveals important roles of N-glycosylation on ER quality control system for development and pathogenesis in <i>Magnaporthe oryzae</i> . <i>PLoS Pathogens</i> , 2020, 16, e1008355.	2.1	26
34	Achieving broad-spectrum resistance against rice bacterial blight through targeted promoter editing and pathogen population monitoring. <i>ABIOTECH</i> , 2020, 1, 119-122.	1.8	0
35	Molecular Basis of Disease Resistance and Perspectives on Breeding Strategies for Resistance Improvement in Crops. <i>Molecular Plant</i> , 2020, 13, 1402-1419.	3.9	59
36	Machine Learning-Based Presymptomatic Detection of Rice Sheath Blight Using Spectral Profiles. <i>Plant Phenomics</i> , 2020, 2020, 8954085.	2.5	28

#	ARTICLE	IF	CITATIONS
37	Title is missing!. , 2020, 16, e1008355.		0
38	Title is missing!. , 2020, 16, e1008355.		0
39	Title is missing!. , 2020, 16, e1008355.		0
40	Title is missing!. , 2020, 16, e1008355.		0
41	Phosphorylation-guarded light-harvesting complex II contributes to broad-spectrum blast resistance in rice. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 17572-17577.	3.3	68
42	PALs: Emerging Key Players in Broad-Spectrum Disease Resistance. Trends in Plant Science, 2019, 24, 785-787.	4.3	26
43	Genome-wide association mapping of resistance against rice blast strains in South China and identification of a new Pik allele. Rice, 2019, 12, 47.	1.7	31
44	Use of genomic selection in breeding rice (<i>Oryza sativa</i> L.) for resistance to rice blast (<i>Magnaporthe</i>) Tj ETQq0 0 0 rBT /Overlock 10 Tf 5	1.0	43
45	A proteomic approach identifies novel proteins and metabolites for lesion mimic formation and disease resistance enhancement in rice. Plant Science, 2019, 287, 110182.	1.7	10
46	Identification of new rice cultivars and resistance loci against rice black-streaked dwarf virus disease through genome-wide association study. Rice, 2019, 12, 49.	1.7	26
47	Dissection of the Genetic Architecture of Rice Tillering using a Genome-wide Association Study. Rice, 2019, 12, 43.	1.7	22
48	An improved heteroduplex analysis for rapid genotyping of SNPs and single base pair indels. BioTechniques, 2019, 67, 6-10.	0.8	8
49	SINA E3 Ubiquitin Ligases: Versatile Moderators of Plant Growth and Stress Response. Molecular Plant, 2019, 12, 610-612.	3.9	21
50	The Rice Phosphate Transporter Protein OsPT8 Regulates Disease Resistance and Plant Growth. Scientific Reports, 2019, 9, 5408.	1.6	28
51	Global Proteomic Analysis Reveals Widespread Lysine Succinylation in Rice Seedlings. International Journal of Molecular Sciences, 2019, 20, 5911.	1.8	10
52	Identification of New Resistance Loci Against Sheath Blight Disease in Rice Through Genome-Wide Association Study. Rice Science, 2019, 26, 21-31.	1.7	31
53	Role of lysine residues of the <i>Magnaporthe oryzae</i> effector AvrPiz-t in effector- and PAMP-triggered immunity. Molecular Plant Pathology, 2019, 20, 599-608.	2.0	18
54	Breeding plant broad-spectrum resistance without yield penalties. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 2859-2861.	3.3	27

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55	Dissection of the genetic architecture of rice resistance to <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> using a genomewide association study. <i>Journal of Phytopathology</i> , 2018, 166, 470-476.	0.5	7
56	The Monocot-Specific Receptor-like Kinase SDS2 Controls Cell Death and Immunity in Rice. <i>Cell Host and Microbe</i> , 2018, 23, 498-510.e5.	5.1	96
57	The DnaJ protein OsDjA6 negatively regulates rice innate immunity to the blast fungus <i>Magnaporthe oryzae</i> . <i>Molecular Plant Pathology</i> , 2018, 19, 607-614.	2.0	27
58	The major leaf ferredoxin Fd2 regulates plant innate immunity in Arabidopsis. <i>Molecular Plant Pathology</i> , 2018, 19, 1377-1390.	2.0	32
59	The Kinase OsCPK4 Regulates a Buffering Mechanism That Fine-Tunes Innate Immunity. <i>Plant Physiology</i> , 2018, 176, 1835-1849.	2.3	66
60	Comparative Transcriptome Analysis of <i>Rhizoctonia solani</i> -resistant and -susceptible Rice Cultivars Reveals the Importance of Pathogen Recognition and Active Immune Responses in Host Resistance. <i>Journal of Plant Biology</i> , 2018, 61, 143-158.	0.9	14
61	The rice blast resistance gene Ptr encodes an atypical protein required for broad-spectrum disease resistance. <i>Nature Communications</i> , 2018, 9, 2039.	5.8	128
62	A Versatile Vector Toolkit for Functional Analysis of Rice Genes. <i>Rice</i> , 2018, 11, 27.	1.7	50
63	Proteomic Analysis of Ubiquitinated Proteins in Rice (<i>Oryza sativa</i>) After Treatment With Pathogen-Associated Molecular Pattern (PAMP) Elicitors. <i>Frontiers in Plant Science</i> , 2018, 9, 1064.	1.7	44
64	The fungal pathogen <i>Magnaporthe oryzae</i> suppresses innate immunity by modulating a host potassium channel. <i>PLoS Pathogens</i> , 2018, 14, e1006878.	2.1	94
65	OsCUL3a Negatively Regulates Cell Death and Immunity by Degrading OsNPR1 in Rice. <i>Plant Cell</i> , 2017, 29, 345-359.	3.1	121
66	The Nup98 Homolog APIP12 Targeted by the Effector AvrPiz-t is Involved in Rice Basal Resistance Against <i>Magnaporthe oryzae</i> . <i>Rice</i> , 2017, 10, 5.	1.7	52
67	Durable resistance to rice blast. <i>Science</i> , 2017, 355, 906-907.	6.0	53
68	Balancing Immunity and Yield in Crop Plants. <i>Trends in Plant Science</i> , 2017, 22, 1069-1079.	4.3	186
69	Genotyping-by-Sequencing-Based Genetic Analysis of African Rice Cultivars and Association Mapping of Blast Resistance Genes Against <i>Magnaporthe oryzae</i> Populations in Africa. <i>Phytopathology</i> , 2017, 107, 1039-1046.	1.1	14
70	A Chemical-Induced, Seed-Soaking Activation Procedure for Regulated Gene Expression in Rice. <i>Frontiers in Plant Science</i> , 2017, 8, 1447.	1.7	8
71	OsWRKY67 Plays a Positive Role in Basal and XA21-Mediated Resistance in Rice. <i>Frontiers in Plant Science</i> , 2017, 8, 2220.	1.7	49
72	The Rice Dynamin-Related Protein OsDRP1E Negatively Regulates Programmed Cell Death by Controlling the Release of Cytochrome c from Mitochondria. <i>PLoS Pathogens</i> , 2017, 13, e1006157.	2.1	50

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73	A Layered Defense Strategy Mediated by Rice E3 Ubiquitin Ligases against Diverse Pathogens. <i>Molecular Plant</i> , 2016, 9, 1096-1098.	3.9	17
74	Genome-Wide Association Mapping of Rice Resistance Genes Against <i>Magnaporthe oryzae</i> Isolates from Four African Countries. <i>Phytopathology</i> , 2016, 106, 1359-1365.	1.1	25
75	A novel method for identifying polymorphic transposable elements via scanning of high-throughput short reads. <i>DNA Research</i> , 2016, 23, 241-251.	1.5	18
76	Plant innate immunity in rice: a defense against pathogen infection. <i>National Science Review</i> , 2016, 3, 295-308.	4.6	57
77	Indica rice genome assembly, annotation and mining of blast disease resistance genes. <i>BMC Genomics</i> , 2016, 17, 242.	1.2	51
78	A Genome-Wide Association Study of Field Resistance to <i>Magnaporthe Oryzae</i> in Rice. <i>Rice</i> , 2016, 9, 44.	1.7	55
79	Quantification of hydrogen peroxide in plant tissues using Amplex Red. <i>Methods</i> , 2016, 109, 105-113.	1.9	35
80	Rice (<i>Oryza sativa</i>) Protoplast Isolation and Its Application for Transient Expression Analysis. <i>Current Protocols in Plant Biology</i> , 2016, 1, 373-383.	2.8	61
81	Immunity to Rice Blast Disease by Suppression of Effector-Triggered Necrosis. <i>Current Biology</i> , 2016, 26, 2399-2411.	1.8	108
82	Genome-wide Association Mapping of Cold Tolerance Genes at the Seedling Stage in Rice. <i>Rice</i> , 2016, 9, 61.	1.7	75
83	Dissection of the genetic architecture of rice resistance to the blast fungus <i>Magnaporthe oryzae</i> . <i>Molecular Plant Pathology</i> , 2016, 17, 959-972.	2.0	66
84	A comprehensive catalog of the lysine-acetylation targets in rice (<i>Oryza sativa</i>) based on proteomic analyses. <i>Journal of Proteomics</i> , 2016, 138, 20-29.	1.2	100
85	Data for global lysine-acetylation analysis in rice (<i>Oryza sativa</i>). <i>Data in Brief</i> , 2016, 7, 411-417.	0.5	5
86	The E3 Ligase APIP10 Connects the Effector AvrPiz-t to the NLR Receptor Piz-t in Rice. <i>PLoS Pathogens</i> , 2016, 12, e1005529.	2.1	128
87	Chromatin versus pathogens: the function of epigenetics in plant immunity. <i>Frontiers in Plant Science</i> , 2015, 6, 675.	1.7	103
88	Comparative phosphoproteome analysis of <i>Magnaporthe oryzae</i> -responsive proteins in susceptible and resistant rice cultivars. <i>Journal of Proteomics</i> , 2015, 115, 66-80.	1.2	33
89	Data set from the phosphoproteomic analysis of <i>Magnaporthe oryzae</i> -responsive proteins in susceptible and resistant rice cultivars. <i>Data in Brief</i> , 2015, 3, 7-11.	0.5	1
90	The NAC transcription factor OsSWN1 regulates secondary cell wall development in <i>Oryza sativa</i> . <i>Journal of Plant Biology</i> , 2015, 58, 44-51.	0.9	63

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91	The RhoGAP SPIN6 Associates with SPL11 and OsRac1 and Negatively Regulates Programmed Cell Death and Innate Immunity in Rice. <i>PLoS Pathogens</i> , 2015, 11, e1004629.	2.1	99
92	Genetic analysis and molecular mapping of QTLs for resistance to rice black-streaked dwarf disease in rice. <i>Scientific Reports</i> , 2015, 5, 10509.	1.6	23
93	OsHUB1 and OsHUB2 interact with SPIN6 and form homo- and hetero-dimers in rice. <i>Plant Signaling and Behavior</i> , 2015, 10, e1039212.	1.2	6
94	OsELF3-2, an Ortholog of Arabidopsis ELF3, Interacts with the E3 Ligase APIP6 and Negatively Regulates Immunity against <i>Magnaporthe oryzae</i> in Rice. <i>Molecular Plant</i> , 2015, 8, 1679-1682.	3.9	28
95	RBS1, an RNA Binding Protein, Interacts with SPIN1 and Is Involved in Flowering Time Control in Rice. <i>PLoS ONE</i> , 2014, 9, e87258.	1.1	4
96	Identification of Candidate Genes Associated with Positive and Negative Heterosis in Rice. <i>PLoS ONE</i> , 2014, 9, e95178.	1.1	11
97	The role of effectors and host immunity in plant–necrotrophic fungal interactions. <i>Virulence</i> , 2014, 5, 722-732.	1.8	157
98	Novel Insights into Rice Innate Immunity Against Bacterial and Fungal Pathogens. <i>Annual Review of Phytopathology</i> , 2014, 52, 213-241.	3.5	331
99	Identification and Characterization of Suppressor Mutants of <i>spl11</i> -Mediated Cell Death in Rice. <i>Molecular Plant-Microbe Interactions</i> , 2014, 27, 528-536.	1.4	36
100	Mapped Clone and Functional Analysis of Leaf-Color Gene <i>Ygl7</i> in a Rice Hybrid (<i>Oryza sativa</i> L. ssp.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.1	70
101	Fine-mapping and molecular marker development for Pi56(t), a NBS-LRR gene conferring broad-spectrum resistance to <i>Magnaporthe oryzae</i> in rice. <i>Theoretical and Applied Genetics</i> , 2013, 126, 985-998.	1.8	66
102	Molecular mapping of the blast resistance gene Pi49 in the durably resistant rice cultivar Mowanggu. <i>Euphytica</i> , 2013, 192, 45-54.	0.6	21
103	Deep transcriptome sequencing reveals the expression of key functional and regulatory genes involved in the abiotic stress signaling pathways in rice. <i>Journal of Plant Biology</i> , 2013, 56, 216-231.	0.9	27
104	Molecular mapping of four blast resistance genes using recombinant inbred lines of 93-11 and nipponbare. <i>Journal of Plant Biology</i> , 2013, 56, 91-97.	0.9	6
105	Loving memories of Dr. Ko Shimamoto. <i>Rice</i> , 2013, 6, 34.	1.7	0
106	Identification and Characterization of In planta-Expressed Secreted Effector Proteins from <i>Magnaporthe oryzae</i> That Induce Cell Death in Rice. <i>Molecular Plant-Microbe Interactions</i> , 2013, 26, 191-202.	1.4	141
107	Recent Progress in Understanding PAMP- and Effector-Triggered Immunity against the Rice Blast Fungus <i>Magnaporthe oryzae</i> . <i>Molecular Plant</i> , 2013, 6, 605-620.	3.9	141
108	The U-Box/ARM E3 Ligase PUB13 Regulates Cell Death, Defense, and Flowering Time in Arabidopsis. <i>Plant Physiology</i> , 2012, 159, 239-250.	2.3	129

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109	HDT701, a Histone H4 Deacetylase, Negatively Regulates Plant Innate Immunity by Modulating Histone H4 Acetylation of Defense-Related Genes in Rice. <i>Plant Cell</i> , 2012, 24, 3783-3794.	3.1	183
110	The <i>Magnaporthe oryzae</i> Effector AvrPiz-t Targets the RING E3 Ubiquitin Ligase APIP6 to Suppress Pathogen-Associated Molecular Pattern-Triggered Immunity in Rice. <i>Plant Cell</i> , 2012, 24, 4748-4762.	3.1	472
111	The U-Box E3 Ligase SPL11/PUB13 Is a Convergence Point of Defense and Flowering Signaling in Plants. <i>Plant Physiology</i> , 2012, 160, 28-37.	2.3	73
112	PAPP2C Interacts with the Atypical Disease Resistance Protein RPW8.2 and Negatively Regulates Salicylic Acid-Dependent Defense Responses in Arabidopsis. <i>Molecular Plant</i> , 2012, 5, 1125-1137.	3.9	25
113	Molecular Mapping of the Blast Resistance Genes <i>Pi2-1</i> and <i>Pi51(t)</i> in the Durably Resistant Rice "Tianjingyeshengdao". <i>Phytopathology</i> , 2012, 102, 779-786.	1.1	33
114	Molecular mapping of the Pi2/9 allelic gene Pi2-2 conferring broad-spectrum resistance to <i>Magnaporthe oryzae</i> in the rice cultivar Jefferson. <i>Rice</i> , 2012, 5, 29.	1.7	43
115	Development of a Simple and Efficient System for Excising Selectable Markers in Arabidopsis Using a Minimal Promoter:: Cre Fusion Construct. <i>Molecules and Cells</i> , 2012, 33, 61-70.	1.0	6
116	Large Scale Identification of Genes Involved in Plant-Fungal Interactions Using Illumina's Sequencing-by-Synthesis Technology. <i>Methods in Molecular Biology</i> , 2011, 722, 167-178.	0.4	16
117	Molecular Mapping of the New Blast Resistance Genes Pi47 and Pi48 in the Durably Resistant Local Rice Cultivar Xiangzi 3150. <i>Phytopathology</i> , 2011, 101, 620-626.	1.1	49
118	Quantitative trait loci associated with seed set under high temperature stress at the flowering stage in rice (<i>Oryza sativa</i> L.). <i>Euphytica</i> , 2011, 178, 331-338.	0.6	74
119	Genetic Variation and Evolution of the Pi9 Blast Resistance Locus in the AA Genome <i>Oryza</i> Species. <i>Journal of Plant Biology</i> , 2011, 54, 294-302.	0.9	27
120	Deep sequencing reveals the complex and coordinated transcriptional regulation of genes related to grain quality in rice cultivars. <i>BMC Genomics</i> , 2011, 12, 190.	1.2	38
121	OsDIS1-mediated stress response pathway in rice. <i>Plant Signaling and Behavior</i> , 2011, 6, 1684-1686.	1.2	15
122	The SINA E3 Ligase OsDIS1 Negatively Regulates Drought Response in Rice. <i>Plant Physiology</i> , 2011, 157, 242-255.	2.3	158
123	Genomic structure and evolution of the Pi2/9 locus in wild rice species. <i>Theoretical and Applied Genetics</i> , 2010, 121, 295-309.	1.8	25
124	Deep and Comparative Transcriptome Analysis of Rice Plants Infested by the Beet Armyworm (<i>Spodoptera exigua</i>) and Water Weevil (<i>Lissorhoptrus oryzophilus</i>). <i>Rice</i> , 2010, 3, 22-35.	1.7	18
125	Role of Ubiquitination in Plant Innate Immunity and Pathogen Virulence. <i>Journal of Plant Biology</i> , 2010, 53, 10-18.	0.9	20
126	Recent progress and understanding of the molecular mechanisms of the rice- <i>Magnaporthe oryzae</i> interaction. <i>Molecular Plant Pathology</i> , 2010, 11, 419-427.	2.0	180

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127	The <i>Magnaporthe oryzae</i> Avirulence Gene <i>AvrPiz-t</i> Encodes a Predicted Secreted Protein That Triggers the Immunity in Rice Mediated by the Blast Resistance Gene <i>Piz-t</i> . <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 411-420.	1.4	240
128	A Versatile Zero Background T-Vector System for Gene Cloning and Functional Genomics. <i>Plant Physiology</i> , 2009, 150, 1111-1121.	2.3	383
129	Construction and Application of Efficient Δ Transposon Tagging Vectors in Rice. <i>Journal of Integrative Plant Biology</i> , 2009, 51, 982-992.	4.1	18
130	Rice <i>Pi5</i> -Mediated Resistance to <i>Magnaporthe oryzae</i> Requires the Presence of Two Coiled-Coil Nucleotide-Binding Leucine-Rich Repeat Genes. <i>Genetics</i> , 2009, 181, 1627-1638.	1.2	239
131	Isolation and Functional Analysis of Putative Effectors from <i>Magnaporthe oryzae</i> Using Integrated Genomic Approaches. , 2009, , 93-103.		1
132	Transposable Element Regulation in Rice and Arabidopsis: Diverse Patterns of Active Expression and siRNA-mediated Silencing. <i>Tropical Plant Biology</i> , 2008, 1, 72-84.	1.0	6
133	Rice lesion mimic mutants with enhanced resistance to diseases. <i>Molecular Genetics and Genomics</i> , 2008, 279, 605-619.	1.0	103
134	SPIN1, a K Homology Domain Protein Negatively Regulated and Ubiquitinated by the E3 Ubiquitin Ligase SPL11, Is Involved in Flowering Time Control in Rice. <i>Plant Cell</i> , 2008, 20, 1456-1469.	3.1	91
135	Classification, Expression Pattern, and E3 Ligase Activity Assay of Rice U-Box-Containing Proteins. <i>Molecular Plant</i> , 2008, 1, 800-815.	3.9	139
136	An Inositolphosphorylceramide Synthase Is Involved in Regulation of Plant Programmed Cell Death Associated with Defense in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2008, 20, 3163-3179.	3.1	193
137	<i>Magnaporthe grisea</i> Infection Triggers RNA Variation and Antisense Transcript Expression in Rice. <i>Plant Physiology</i> , 2007, 144, 524-533.	2.3	29
138	The Genomic Dynamics and Evolutionary Mechanism of the <i>Pi2/9</i> Locus in Rice. <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 63-71.	1.4	73
139	Resistance of transgenic tall fescue to two major fungal diseases. <i>Plant Science</i> , 2007, 173, 501-509.	1.7	35
140	Recent Progress in Elucidating the Structure, Function and Evolution of Disease Resistance Genes in Plants. <i>Journal of Genetics and Genomics</i> , 2007, 34, 765-776.	1.7	198
141	An expression atlas of rice mRNAs and small RNAs. <i>Nature Biotechnology</i> , 2007, 25, 473-477.	9.4	246
142	Recent Advances in Cloning and Characterization of Disease Resistance Genes in Rice. <i>Journal of Integrative Plant Biology</i> , 2007, 49, 112-119.	4.1	59
143	The <i>COI1</i> and <i>DFR</i> Genes are Essential for Regulation of Jasmonate-Induced Anthocyanin Accumulation in <i>Arabidopsis</i> . <i>Journal of Integrative Plant Biology</i> , 2007, 49, 1370-1377.	4.1	21
144	BWMK1 Responds to Multiple Environmental Stresses and Plant Hormones. <i>Journal of Integrative Plant Biology</i> , 2007, 49, 843-851.	4.1	7

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145	RL-SAGE and microarray analysis of the rice transcriptome after <i>Rhizoctonia solani</i> infection. <i>Molecular Genetics and Genomics</i> , 2007, 278, 421-431.	1.0	50
146	The Eight Amino-Acid Differences Within Three Leucine-Rich Repeats Between Pi2 and Piz-t Resistance Proteins Determine the Resistance Specificity to <i>Magnaporthe grisea</i> . <i>Molecular Plant-Microbe Interactions</i> , 2006, 19, 1216-1228.	1.4	357
147	A highly efficient transient protoplast system for analyzing defence gene expression and protein-protein interactions in rice. <i>Molecular Plant Pathology</i> , 2006, 7, 417-427.	2.0	396
148	Ubiquitination-mediated protein degradation and modification: an emerging theme in plant-microbe interactions. <i>Cell Research</i> , 2006, 16, 413-426.	5.7	176
149	A comprehensive expression analysis of the WRKY gene superfamily in rice plants during defense response. <i>Plant Cell Reports</i> , 2006, 25, 836-847.	2.8	243
150	The Broad-Spectrum Blast Resistance Gene Pi9 Encodes a Nucleotide-Binding Site-Leucine-Rich Repeat Protein and Is a Member of a Multigene Family in Rice. <i>Genetics</i> , 2006, 172, 1901-1914.	1.2	479
151	A Phylogeny of <i>Pelargonium</i> Based on TRAP Markers. <i>Hortscience: A Publication of the American Society for Horticultural Science</i> , 2006, 41, 1001C-1001.	0.5	0
152	R gene expression induced by a type-III effector triggers disease resistance in rice. <i>Nature</i> , 2005, 435, 1122-1125.	13.7	502
153	Large-Scale Identification of Expressed Sequence Tags Involved in Rice and Rice Blast Fungus Interaction. <i>Plant Physiology</i> , 2005, 138, 105-115.	2.3	96
154	(17) TRAP Markers Help Categorize a <i>Pelargonium</i> Collection. <i>Hortscience: A Publication of the American Society for Horticultural Science</i> , 2005, 40, 1067C-1067.	0.5	1
155	Spotted leaf11, a Negative Regulator of Plant Cell Death and Defense, Encodes a U-Box/Armadillo Repeat Protein Endowed with E3 Ubiquitin Ligase Activity. <i>Plant Cell</i> , 2004, 16, 2795-2808.	3.1	385
156	Isolation and characterization of novel defense response genes involved in compatible and incompatible interactions between rice and <i>Magnaporthe grisea</i> . <i>Theoretical and Applied Genetics</i> , 2004, 108, 525-534.	1.8	44
157	Isolation and characterization of rice mutants compromised in Xa21-mediated resistance to <i>X. oryzae</i> pv. <i>oryzae</i> . <i>Theoretical and Applied Genetics</i> , 2004, 108, 379-384.	1.8	22
158	Robust-LongSAGE (RL-SAGE): A Substantially Improved LongSAGE Method for Gene Discovery and Transcriptome Analysis. <i>Plant Physiology</i> , 2004, 134, 890-897.	2.3	115
159	Development of a new transformation-competent artificial chromosome (TAC) vector and construction of tomato and rice TAC libraries. <i>Molecular Breeding</i> , 2003, 12, 297-308.	1.0	17
160	Two broad-spectrum blast resistance genes, Pi9(t) and Pi2(t), are physically linked on rice chromosome 6. <i>Molecular Genetics and Genomics</i> , 2002, 267, 472-480.	1.0	181
161	Fine genetic mapping and physical delimitation of the lesion mimic gene Spl11 to a 160-kb DNA segment of the rice genome. <i>Molecular Genetics and Genomics</i> , 2002, 268, 253-261.	1.0	31
162	Dissection of Defence Response Pathways in Rice. <i>Novartis Foundation Symposium</i> , 2001, 236, 190-204.	1.2	0

#	ARTICLE	IF	CITATIONS
163	Characterizing Rice Lesion Mimic Mutants and Identifying a Mutant with Broad-Spectrum Resistance to Rice Blast and Bacterial Blight. <i>Molecular Plant-Microbe Interactions</i> , 2000, 13, 869-876.	1.4	241
164	BWMK1, a Novel MAP Kinase Induced by Fungal Infection and Mechanical Wounding in Rice. <i>Molecular Plant-Microbe Interactions</i> , 1999, 12, 1064-1073.	1.4	120
165	Xa21D Encodes a Receptor-like Molecule with a Leucine-Rich Repeat Domain That Determines Race-Specific Recognition and Is Subject to Adaptive Evolution. <i>Plant Cell</i> , 1998, 10, 765-779.	3.1	304
166	Construction of an arabidopsis BAC library and isolation of clones hybridizing with disease-resistance, gene-like sequences. <i>Plant Molecular Biology Reporter</i> , 1996, 14, 107-114.	1.0	18
167	The Cloned Gene, <i>Xa21</i> , Confers Resistance to Multiple <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> Isolates in Transgenic Plants. <i>Molecular Plant-Microbe Interactions</i> , 1996, 9, 850.	1.4	240
168	Construction of a rice bacterial artificial chromosome library and identification of clones linked to the Xa-21 disease resistance locus. <i>Plant Journal</i> , 1995, 7, 525-533.	2.8	209