

# Guo-Liang Wang

## List of Publications by Year in descending order

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168  
papers

12,488  
citations

26630

56  
h-index

28297

105  
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175  
all docs

175  
docs citations

175  
times ranked

9381  
citing authors

#	ARTICLE	IF	CITATIONS
1	R gene expression induced by a type-III effector triggers disease resistance in rice. <i>Nature</i> , 2005, 435, 1122-1125.	27.8	502
2	The Broad-Spectrum Blast Resistance Gene Pi9 Encodes a Nucleotide-Binding Siteâ€“Leucine-Rich Repeat Protein and Is a Member of a Multigene Family in Rice. <i>Genetics</i> , 2006, 172, 1901-1914.	2.9	479
3	The <i>Magnaporthe oryzae</i> Effector AvrPiz-t Targets the RING E3 Ubiquitin Ligase APIP6 to Suppress Pathogen-Associated Molecular Patternâ€“Triggered Immunity in Rice. <i>Plant Cell</i> , 2012, 24, 4748-4762.	6.6	472
4	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.	4.2	396
5	Spotted leaf11, a Negative Regulator of Plant Cell Death and Defense, Encodes a U-Box/Armadillo Repeat Protein Endowed with E3 Ubiquitin Ligase Activitywâfž. <i>Plant Cell</i> , 2004, 16, 2795-2808.	6.6	385
6	A Versatile Zero Background T-Vector System for Gene Cloning and Functional Genomics Â Â Â. <i>Plant Physiology</i> , 2009, 150, 1111-1121.	4.8	383
7	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.	2.6	357
8	Novel Insights into Rice Innate Immunity Against Bacterial and Fungal Pathogens. <i>Annual Review of Phytopathology</i> , 2014, 52, 213-241.	7.8	331
9	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.	6.6	304
10	An expression atlas of rice mRNAs and small RNAs. <i>Nature Biotechnology</i> , 2007, 25, 473-477.	17.5	246
11	A comprehensive expression analysis of the WRKY gene superfamily in rice plants during defense response. <i>Plant Cell Reports</i> , 2006, 25, 836-847.	5.6	243
12	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.	2.6	241
13	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.	2.6	240
14	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.	2.6	240
15	Rice <i>Pi5</i> -Mediated Resistance to <i>Magnaporthe oryzae</i> Requires the Presence of Two Coiled-Coilâ€“Nucleotide-Bindingâ€“Leucine-Rich Repeat Genes. <i>Genetics</i> , 2009, 181, 1627-1638.	2.9	239
16	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.	5.7	209
17	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.	3.9	198
18	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.	6.6	193

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19	Balancing Immunity and Yield in Crop Plants. <i>Trends in Plant Science</i> , 2017, 22, 1069-1079.	8.8	186
20	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.	6.6	183
21	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.	2.1	181
22	Recent progress and understanding of the molecular mechanisms of the rice-Magnaporthe oryzae interaction. <i>Molecular Plant Pathology</i> , 2010, 11, 419-427.	4.2	180
23	Ubiquitination-mediated protein degradation and modification: an emerging theme in plant-microbe interactions. <i>Cell Research</i> , 2006, 16, 413-426.	12.0	176
24	The SINA E3 Ligase OsDIS1 Negatively Regulates Drought Response in Rice. <i>Plant Physiology</i> , 2011, 157, 242-255.	4.8	158
25	The role of effectors and host immunity in plant-necrotrophic fungal interactions. <i>Virulence</i> , 2014, 5, 722-732.	4.4	157
26	Identification and Characterization of In planta-Expressed Secreted Effector Proteins from Magnaporthe oryzae That Induce Cell Death in Rice. <i>Molecular Plant-Microbe Interactions</i> , 2013, 26, 191-202.	2.6	141
27	Recent Progress in Understanding PAMP- and Effector-Triggered Immunity against the Rice Blast Fungus Magnaporthe oryzae. <i>Molecular Plant</i> , 2013, 6, 605-620.	8.3	141
28	Classification, Expression Pattern, and E3 Ligase Activity Assay of Rice U-Box-Containing Proteins. <i>Molecular Plant</i> , 2008, 1, 800-815.	8.3	139
29	The U-Box/ARM E3 Ligase PUB13 Regulates Cell Death, Defense, and Flowering Time in Arabidopsis. <i>Plant Physiology</i> , 2012, 159, 239-250.	4.8	129
30	The rice blast resistance gene Ptr encodes an atypical protein required for broad-spectrum disease resistance. <i>Nature Communications</i> , 2018, 9, 2039.	12.8	128
31	The E3 Ligase APIP10 Connects the Effector AvrPiz-t to the NLR Receptor Piz-t in Rice. <i>PLoS Pathogens</i> , 2016, 12, e1005529.	4.7	128
32	Exploiting Broad-Spectrum Disease Resistance in Crops: From Molecular Dissection to Breeding. <i>Annual Review of Plant Biology</i> , 2020, 71, 575-603.	18.7	125
33	OsCUL3a Negatively Regulates Cell Death and Immunity by Degrading OsNPR1 in Rice. <i>Plant Cell</i> , 2017, 29, 345-359.	6.6	121
34	BWMK1, a Novel MAP Kinase Induced by Fungal Infection and Mechanical Wounding in Rice. <i>Molecular Plant-Microbe Interactions</i> , 1999, 12, 1064-1073.	2.6	120
35	Ca <sup>2+</sup> sensor-mediated ROS scavenging suppresses rice immunity and is exploited by a fungal effector. <i>Cell</i> , 2021, 184, 5391-5404.e17.	28.9	117
36	Robust-LongSAGE (RL-SAGE): A Substantially Improved LongSAGE Method for Gene Discovery and Transcriptome Analysis. <i>Plant Physiology</i> , 2004, 134, 890-897.	4.8	115

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37	Immunity to Rice Blast Disease by Suppression of Effector-Triggered Necrosis. <i>Current Biology</i> , 2016, 26, 2399-2411.	3.9	108
38	Rice lesion mimic mutants with enhanced resistance to diseases. <i>Molecular Genetics and Genomics</i> , 2008, 279, 605-619.	2.1	103
39	Chromatin versus pathogens: the function of epigenetics in plant immunity. <i>Frontiers in Plant Science</i> , 2015, 6, 675.	3.6	103
40	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.	2.4	100
41	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.	4.7	99
42	Large-Scale Identification of Expressed Sequence Tags Involved in Rice and Rice Blast Fungus Interaction. <i>Plant Physiology</i> , 2005, 138, 105-115.	4.8	96
43	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.	11.0	96
44	The fungal pathogen <i>Magnaporthe oryzae</i> suppresses innate immunity by modulating a host potassium channel. <i>PLoS Pathogens</i> , 2018, 14, e1006878.	4.7	94
45	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.	6.6	91
46	Genome-wide Association Mapping of Cold Tolerance Genes at the Seedling Stage in Rice. <i>Rice</i> , 2016, 9, 61.	4.0	75
47	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.	1.2	74
48	The Genomic Dynamics and Evolutionary Mechanism of the Pi2/9 Locus in Rice. <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 63-71.	2.6	73
49	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.	4.8	73
50	Mapped Clone and Functional Analysis of Leaf-Color Gene Ygl7 in a Rice Hybrid ( <i>Oryza sativa</i> L. ssp.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	2.5	70
51	Phosphorylation-guarded light-harvesting complex II contributes to broad-spectrum blast resistance in rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 17572-17577.	7.1	68
52	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.	3.6	66
53	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.	4.2	66
54	The Kinase OsCPK4 Regulates a Buffering Mechanism That Fine-Tunes Innate Immunity. <i>Plant Physiology</i> , 2018, 176, 1835-1849.	4.8	66

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55	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.	2.1	63
56	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
57	Recent Advances in Cloning and Characterization of Disease Resistance Genes in Rice. <i>Journal of Integrative Plant Biology</i> , 2007, 49, 112-119.	8.5	59
58	Molecular Basis of Disease Resistance and Perspectives on Breeding Strategies for Resistance Improvement in Crops. <i>Molecular Plant</i> , 2020, 13, 1402-1419.	8.3	59
59	Plant innate immunity in rice: a defense against pathogen infection. <i>National Science Review</i> , 2016, 3, 295-308.	9.5	57
60	A Genome-Wide Association Study of Field Resistance to <i>Magnaporthe Oryzae</i> in Rice. <i>Rice</i> , 2016, 9, 44.	4.0	55
61	Durable resistance to rice blast. <i>Science</i> , 2017, 355, 906-907.	12.6	53
62	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.	4.0	52
63	Indica rice genome assembly, annotation and mining of blast disease resistance genes. <i>BMC Genomics</i> , 2016, 17, 242.	2.8	51
64	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.	2.1	50
65	A Versatile Vector Toolkit for Functional Analysis of Rice Genes. <i>Rice</i> , 2018, 11, 27.	4.0	50
66	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.	4.7	50
67	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.	2.2	49
68	OsWRKY67 Plays a Positive Role in Basal and XA21-Mediated Resistance in Rice. <i>Frontiers in Plant Science</i> , 2017, 8, 2220.	3.6	49
69	Wheat blast: a new threat to food security. <i>Phytopathology Research</i> , 2020, 2, .	2.4	49
70	Fine-Tuning of RBOH-Mediated ROS Signaling in Plant Immunity. <i>Trends in Plant Science</i> , 2020, 25, 1060-1062.	8.8	47
71	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.	3.6	44
72	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.	3.6	44

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73	Molecular mapping of the Pi2/9 allelic gene Pi2-2 conferring broad-spectrum resistance to Magnaporthe oryzae in the rice cultivar Jefferson. Rice, 2012, 5, 29.	4.0	43
74	Use of genomic selection in breeding rice (Oryza sativa L.) for resistance to rice blast (Magnaporthe Tj ETQq0 0 0 rBT /Overlock 10 Tf 5	2.1	43
75	Two VOZ transcription factors link an E3 ligase and an NLR immune receptor to modulate immunity in rice. Molecular Plant, 2021, 14, 253-266.	8.3	43
76	A fungal effector targets a heat shockâ€“dynamin protein complex to modulate mitochondrial dynamics and reduce plant immunity. Science Advances, 2020, 6, .	10.3	39
77	A fungal effector and a rice NLR protein have antagonistic effects on a Bowmanâ€“Birk trypsin inhibitor. Plant Biotechnology Journal, 2020, 18, 2354-2363.	8.3	39
78	Deep sequencing reveals the complex and coordinated transcriptional regulation of genes related to grain quality in rice cultivars. BMC Genomics, 2011, 12, 190.	2.8	38
79	Identification and Characterization of Suppressor Mutants of <i>spl11</i> Mediated Cell Death in Rice. Molecular Plant-Microbe Interactions, 2014, 27, 528-536.	2.6	36
80	Resistance of transgenic tall fescue to two major fungal diseases. Plant Science, 2007, 173, 501-509.	3.6	35
81	Quantification of hydrogen peroxide in plant tissues using Amplex Red. Methods, 2016, 109, 105-113.	3.8	35
82	Genomeâ€“wide association study identifies an NLR gene that confers partial resistance to <i>Magnaporthe oryzae</i> in rice. Plant Biotechnology Journal, 2020, 18, 1376-1383.	8.3	35
83	An Oryza-specific hydroxycinnamoyl tyramine gene cluster contributes to enhanced disease resistance. Science Bulletin, 2021, 66, 2369-2380.	9.0	35
84	Molecular Mapping of the Blast Resistance Genes <i>Pi2-1</i> and <i>Pi51(t)</i> in the Durably Resistant Rice â€“Tianjingyeshengdaoâ€“™. Phytopathology, 2012, 102, 779-786.	2.2	33
85	Comparative phosphoproteome analysis of Magnaporthe oryzae-responsive proteins in susceptible and resistant rice cultivars. Journal of Proteomics, 2015, 115, 66-80.	2.4	33
86	The major leaf ferredoxin Fd2 regulates plant innate immunity in Arabidopsis. Molecular Plant Pathology, 2018, 19, 1377-1390.	4.2	32
87	Fine genetic mapping and physical delimitation of the lesion mimic gene Spl11 to a 160-kb DNA segment of the rice genome. Molecular Genetics and Genomics, 2002, 268, 253-261.	2.1	31
88	Genome-wide association mapping of resistance against rice blast strains in South China and identification of a new Pik allele. Rice, 2019, 12, 47.	4.0	31
89	Identification of New Resistance Loci Against Sheath Blight Disease in Rice Through Genome-Wide Association Study. Rice Science, 2019, 26, 21-31.	3.9	31
90	Magnaporthe grisea Infection Triggers RNA Variation and Antisense Transcript Expression in Rice. Plant Physiology, 2007, 144, 524-533.	4.8	29

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91	OsELF3-2, an Ortholog of Arabidopsis ELF3, Interacts with the E3 Ligase APIP6 and Negatively Regulates Immunity against Magnaporthe oryzae in Rice. <i>Molecular Plant</i> , 2015, 8, 1679-1682.	8.3	28
92	The Rice Phosphate Transporter Protein OsPT8 Regulates Disease Resistance and Plant Growth. <i>Scientific Reports</i> , 2019, 9, 5408.	3.3	28
93	Machine Learning-Based Presymptomatic Detection of Rice Sheath Blight Using Spectral Profiles. <i>Plant Phenomics</i> , 2020, 2020, 8954085.	5.9	28
94	Genetic Variation and Evolution of the Pi9 Blast Resistance Locus in the AA Genome Oryza Species. <i>Journal of Plant Biology</i> , 2011, 54, 294-302.	2.1	27
95	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.	2.1	27
96	Breeding plant broad-spectrum resistance without yield penalties. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 2859-2861.	7.1	27
97	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.	4.2	27
98	A monocot-specific hydroxycinnamoylputrescine gene cluster contributes to immunity and cell death in rice. <i>Science Bulletin</i> , 2021, 66, 2381-2393.	9.0	27
99	Engineering broad-spectrum disease-resistant rice by editing multiple susceptibility genes. <i>Journal of Integrative Plant Biology</i> , 2021, 63, 1639-1648.	8.5	27
100	PALs: Emerging Key Players in Broad-Spectrum Disease Resistance. <i>Trends in Plant Science</i> , 2019, 24, 785-787.	8.8	26
101	Identification of new rice cultivars and resistance loci against rice black-streaked dwarf virus disease through genome-wide association study. <i>Rice</i> , 2019, 12, 49.	4.0	26
102	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.	4.7	26
103	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.	6.7	26
104	Genomic structure and evolution of the Pi2/9 locus in wild rice species. <i>Theoretical and Applied Genetics</i> , 2010, 121, 295-309.	3.6	25
105	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.	8.3	25
106	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.	2.2	25
107	Genetic analysis and molecular mapping of QTLs for resistance to rice black-streaked dwarf disease in rice. <i>Scientific Reports</i> , 2015, 5, 10509.	3.3	23
108	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.	3.6	22



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109	Dissection of the Genetic Architecture of Rice Tillering using a Genome-wide Association Study. <i>Rice</i> , 2019, 12, 43.	4.0	22
110	The WRKY10â€VQ8 module safely and effectively regulates rice thermotolerance. <i>Plant, Cell and Environment</i> , 2022, 45, 2126-2144.	5.7	22
111	The <i>COI1</i> and <i>DFR</i> Genes are Essential for Regulation of Jasmonateâ€Induced Anthocyanin Accumulation in <i>Arabidopsis</i> . <i>Journal of Integrative Plant Biology</i> , 2007, 49, 1370-1377.	8.5	21
112	Molecular mapping of the blast resistance gene Pi49 in the durably resistant rice cultivar Mowanggu. <i>Euphytica</i> , 2013, 192, 45-54.	1.2	21
113	SINA E3â€Ubiquitin Ligases: Versatile Moderators of Plant Growth and Stress Response. <i>Molecular Plant</i> , 2019, 12, 610-612.	8.3	21
114	A CRISPR/dCas9 toolkit for functional analysis of maize genes. <i>Plant Methods</i> , 2020, 16, 133.	4.3	21
115	Multilayer regulatory landscape during patternâ€triggered immunity in rice. <i>Plant Biotechnology Journal</i> , 2021, 19, 2629-2645.	8.3	21
116	Role of Ubiquitination in Plant Innate Immunity and Pathogen Virulence. <i>Journal of Plant Biology</i> , 2010, 53, 10-18.	2.1	20
117	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.	1.8	18
118	Construction and Application of Efficient <i>Acâ€Ds</i> Transposon Tagging Vectors in Rice. <i>Journal of Integrative Plant Biology</i> , 2009, 51, 982-992.	8.5	18
119	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.	4.0	18
120	A novel method for identifying polymorphic transposable elements via scanning of high-throughput short reads. <i>DNA Research</i> , 2016, 23, 241-251.	3.4	18
121	Role of lysine residues of the <i>Magnaporthe oryzae</i> effector AvrPizâ€ in effectorâ€and PAMPâ€triggered immunity. <i>Molecular Plant Pathology</i> , 2019, 20, 599-608.	4.2	18
122	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.	2.8	18
123	Mitochondrial functions in plant immunity. <i>Trends in Plant Science</i> , 2022, 27, 1063-1076.	8.8	18
124	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.	2.1	17
125	A Layered Defense Strategy Mediated by Rice E3â€Ubiquitin Ligases against Diverse Pathogens. <i>Molecular Plant</i> , 2016, 9, 1096-1098.	8.3	17
126	Large Scale Identification of Genes Involved in Plantâ€Fungal Interactions Using Illuminaâ€™s Sequencing-by-Synthesis Technology. <i>Methods in Molecular Biology</i> , 2011, 722, 167-178.	0.9	16



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127	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.	14.5	16
128	OsDIS1-mediated stress response pathway in rice. <i>Plant Signaling and Behavior</i> , 2011, 6, 1684-1686.	2.4	15
129	Phenylalanine ammonia lyases mediate broad-spectrum resistance to pathogens and insect pests in plants. <i>Science Bulletin</i> , 2020, 65, 1425-1427.	9.0	15
130	Integrated Strategies for Durable Rice Blast Resistance in Sub-Saharan Africa. <i>Plant Disease</i> , 2021, 105, 2749-2770.	1.4	15
131	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.	2.2	14
132	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.	2.1	14
133	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.	8.3	14
134	VICE: virus-induced genome editing for improving abiotic and biotic stress traits in plants. <i>Stress Biology</i> , 2022, 2, 1.	3.1	14
135	Rice catalase OsCATC is degraded by E3 ligase APIP6 to negatively regulate immunity. <i>Plant Physiology</i> , 2022, 190, 1095-1099.	4.8	14
136	An ORFeome of rice E3 ubiquitin ligases for global analysis of the ubiquitination interactome. <i>Genome Biology</i> , 2022, 23, .	8.8	13
137	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, , .	3.9	12
138	Identification of Candidate Genes Associated with Positive and Negative Heterosis in Rice. <i>PLoS ONE</i> , 2014, 9, e95178.	2.5	11
139	A proteomic approach identifies novel proteins and metabolites for lesion mimic formation and disease resistance enhancement in rice. <i>Plant Science</i> , 2019, 287, 110182.	3.6	10
140	Global Proteomic Analysis Reveals Widespread Lysine Succinylation in Rice Seedlings. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5911.	4.1	10
141	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.	8.3	10
142	A Chemical-Induced, Seed-Soaking Activation Procedure for Regulated Gene Expression in Rice. <i>Frontiers in Plant Science</i> , 2017, 8, 1447.	3.6	8
143	An improved heteroduplex analysis for rapid genotyping of SNPs and single base pair indels. <i>BioTechniques</i> , 2019, 67, 6-10.	1.8	8
144	BWMK1 Responds to Multiple Environmental Stresses and Plant Hormones. <i>Journal of Integrative Plant Biology</i> , 2007, 49, 843-851.	8.5	7

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145	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.	1.0	7
146	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.	1.9	6
147	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.	2.6	6
148	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.	2.1	6
149	OsHUB1 and OsHUB2 interact with SPIN6 and form homo- and hetero-dimers in rice. <i>Plant Signaling and Behavior</i> , 2015, 10, e1039212.	2.4	6
150	Data for global lysine-acetylation analysis in rice ( <i>Oryza sativa</i> ). <i>Data in Brief</i> , 2016, 7, 411-417.	1.0	5
151	In planta transcriptome analysis reveals tissue-specific expression of pathogenicity genes and microRNAs during rice-Magnaporthe interactions. <i>Genomics</i> , 2021, 113, 265-275.	2.9	5
152	RBS1, an RNA Binding Protein, Interacts with SPIN1 and Is Involved in Flowering Time Control in Rice. <i>PLoS ONE</i> , 2014, 9, e87258.	2.5	4
153	<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, .	2.4	4
154	Association Mapping and Functional Analysis of Rice Cold Tolerance QTLs at the Bud Burst Stage. <i>Rice</i> , 2021, 14, 98.	4.0	3
155	Next Generation Rice Disease Research. <i>Rice</i> , 2021, 14, 84.	4.0	2
156	Ubiquitination of susceptibility proteins modulates rice broad-spectrum resistance. <i>Trends in Plant Science</i> , 2022, 27, 322-324.	8.8	2
157	Nuclear EPL-HAM complex is essential for the development of chloroplasts. <i>Journal of Genetics and Genomics</i> , 2022, 49, 1165-1168.	3.9	2
158	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.	1.0	1
159	(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.	1.0	1
160	Isolation and Functional Analysis of Putative Effectors from <i>Magnaporthe oryzae</i> Using Integrated Genomic Approaches. , 2009, , 93-103.		1
161	Loving memories of Dr. Ko Shimamoto. <i>Rice</i> , 2013, 6, 34.	4.0	0
162	Achieving broad-spectrum resistance against rice bacterial blight through targeted promoter editing and pathogen population monitoring. <i>ABIOTECH</i> , 2020, 1, 119-122.	3.9	0

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163	A Phylogeny of Pelargonium Based on TRAP Markers. Hortscience: A Publication of the American Society for Horticultural Science, 2006, 41, 1001C-1001.	1.0	0
164	Dissection of Defence Response Pathways in Rice. Novartis Foundation Symposium, 2001, 236, 190-204.	1.1	0
165	Title is missing!., 2020, 16, e1008355.		0
166	Title is missing!., 2020, 16, e1008355.		0
167	Title is missing!., 2020, 16, e1008355.		0
168	Title is missing!., 2020, 16, e1008355.		0