

Wang Shuaishuai

List of Publications by Year in descending order

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98
papers

3,422
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136740

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168136

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docs citations

102
times ranked

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#	ARTICLE	IF	CITATIONS
1	ATAC-seq reveals the landscape of open chromatin and cis-regulatory elements in the <i>Phytophthora sojae</i> genome. <i>Molecular Plant-Microbe Interactions</i> , 2022, , .	1.4	5
2	A novel LAMP assay using hot water in vacuum insulated bottle for rapid detection of the soybean red crown rot pathogen <i>Calonectria ilicicola</i> . <i>Australasian Plant Pathology</i> , 2022, 51, 251-259.	0.5	1
3	Wheat Straw Return Influences Soybean Root-Associated Bacterial and Fungal Microbiota in a Wheat–Soybean Rotation System. <i>Microorganisms</i> , 2022, 10, 667.	1.6	4
4	<i>Diaporthe</i> Diversity and Pathogenicity Revealed from a Broad Survey of Soybean Stem Blight in China. <i>Plant Disease</i> , 2022, 106, 2892-2903.	0.7	4
5	Molug4 is a novel secreted effector promoting rice blast by counteracting host OsAHL1-regulated ethylene gene transcription. <i>New Phytologist</i> , 2022, 235, 1163-1178.	3.5	7
6	Transcription factor MoMsn2 targets the putative 3-methylglutaconyl-CoA hydratase-encoding gene MoAUH1 to govern infectious growth via mitochondrial fusion/fission balance in <i>Magnaporthe oryzae</i> . <i>Environmental Microbiology</i> , 2021, 23, 774-790.	1.8	9
7	Phosphatase-associated protein MoTip41 interacts with the phosphatase MoPpe1 to mediate crosstalk between TOR and cell wall integrity signalling during infection by the rice blast fungus <i>Magnaporthe oryzae</i> . <i>Environmental Microbiology</i> , 2021, 23, 791-809.	1.8	18
8	Genome Analysis of Two Newly Emerged Potato Late Blight Isolates Sheds Light on Pathogen Adaptation and Provides Tools for Disease Management. <i>Phytopathology</i> , 2021, 111, 96-107.	1.1	9
9	Cleavage of a pathogen apoplastic protein by plant subtilases activates host immunity. <i>New Phytologist</i> , 2021, 229, 3424-3439.	3.5	24
10	Auxilin-like protein MoSwa2 promotes effector secretion and virulence as a clathrin uncoating factor in the rice blast fungus <i>Magnaporthe oryzae</i> . <i>New Phytologist</i> , 2021, 230, 720-736.	3.5	33
11	<i>Pythium huanghuaiense</i> sp. nov. isolated from soybean: morphology, molecular phylogeny and pathogenicity. <i>Biodiversity Data Journal</i> , 2021, 9, e65227.	0.4	2
12	Development of LAMP Assays Using a Novel Target Gene for Specific Detection of <i>Pythium terrestris</i> , <i>Pythium spinosum</i> , and <i>Candidatus Pythium huanghuaiense</i> ™. <i>Plant Disease</i> , 2021, 105, 2888-2897.	0.7	3
13	First report of soybean stem blight caused by <i>Diaporthe phaseolorum</i> in Sichuan province, China. <i>Plant Disease</i> , 2021, , .	0.7	1
14	The rice blast fungus MoRgs1 functioning in cAMP signaling and pathogenicity is regulated by casein kinase MoCk2 phosphorylation and modulated by membrane protein MoEmc2. <i>PLoS Pathogens</i> , 2021, 17, e1009657.	2.1	22
15	Genome Sequence Resource of <i>Phomopsis longicolla</i> YC2-1, a Fungal Pathogen Causing <i>Phomopsis</i> Stem Blight in Soybean. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 842-844.	1.4	6
16	A CRISPR/Cas9-mediated in situ complementation method for <i>Phytophthora sojae</i> mutants. <i>Molecular Plant Pathology</i> , 2021, 22, 373-381.	2.0	25
17	Balancing of the mitotic exit network and cell wall integrity signaling governs the development and pathogenicity in <i>Magnaporthe oryzae</i> . <i>PLoS Pathogens</i> , 2021, 17, e1009080.	2.1	24
18	Specific interaction of an RNA-binding protein with the 3'-UTR of its target mRNA is critical to oomycete sexual reproduction. <i>PLoS Pathogens</i> , 2021, 17, e1010001.	2.1	13

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19	An atypical <i>Phytophthora sojae</i> RxLR effector manipulates host vesicle trafficking to promote infection. <i>PLoS Pathogens</i> , 2021, 17, e1010104.	2.1	9
20	The Peroxisomal-CoA Synthetase MoPcs60 Is Important for Fatty Acid Metabolism and Infectious Growth of the Rice Blast Fungus. <i>Frontiers in Plant Science</i> , 2021, 12, 811041.	1.7	6
21	An Improved Method for the Identification of Soybean Resistance to <i>Phytophthora sojae</i> Applied to Germplasm Resources from the Huanghuaihai and Dongbei Regions of China. <i>Plant Disease</i> , 2020, 104, 408-413.	0.7	5
22	Shedding light on autophagy coordinating with cell wall integrity signaling to govern pathogenicity of <i>Magnaporthe oryzae</i> . <i>Autophagy</i> , 2020, 16, 900-916.	4.3	72
23	Conserved Subgroups of the Plant-Specific RWP-RK Transcription Factor Family Are Present in Oomycete Pathogens. <i>Frontiers in Microbiology</i> , 2020, 11, 1724.	1.5	11
24	Identification of Resistance Genes to <i>Phytophthora sojae</i> in Domestic Soybean Cultivars from China Using Particle Bombardment. <i>Plant Disease</i> , 2020, 104, 1888-1893.	0.7	3
25	Extracellular proteolytic cascade in tomato activates immune protease Rcr3. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 17409-17417.	3.3	55
26	G protein β subunit suppresses sporangium formation through a serine/threonine protein kinase in <i>Phytophthora sojae</i> . <i>PLoS Pathogens</i> , 2020, 16, e1008138.	2.1	13
27	MicroRNA-like millR236, regulated by transcription factor MoMsn2, targets histone acetyltransferase MoHat1 to play a role in appressorium formation and virulence of the rice blast fungus <i>Magnaporthe oryzae</i> . <i>Fungal Genetics and Biology</i> , 2020, 137, 103349.	0.9	11
28	Pathogenicity and fungicide sensitivity of <i>Pythium</i> and <i>Phytophthora</i> spp. associated with soybean in the Huanghuai region of China. <i>Plant Pathology</i> , 2020, 69, 1083-1092.	1.2	14
29	<i>Magnaporthe oryzae</i> Auxiliary Activity Protein MoAa91 Functions as Chitin-Binding Protein To Induce Appressorium Formation on Artificial Inductive Surfaces and Suppress Plant Immunity. <i>MBio</i> , 2020, 11, .	1.8	38
30	A self-balancing circuit centered on MoOsm1 kinase governs adaptive responses to host-derived ROS in <i>Magnaporthe oryzae</i> . <i>ELife</i> , 2020, 9, .	2.8	47
31	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.	3.3	68
32	Wheat Straw Return Influences Nitrogen-Cycling and Pathogen Associated Soil Microbiota in a Wheat-Soybean Rotation System. <i>Frontiers in Microbiology</i> , 2019, 10, 1811.	1.5	36
33	Comparative Evaluation of a Novel Recombinase Polymerase Amplification-Lateral Flow Dipstick (RPA-LFD) Assay, LAMP, Conventional PCR, and Leaf-Disc Baiting Methods for Detection of <i>Phytophthora sojae</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 1884.	1.5	56
34	A loop-mediated isothermal amplification assay can rapidly diagnose soybean root-rot and damping-off diseases caused by <i>Pythium spinosum</i> . <i>Australasian Plant Pathology</i> , 2019, 48, 553-562.	0.5	4
35	The inhibitor of apoptosis protein MoBir1 is involved in the suppression of hydrogen peroxide-induced fungal cell death, reactive oxygen species generation, and pathogenicity of rice blast fungus. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 6617-6627.	1.7	8
36	The t-SNARE protein FgPep12, associated with FgVam7, is essential for ascospore discharge and plant infection by trafficking Ca ²⁺ ATPase FgNeo1 between Golgi and endosome/vacuole in <i>Fusarium graminearum</i> . <i>PLoS Pathogens</i> , 2019, 15, e1007754.	2.1	35

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37	The seven transmembrane domain protein MoRgs7 functions in surface perception and undergoes coronin MoCrm1-dependent endocytosis in complex with GÎ± subunit MoMagA to promote cAMP signaling and appressorium formation in <i>Magnaporthe oryzae</i> . <i>PLoS Pathogens</i> , 2019, 15, e1007382.	2.1	28
38	Histone acetyltransferase MoHat1 acetylates autophagy-related proteins MoAtg3 and MoAtg9 to orchestrate functional appressorium formation and pathogenicity in <i>Magnaporthe oryzae</i> . <i>Autophagy</i> , 2019, 15, 1234-1257.	4.3	69
39	System-Wide Characterization of MoArf GTPase Family Proteins and Adaptor Protein MoGga1 Involved in the Development and Pathogenicity of <i>Magnaporthe oryzae</i> . <i>MBio</i> , 2019, 10, .	1.8	14
40	Natural allelic variations provide insights into host adaptation of <i>Phytophthora</i> avirulence effector PsAvr3c. <i>New Phytologist</i> , 2019, 221, 1010-1022.	3.5	37
41	Development of seven novel specific SCAR markers for rapid identification of <i>Phytophthora sojae</i> : the cause of root- and stem-rot disease of soybean. <i>European Journal of Plant Pathology</i> , 2019, 153, 517-531.	0.8	4
42	Molmd4 mediates crosstalk between MoPdeH cAMP signalling and purine metabolism to govern growth and pathogenicity in <i>Magnaporthe oryzae</i> . <i>Molecular Plant Pathology</i> , 2019, 20, 500-518.	2.0	11
43	<i>Magnaporthe oryzae</i> Abp1, a MoArk1 Kinase-Interacting Actin Binding Protein, Links Actin Cytoskeleton Regulation to Growth, Endocytosis, and Pathogenesis. <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 437-451.	1.4	11
44	A subunit of the HOPS endocytic tethering complex, FgVps41, is important for fungal development and plant infection in <i>Fusarium graminearum</i> . <i>Environmental Microbiology</i> , 2018, 20, 1436-1451.	1.8	22
45	Rapid diagnosis of rice bakanae caused by <i>Fusarium fujikuroi</i> and <i>F. proliferatum</i> using loop-mediated isothermal amplification assays. <i>Journal of Phytopathology</i> , 2018, 166, 283-290.	0.5	11
46	Disruption of actin motor function due to MoMyo5 mutation impairs host penetration and pathogenicity in <i>Magnaporthe oryzae</i> . <i>Molecular Plant Pathology</i> , 2018, 19, 689-699.	2.0	13
47	New findings on phosphodiesterases, MoPdeH and MoPdeL, in <i>Magnaporthe oryzae</i> revealed by structural analysis. <i>Molecular Plant Pathology</i> , 2018, 19, 1061-1074.	2.0	8
48	MoPpe1 partners with MoSap1 to mediate TOR and cell wall integrity signalling in growth and pathogenicity of the rice blast fungus <i>Magnaporthe oryzae</i> . <i>Environmental Microbiology</i> , 2018, 20, 3964-3979.	1.8	35
49	MoYvh1 subverts rice defense through functions of ribosomal protein MoMrt4 in <i>Magnaporthe oryzae</i> . <i>PLoS Pathogens</i> , 2018, 14, e1007016.	2.1	32
50	A 2-year field trial reveals no significant effects of GM high-methionine soybean on the rhizosphere bacterial communities. <i>World Journal of Microbiology and Biotechnology</i> , 2018, 34, 113.	1.7	10
51	Endophytic fungal communities associated with field-grown soybean roots and seeds in the Huang-Huai region of China. <i>PeerJ</i> , 2018, 6, e4713.	0.9	35
52	MoMip11, a MoRgs7-interacting protein, functions as a scaffolding protein to regulate cAMP signaling and pathogenicity in the rice blast fungus <i>Magnaporthe oryzae</i> . <i>Environmental Microbiology</i> , 2018, 20, 3168-3185.	1.8	16
53	Heat-Shock Proteins MoSsb1, MoSsz1, and MoZuo1 Attenuate MoMkk1-Mediated Cell-Wall Integrity Signaling and Are Important for Growth and Pathogenicity of <i>Magnaporthe oryzae</i> . <i>Molecular Plant-Microbe Interactions</i> , 2018, 31, 1211-1221.	1.4	42
54	A paralogous decoy protects <i>Phytophthora sojae</i> apoplastic effector PsXEG1 from a host inhibitor. <i>Science</i> , 2017, 355, 710-714.	6.0	236

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55	The FgVps39-FgVam7-FgSso1 Complex Mediates Vesicle Trafficking and Is Important for the Development and Virulence of <i>Fusarium graminearum</i> . <i>Molecular Plant-Microbe Interactions</i> , 2017, 30, 410-422.	1.4	38
56	MoVrp1, a putative verprolin protein, is required for asexual development and infection in the rice blast fungus <i>Magnaporthe oryzae</i> . <i>Scientific Reports</i> , 2017, 7, 41148.	1.6	13
57	Rapid diagnosis of wheat head blight caused by <i>Fusarium asiaticum</i> using a loop-mediated isothermal amplification assay. <i>Australasian Plant Pathology</i> , 2017, 46, 261-266.	0.5	11
58	The ArfGAP protein MoGlo3 regulates the development and pathogenicity of <i>Magnaporthe oryzae</i> . <i>Environmental Microbiology</i> , 2017, 19, 3982-3996.	1.8	18
59	Rapid diagnosis of soybean anthracnose caused by <i>Colletotrichum truncatum</i> using a loop-mediated isothermal amplification (LAMP) assay. <i>European Journal of Plant Pathology</i> , 2017, 148, 785-793.	0.8	21
60	Rapid Diagnosis of Soya Bean Root Rot Caused by <i>Fusarium culmorum</i> Using a Loop-Mediated Isothermal Amplification Assay. <i>Journal of Phytopathology</i> , 2017, 165, 249-256.	0.5	15
61	Rapid detection of <i>Colletotrichum gloeosporioides</i> using a loop-mediated isothermal amplification assay. <i>Australasian Plant Pathology</i> , 2017, 46, 493-498.	0.5	12
62	An oomycete plant pathogen reprograms host pre-mRNA splicing to subvert immunity. <i>Nature Communications</i> , 2017, 8, 2051.	5.8	84
63	The thioredoxin MoTrx2 protein mediates reactive oxygen species (ROS) balance and controls pathogenicity as a target of the transcription factor MoAP1 in <i>Magnaporthe oryzae</i> . <i>Molecular Plant Pathology</i> , 2017, 18, 1199-1209.	2.0	37
64	The Atypical Guanylate Kinase MoGuk2 Plays Important Roles in Asexual/Sexual Development, Conidial Septation, and Pathogenicity in the Rice Blast Fungus. <i>Frontiers in Microbiology</i> , 2017, 8, 2467.	1.5	11
65	MoCAP proteins regulated by MoArk1-mediated phosphorylation coordinate endocytosis and actin dynamics to govern development and virulence of <i>Magnaporthe oryzae</i> . <i>PLoS Genetics</i> , 2017, 13, e1006814.	1.5	46
66	MoEnd3 regulates appressorium formation and virulence through mediating endocytosis in rice blast fungus <i>Magnaporthe oryzae</i> . <i>PLoS Pathogens</i> , 2017, 13, e1006449.	2.1	81
67	Carbamoyl Phosphate Synthetase Subunit MoCpa2 Affects Development and Pathogenicity by Modulating Arginine Biosynthesis in <i>Magnaporthe oryzae</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 2023.	1.5	18
68	Phosphodiesterase MoPdeH targets MoMck1 of the conserved mitogen-activated protein (MAP) kinase signalling pathway to regulate cell wall integrity in rice blast fungus <i>Magnaporthe oryzae</i> . <i>Molecular Plant Pathology</i> , 2016, 17, 654-668.	2.0	59
69	The <i>Magnaporthe grisea</i> species complex and plant pathogenesis. <i>Molecular Plant Pathology</i> , 2016, 17, 796-804.	2.0	100
70	The syntaxin protein (MoSyn8) mediates intracellular trafficking to regulate conidiogenesis and pathogenicity of rice blast fungus. <i>New Phytologist</i> , 2016, 209, 1655-1667.	3.5	87
71	Sequencing of the Litchi Downy Blight Pathogen Reveals It Is a <i>Phytophthora</i> Species With Downy Mildew-Like Characteristics. <i>Molecular Plant-Microbe Interactions</i> , 2016, 29, 573-583.	1.4	73
72	FgMon1, a guanine nucleotide exchange factor of FgRab7, is important for vacuole fusion, autophagy and plant infection in <i>Fusarium graminearum</i> . <i>Scientific Reports</i> , 2016, 5, 18101.	1.6	57

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73	The Putative Protein Phosphatase MoYvh1 Functions Upstream of MoPdeH to Regulate the Development and Pathogenicity in <i>Magnaporthe oryzae</i> . <i>Molecular Plant-Microbe Interactions</i> , 2016, 29, 496-507.	1.4	49
74	Orotate phosphoribosyl transferase MoPyr5 is involved in uridine 5â€²-phosphate synthesis and pathogenesis of <i>Magnaporthe oryzae</i> . <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 3655-3666.	1.7	9
75	Genome plasticity in filamentous plant pathogens contributes to the emergence of novel effectors and their cellular processes in the host. <i>Current Genetics</i> , 2016, 62, 47-51.	0.8	9
76	MADS1, a novel MADS-box protein, is involved in the response of <i>Nicotiana benthamiana</i> to bacterial harpin _{Xoo} . <i>Journal of Experimental Botany</i> , 2016, 67, 131-141.	2.4	41
77	SNARE protein FgVam7 controls growth, asexual and sexual development, and plant infection in <i>Fusarium graminearum</i> . <i>Molecular Plant Pathology</i> , 2016, 17, 108-119.	2.0	45
78	Glycoside Hydrolase MoGls2 Controls Asexual/Sexual Development, Cell Wall Integrity and Infectious Growth in the Rice Blast Fungus. <i>PLoS ONE</i> , 2016, 11, e0162243.	1.1	21
79	MoDnm1 Dynamin Mediating Peroxisomal and Mitochondrial Fission in Complex with MoFis1 and MoMdv1 Is Important for Development of Functional Appressorium in <i>Magnaporthe oryzae</i> . <i>PLoS Pathogens</i> , 2016, 12, e1005823.	2.1	62
80	Rapid Diagnosis of Soybean Seedling Blight Caused by <i>Rhizoctonia solani</i> and Soybean Charcoal Rot Caused by <i>Macrophomina phaseolina</i> Using LAMP Assays. <i>Phytopathology</i> , 2015, 105, 1612-1617.	1.1	21
81	MoTup1 is required for growth, conidiogenesis and pathogenicity of <i>Magnaporthe oryzae</i> . <i>Molecular Plant Pathology</i> , 2015, 16, 799-810.	2.0	30
82	Global Genome and Transcriptome Analyses of <i>Magnaporthe oryzae</i> Epidemic Isolate 98-06 Uncover Novel Effectors and Pathogenicity-Related Genes, Revealing Gene Gain and Lose Dynamics in Genome Evolution. <i>PLoS Pathogens</i> , 2015, 11, e1004801.	2.1	148
83	A <i>Phytophthora sojae</i> Glycoside Hydrolase 12 Protein Is a Major Virulence Factor during Soybean Infection and Is Recognized as a PAMP. <i>Plant Cell</i> , 2015, 27, 2057-2072.	3.1	335
84	MoMyb1 is required for asexual development and tissue-specific infection in the rice blast fungus <i>Magnaporthe oryzae</i> . <i>BMC Microbiology</i> , 2015, 15, 37.	1.3	21
85	The importin Î± subunit PsIMPA1 mediates the oxidative stress response and is required for the pathogenicity of <i>Phytophthora sojae</i> . <i>Fungal Genetics and Biology</i> , 2015, 82, 108-115.	0.9	11
86	Development of a Loop-Mediated Isothermal Amplification Assay to Detect <i>Fusarium oxysporum</i> . <i>Journal of Phytopathology</i> , 2015, 163, 63-66.	0.5	19
87	Community Structure of Arbuscular Mycorrhizal Fungi in Rhizospheric Soil of a Transgenic High-Methionine Soybean and a Near Isogenic Variety. <i>PLoS ONE</i> , 2015, 10, e0145001.	1.1	18
88	Comparison of the Rhizosphere Bacterial Communities of Zigongdongdou Soybean and a High-Methionine Transgenic Line of This Cultivar. <i>PLoS ONE</i> , 2014, 9, e103343.	1.1	55
89	ALY proteins participate in multifaceted Nep1Mo-triggered responses in <i>Nicotiana benthamiana</i> and <i>Arabidopsis thaliana</i> . <i>Journal of Experimental Botany</i> , 2014, 65, 2483-2494.	2.4	23
90	Threonine deaminase Mollv1 is important for conidiogenesis and pathogenesis in the rice blast fungus <i>Magnaporthe oryzae</i> . <i>Fungal Genetics and Biology</i> , 2014, 73, 53-60.	0.9	27

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91	MoLys2 is necessary for growth, conidiogenesis, lysine biosynthesis, and pathogenicity in <i>Magnaporthe oryzae</i> . <i>Fungal Genetics and Biology</i> , 2014, 67, 51-57.	0.9	36
92	The RxLR effector Avh241 from <i>Phytophthora sojae</i> requires plasma membrane localization to induce plant cell death. <i>New Phytologist</i> , 2012, 196, 247-260.	3.5	151
93	Development of a loop-mediated isothermal amplification assay for detection of <i>Phytophthora sojae</i> . <i>FEMS Microbiology Letters</i> , 2012, 334, 27-34.	0.7	83
94	Distribution, Pathotypes, and Metalaxyl Sensitivity of <i>Phytophthora sojae</i> from Heilongjiang and Fujian Provinces in China. <i>Plant Disease</i> , 2010, 94, 881-884.	0.7	50
95	Green fluorescent protein (GFP) as a vital marker for studying the interaction of <i>Phytophthora sojae</i> and soybean. <i>Science Bulletin</i> , 2009, 54, 2822-2829.	4.3	2
96	The LCB ₂ subunit of the sphingolip biosynthesis enzyme serine palmitoyltransferase can function as an attenuator of the hypersensitive response and Bax-induced cell death. <i>New Phytologist</i> , 2009, 181, 127-146.	3.5	32
97	Cloning of genes encoding nonhost hypersensitive response-inducing elicitors from <i>Phytophthora boehmeriae</i> . <i>Science Bulletin</i> , 2007, 52, 231-237.	1.7	2
98	A <i>Phytophthora sojae</i> gene of glyceraldehyde-3-phosphate dehydrogenase (GAPDH) induced in host infection and its anti-oxidative function in yeast. <i>Science Bulletin</i> , 2006, 51, 1316-1323.	1.7	5