Yulin Jia

List of Publications by Year in descending order

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116	6,016	36	73
papers	citations	h-index	g-index
118	118	118	4167 citing authors
all docs	docs citations	times ranked	

#	Article	IF	CITATIONS
1	Direct interaction of resistance gene and avirulence gene products confers rice blast resistance. EMBO Journal, 2000, 19, 4004-4014.	3.5	943
2	Initiation of Plant Disease Resistance by Physical Interaction of AvrPto and Pto Kinase. Science, 1996, 274, 2060-2063.	6.0	630
3	A Single Amino Acid Difference Distinguishes Resistant and Susceptible Alleles of the Rice Blast Resistance Gene Pi-ta. Plant Cell, 2000, 12, 2033-2045.	3.1	544
4	Transcriptome and methylome interactions in rice hybrids. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 12040-12045.	3.3	203
5	Instability of the Magnaporthe oryzae avirulence gene AVR-Pita alters virulence. Fungal Genetics and Biology, 2007, 44, 1024-1034.	0.9	157
6	Signatures of adaptation in the weedy rice genome. Nature Genetics, 2017, 49, 811-814.	9.4	146
7	The rice blast resistance gene Ptr encodes an atypical protein required for broad-spectrum disease resistance. Nature Communications, 2018, 9, 2039.	5 . 8	128
8	An early response regulatory cluster induced by low temperature and hydrogen peroxide in seedlings of chilling-tolerant japonica rice. BMC Genomics, 2007, 8, 175.	1.2	123
9	Diversification and evolution of the avirulence gene AVR-Pita1 in field isolates of Magnaporthe oryzae. Fungal Genetics and Biology, 2010, 47, 973-980.	0.9	116
10	Mapping Quantitative Trait Loci Responsible for Resistance to Sheath Blight in Rice. Phytopathology, 2009, 99, 1078-1084.	1.1	115
11	Development of Dominant Rice Blast <i>Piâ€ŧa</i> Resistance Gene Markers. Crop Science, 2002, 42, 2145-2149.	0.8	112
12	Molecular evolution of shattering loci in U.S. weedy rice. Molecular Ecology, 2010, 19, 3271-3284.	2.0	112
13	Genomic patterns of nucleotide diversity in divergent populations of U.S. weedy rice. BMC Evolutionary Biology, 2010, 10, 180.	3.2	98
14	Rapid Determination of Rice Cultivar Responses to the Sheath Blight Pathogen Rhizoctonia solani Using a Micro-Chamber Screening Method. Plant Disease, 2007, 91, 485-489.	0.7	92
15	Determination of Host Responses to Magnaporthe grisea on Detached Rice Leaves Using a Spot Inoculation Method. Plant Disease, 2003, 87, 129-133.	0.7	86
16	Seeing red: the origin of grain pigmentation in US weedy rice. Molecular Ecology, 2010, 19, 3380-3393.	2.0	79
17	Rice Pi-ta gene Confers Resistance to the Major Pathotypes of the Rice Blast Fungus in the United States. Phytopathology, 2004, 94, 296-301.	1.1	78
18	Natural Variation at the Pi-ta Rice Blast Resistance Locus. Phytopathology, 2003, 93, 1452-1459.	1.1	70

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19	Sequence variation at the rice blast resistance gene Pi-km locus: Implications for the development of allele specific markers. Plant Science, 2010, 178, 523-530.	1.7	68
20	Genome-Wide Association of Rice Blast Disease Resistance and Yield-Related Components of Rice. Molecular Plant-Microbe Interactions, 2015, 28, 1383-1392.	1.4	68
21	Rapid transcript accumulation of pathogenesis-related genes during an incompatible interaction in bacterial speck disease-resistant tomato plants. , 1999, 40, 455-465.		61
22	Rapid survey for presence of a blast resistance gene Pi-ta in rice cultivars using the dominant DNA markers derived from portions of the Pi-ta gene. Plant Breeding, 2007, 126, 36-42.	1.0	54
23	Identification of a New Locus, Ptr(t), Required for Rice Blast Resistance Gene Pi-ta–Mediated Resistance. Molecular Plant-Microbe Interactions, 2008, 21, 396-403.	1.4	53
24	Development of a SNLP marker from the Pi-ta blast resistance gene by tri-primer PCR. Euphytica, 2004, 138, 97-105.	0.6	52
25	Identifying Novel Resistance Genes in Newly Introduced Blast Resistant Rice Germplasm. Crop Science, 2006, 46, 1870-1878.	0.8	51
26	More than one way to evolve a weed: parallel evolution of <scp>US</scp> weedy rice through independent genetic mechanisms. Molecular Ecology, 2015, 24, 3329-3344.	2.0	51
27	All roads lead to weediness: Patterns of genomic divergence reveal extensive recurrent weedy rice origins from South Asian <i>Oryza</i> . Molecular Ecology, 2017, 26, 3151-3167.	2.0	51
28	RL-SAGE and microarray analysis of the rice transcriptome after Rhizoctonia solani infection. Molecular Genetics and Genomics, 2007, 278, 421-431.	1.0	50
29	Similar traits, different genes? Examining convergent evolution in related weedy rice populations. Molecular Ecology, 2013, 22, 685-698.	2.0	50
30	Identification of SSR markers for a broad-spectrum blast resistance gene Pi20(t) for marker-assisted breeding. Molecular Breeding, 2008, 22, 141-149.	1.0	48
31	Evolutionary Dynamics of the Genomic Region Around the Blast Resistance Gene <i>Pi-ta</i> in AA Genome Oryza Species. Genetics, 2009, 183, 1315-1325.	1.2	48
32	Analysis of rice blast resistance gene Pi-z in rice germplasm using pathogenicity assays and DNA markers. Euphytica, 2012, 184, 35-46.	0.6	48
33	Confirming QTLs and Finding Additional Loci Responsible for Resistance to Rice Sheath Blight Disease. Plant Disease, 2013, 97, 113-117.	0.7	46
34	Call of the wild rice: <i>Oryza rufipogon</i> shapes weedy rice evolution in Southeast Asia. Evolutionary Applications, 2019, 12, 93-104.	1.5	45
35	Haplotype Diversity at the <i>Pi-ta</i> Locus in Cultivated Rice and Its Wild Relatives. Phytopathology, 2008, 98, 1305-1311.	1.1	43
36	Current progress on genetic interactions of rice with rice blast and sheath blight fungi. Frontiers of Agriculture in China, 2009, 3, 231-239.	0.2	40

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37	Evolutionary Genomics of Weedy Rice in the USA. Journal of Integrative Plant Biology, 2007, 49, 811-816.	4.1	39
38	Alternatively spliced transcripts of Pi-ta blast resistance gene in Oryza sativa. Plant Science, 2009, 177, 468-478.	1.7	36
39	The long and the short of it: <i>SD1</i> polymorphism and the evolution of growth trait divergence in U.S. weedy rice. Molecular Ecology, 2011, 20, 3743-3756.	2.0	36
40	Little White Lies: Pericarp Color Provides Insights into the Origins and Evolution of Southeast Asian Weedy Rice. G3: Genes, Genomes, Genetics, 2016, 6, 4105-4114.	0.8	36
41	tA Single Amino Acid Difference Distinguishes Resistant and Susceptible Alleles of the Rice Blast Resistance Gene Pi-ta. Plant Cell, 2000, 12, 2033.	3.1	33
42	Sheath-blight resistance QTLS in japonica rice germplasm. Euphytica, 2012, 184, 23-34.	0.6	33
43	Artificial introgression of a large chromosome fragment around the rice blast resistance gene Pi-ta in backcross progeny and several elite rice cultivars. Heredity, 2009, 103, 333-339.	1.2	32
44	Identification of the Rice Blast Resistance Gene <i>Pib</i> in the National Small Grains Collection. Phytopathology, 2012, 102, 700-706.	1.1	32
45	Exploring genetic diversity and potential novel disease resistance genes in a collection of rice (Oryza) Tj ETQq1	1 0.78431	4 rgBT /Overl
46	Molecular characterization of the recombinant inbred line population derived from a japonica-indica rice cross. Euphytica, 2007, 159, 73-82.	0.6	30
47	Identification of field isolates of Rhizoctonia solani to detect quantitative resistance in rice under greenhouse conditions. Frontiers of Agriculture in China, 2007, 1, 361-367.	0.2	30
48	Coevolutionary Dynamics of Rice Blast Resistance Gene <i>Pi-ta</i> and <i>Magnaporthe oryzae</i> Avirulence Gene <i>AVR-Pita 1</i> Phytopathology, 2016, 106, 676-683.	1.1	30
49	Molecular Evolution of the Rice Blast Resistance Gene Pi-ta in Invasive Weedy Rice in the USA. PLoS ONE, 2011, 6, e26260.	1.1	30
50	The evolution of flowering strategies in US weedy rice. American Journal of Botany, 2014, 101, 1737-1747.	0.8	28
51	Dynamic Changes in the Rice Blast Population in the United States Over Six Decades. Molecular Plant-Microbe Interactions, 2017, 30, 803-812.	1.4	28
52	Identification of two major resistance genes against race IE-1k of Magnaporthe oryzae in the indica rice cultivar Zhe733. Molecular Breeding, 2009, 24, 127-134.	1.0	27
53	Determination of Resistance Spectra of the <i>Pi-ta</i> and <i>Pi-k</i> Genes to U.S. Races of <i>Magnaporthe oryzae</i> Causing Rice Blast in a Recombinant Inbred Line Population. Plant Disease, 2009, 93, 639-644.	0.7	27
54	Deep transcriptome sequencing reveals the expression of key functional and regulatory genes involved in the abiotic stress signaling pathways in rice. Journal of Plant Biology, 2013, 56, 216-231.	0.9	27

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55	Identification of rice blast resistance genes using international monogenic differentials. Crop Protection, 2013, 45, 109-116.	1.0	26
56	Inoculation and Scoring Methods for Rice Sheath Blight Disease. Methods in Molecular Biology, 2013, 956, 257-268.	0.4	26
57	Mapping Quantitative Trait Loci for Resistance to Rice Blast. Phytopathology, 2011, 101, 176-181.	1.1	25
58	Analysis of Genetic and Molecular Identity Among Field Isolates of the Rice Blast Fungus with an International Differential System, Rep-PCR, and DNA Sequencing. Plant Disease, 2013, 97, 491-495.	0.7	25
59	Integration Analysis of Small RNA and Degradome Sequencing Reveals MicroRNAs Responsive to Dickeya zeae in Resistant Rice. International Journal of Molecular Sciences, 2019, 20, 222.	1.8	25
60	Marker assisted selection for the control of rice blast disease. Outlooks on Pest Management, 2003, 14, 150.	0.2	24
61	QTL Analysis for Resistance to Blast Disease in U.S. Weedy Rice. Molecular Plant-Microbe Interactions, 2015, 28, 834-844.	1.4	23
62	Characterization of rice blast resistance genes in rice germplasm with monogenic lines and pathogenicity assays. Crop Protection, 2015, 72, 132-138.	1.0	22
63	Weedy red rice has novel sources of resistance to biotic stress. Crop Journal, 2018, 6, 443-450.	2.3	22
64	Comparative analysis of putative pathogenesis-related gene expression in two Rhizoctonia solani pathosystems. Current Genetics, 2011, 57, 391-408.	0.8	21
65	Indica and Japonica Crosses Resulting in Linkage Block and Recombination Suppression on Rice Chromosome 12. PLoS ONE, 2012, 7, e43066.	1.1	20
66	Characterization of Molecular Identity and Pathogenicity of Rice Blast Fungus in Hunan Province of China. Plant Disease, 2017, 101, 557-561.	0.7	20
67	Registration of TIL:455, TIL:514, and TIL:642, Three Rice Germplasm Lines Containing Introgressed Sheath Blight Resistance Alleles. Journal of Plant Registrations, 2008, 2, 251-254.	0.4	19
68	Identification of Novel QTL Conferring Sheath Blight Resistance in Two Weedy Rice Mapping Populations. Rice, 2020, 13, 21.	1.7	18
69	Structural and expressional analysis of the B-hordein genes in Tibetan hull-less barley. Genetica, 2010, 138, 227-239.	0.5	17
70	Tagging quantitative trait loci for heading date and plant height in important breeding parents of rice (Oryza sativa). Euphytica, 2014, 197, 191-200.	0.6	17
71	Natural variation of rice blast resistance gene Pi-d2. Genetics and Molecular Research, 2015, 14, 1235-1249.	0.3	17
72	The Role of Standing Variation in the Evolution of Weedines Traits in South Asian Weedy Rice (<i>Oryza</i> spp.). G3: Genes, Genomes, Genetics, 2018, 8, 3679-3690.	0.8	17

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7 3	Development of Monogenic and Digenic Rice Lines for Blast Resistance Genes <i>Piâ€ta</i> , <i>Piâ€k^h</i> /i>/ia€k ^s . Journal of Plant Registrations, 2010, 4, 163-166.	0.4	16
74	Three Quantitative Trait Loci Conferring Resistance to Kernel Fissuring in Rice Identified by Selective Genotyping in Two Tropical Japonica Populations. Crop Science, 2013, 53, 2434-2443.	0.8	16
7 5	A User-Friendly Method to Isolate and Single Spore the Fungi Magnaporthe oryzae and Magnaporthe grisea Obtained from Diseased Field Samples. Plant Health Progress, 2009, 10, 37.	0.8	15
76	Effectiveness and Durability of the Rice <i>Pi-ta</i> Gene in Yunnan Province of China. Phytopathology, 2014, 104, 762-768.	1.1	14
77	Registration of a Rice Geneâ€Mapping Population Consisting of â€̃TeQing'â€intoâ€â€̃Lemont' Backcross Introgression Lines. Journal of Plant Registrations, 2012, 6, 128-135.	S 0.4	14
78	Registration of Four Rice Germplasm Lines with Improved Resistance to Sheath Blight and Blast Diseases. Journal of Plant Registrations, 2012, 6, 95-100.	0.4	13
79	Characterization of resistance genes to rice blast fungus Magnaporthe oryzae in a "Green Revolution―rice variety. Molecular Breeding, 2015, 35, 1.	1.0	13
80	Identification of a <i>Pi9</i> -Containing Rice Germplasm with a Newly Developed Robust Marker. Phytopathology, 2016, 106, 871-876.	1.1	12
81	Response to Early Generation Selection for Resistance to Rice Kernel Fissuring. Crop Science, 2012, 52, 1482-1492.	0.8	11
82	Identification of Candidate Genes Associated with Positive and Negative Heterosis in Rice. PLoS ONE, 2014, 9, e95178.	1.1	11
83	Evaluation of Rice Responses to the Blast Fungus <i>Magnaporthe oryzae</i> at Different Growth Stages. Plant Disease, 2019, 103, 132-136.	0.7	11
84	Characterization of Field Isolates of <i>Magnaporthe oryzae</i> with Mating Type, DNA Fingerprinting, and Pathogenicity Assays. Plant Disease, 2016, 100, 298-303.	0.7	10
85	Selection and mutation of the avirulence gene <i>AVRâ€Pii</i> of the rice blast fungus <i>Magnaporthe oryzae</i> . Plant Pathology, 2019, 68, 127-134.	1.2	10
86	Examination of the Rice Blast Pathogen Population Diversity in Arkansas, USA – Stable or Unstable?. , 2009, , 217-228.		9
87	Functional Interactions Between Major Rice Blast Resistance Genes, <i>Pi-ta</i> and <ipi-b< i="">, and Minor Blast Resistance Quantitative Trait Loci. Phytopathology, 2018, 108, 1095-1103.</ipi-b<>	1.1	9
88	Characterization of Rice Blast Resistance Gene <i>Pi61(t)</i> in Rice Germplasm. Plant Disease, 2014, 98, 1200-1204.	0.7	8
89	Transgenic Rice Expressing Isoflavone Synthase Gene from Soybean Shows Resistance Against Blast Fungus (<i>Magnaporthe oryzae</i>). Plant Disease, 2021, 105, 3141-3146.	0.7	8
90	Field Resistance Expressed when the Pi-ta Gene is Compromised by Magnaporthe oryzae., 2009,, 281-289.		8

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91	Carolina Foxtail (<i>Alopecurus carolinianus</i>): Susceptibility and Suitability as an Alternative Host to Rice Blast Disease (<i>Magnaporthe oryzae</i> [formerly <i>M. grisea</i>]). Plant Disease, 2008, 92, 504-507.	0.7	7
92	An expedited method for isolation of DNA for PCR from Magnaporthe oryzae stored on filter paper. Crop Journal, 2014, 2, 267-271.	2.3	7
93	Induction of avirulence by AVR-Pita1 in virulent U.S. field isolates of Magnaporthe oryzae. Crop Journal, 2014, 2, 1-9.	2.3	7
94	Confirming and Identifying New Loci for Rice Blast Disease Resistance using <i>Magnaporthe oryzae</i> Field Isolates in the US. Crop Science, 2015, 55, 2620-2627.	0.8	7
95	Molecular mapping of four blast resistance genes using recombinant inbred lines of 93-11 and nipponbare. Journal of Plant Biology, 2013, 56, 91-97.	0.9	6
96	Statistical Inference of Selection and Divergence of the Rice Blast Resistance Gene <i>Pi-ta</i> Genes, Genomes, Genetics, 2014, 4, 2425-2432.	0.8	6
97	QTLs for Early Tiller Production and Relationships with Rapid Seedling Growth and Increased Panicle Number in Rice. Crop Science, 2016, 56, 505-519.	0.8	6
98	Genetic variation and evolution of the Pit blast resistance locus in rice. Genetic Resources and Crop Evolution, 2014, 61, 473-489.	0.8	5
99	A Toolbox for Managing Blast and Sheath Blight Diseases of Rice in the United States of America. , 2019, , .		5
100	Host Active Defense Responses Occur within 24 Hours after Pathogen Inoculation in the Rice Blast System. Rice Science, 2007, 14, 302-310.	1.7	4
101	Marker Development for Rice Blast Resistance Gene Pi66(t) and Application in the USDA Rice Miniâ€Core Collection. Crop Science, 2016, 56, 1001-1008.	0.8	4
102	Novel QTLs Affecting Rice Kernel Fissure Resistance Discovered in the Cultivar â€~Saber' Augment Those from â€~Cybonnet'. Crop Science, 2018, 58, 1531-1541.	0.8	4
103	<i>Bacillus subtilis</i> GB519 Promotes Rice Growth and Reduces the Damages Caused by Rice Blast Fungus <i>Magnaporthe oryzae</i> . PhytoFrontiers, 2021, 1, 330-338.	0.8	4
104	Analysis of Differentially Expressed Rice Genes Reveals the ATP-Binding Cassette Transporters as Candidate Genes Against the Sheath Blight Pathogen, <i>Rhizoctonia solani</i> . PhytoFrontiers, 2022, 2, 105-115.	0.8	4
105	Understanding the Co-evolution of the Rice Blast Resistance Gene PI-TA and Magnaporthe oryzae Avirulence Gene AVR-PITA., 2009, , 137-147.		4
106	Registration of a Rice Gene Mapping Population of Lemont \tilde{A} — Jasmine 85 Recombinant Inbred Lines. Journal of Plant Registrations, 2015, 9, 128-132.	0.4	3
107	Registration of 42 Blast Resistant Medium Grain Rice Genetic Stocks with Suitable Agronomic, Yield, Milling Yield, and Seed Characteristics. Journal of Plant Registrations, 2016, 10, 316-324.	0.4	3
108	A Rapid Survey of Avirulence Genes in Field Isolates of Magnaporthe oryzae. Plant Disease, 2020, 104, 717-723.	0.7	3

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109	Exploring natural variation for rice sheath blight resistance in Brachypodium distachyon. Plant Signaling and Behavior, 2019, 14, 1546527.	1.2	2
110	Physiological, Ecological and Genetic Interactions of Rice with Harmful Microbes. , 0, , .		2
111	Introductory Chapter: Protecting Rice Grains in the Post-Genomic Era: Are We There Yet?., 0, , .		2
112	An Allelic Variant of the Broad-Spectrum Blast Resistance Gene <i>Ptr</i> in Weedy Rice Is Associated with Resistance to the Most Virulent Blast Race IB-33. Plant Disease, 2022, 106, 1675-1680.	0.7	2
113	Registration of two rice mapping populations using weedy rice ecotypes as a novel germplasm resource. Journal of Plant Registrations, 2022, 16, 162-175.	0.4	2
114	Cloning and Characterization of Two Members of the Pto Gene Family: the Pto Bacterial Resistance Gene and the Fen Insecticide Sensitivity Gene Current Plant Science and Biotechnology in Agriculture, 1994, , 273-282.	0.0	0
115	Effectiveness and durability of the ricePi-tagene in Yunnan province of China. Phytopathology, 0, , PHYTO-11-13-000.	1.1	0
116	Mapping Blast Resistance Genes in Rice Varieties â€~Minghui 63' and â€~M-202'. Plant Disease, 2021, , .	0.7	0