Wenwu Ye

List of Publications by Year in descending order

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85	4,054	159358 30	128067 60
papers	citations	h-index	g-index

90	90	90	2942
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Improved Whole-Genome Sequence of Fusarium meridionale, the Fungal Pathogen Causing Fusarium Head Blight in Rice. Molecular Plant-Microbe Interactions, 2022, 35, 85-89.	1.4	1
2	ATAC-seq reveals the landscape of open chromatin and cis-regulatory elements in the Phytophthora sojae genome. Molecular Plant-Microbe Interactions, 2022, , .	1.4	5
3	Phytophthora sojae Transformation Based on the CRISPR/Cas9 System. Bio-protocol, 2022, 12, e4352.	0.2	4
4	Wheat Straw Return Influences Soybean Root-Associated Bacterial and Fungal Microbiota in a Wheatâ€“Soybean Rotation System. Microorganisms, 2022, 10, 667.	1.6	4
5	A new distinct geminivirus causes soybean stay-green disease. Molecular Plant, 2022, 15, 927-930.	3.9	17
6	Diaporthe Diversity and Pathogenicity Revealed from a Broad Survey of Soybean Stem Blight in China. Plant Disease, 2022, 106, 2892-2903.	0.7	4
7	Transcription factor <scp>MoMsn2</scp> targets the putative <scp>3â€methylglutaconylâ€CoA</scp> hydrataseâ€encoding gene <scp>MoAUH1</scp> to govern infectious growth via mitochondrial fusion/fission balance in Magnaporthe oryzae. Environmental Microbiology, 2021, 23, 774-790.	1.8	9
8	Fg12 ribonuclease secretion contributes to Fusarium graminearum virulence and induces plant cell death. Journal of Integrative Plant Biology, 2021, 63, 365-377.	4.1	47
9	Genome Analysis of Two Newly Emerged Potato Late Blight Isolates Sheds Light on Pathogen Adaptation and Provides Tools for Disease Management. Phytopathology, 2021, 111, 96-107.	1.1	9
10	The bZIP transcription factor PsBZP32 is involved in cyst germination, oxidative stress response, and pathogenicity of Phytophthora sojae. Phytopathology Research, 2021, 3, .	0.9	8
11	Editorial: Genomics and Effectomics of Filamentous Plant Pathogens. Frontiers in Genetics, 2021, 12, 648690.	1.1	2
12	Phytophthora sojae effector Avr1d functions as an E2 competitor and inhibits ubiquitination activity of GmPUB13 to facilitate infection. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	35
13	Pythium huanghuaiense sp. nov. isolated from soybean: morphology, molecular phylogeny and pathogenicity. Biodiversity Data Journal, 2021, 9, e65227.	0.4	2
14	Development of LAMP Assays Using a Novel Target Gene for Specific Detection of Pythium terrestris, Pythium spinosum, and â€˜Candidatus Pythium huanghuaienseâ€™. Plant Disease, 2021, 105, 2888-2897.	0.7	3
15	The Phytophthora effector Avh241 interacts with host NDR1â€like proteins to manipulate plant immunity. Journal of Integrative Plant Biology, 2021, 63, 1382-1396.	4.1	16
16	First report of soybean stem blight caused by Diaporthe phaseolorum in Sichuan province, China. Plant Disease, 2021, , .	0.7	1
17	Genome Sequence Data of three formae speciales of Phytophthora vignae Causing Phytophthora Stem Rot on different Vigna species. Plant Disease, 2021, , PDIS11202546A.	0.7	3
18	Improved Whole-Genome Sequence of Phytophthora capsici Generated by Long-Read Sequencing. Molecular Plant-Microbe Interactions, 2021, 34, 866-869.	1.4	9

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19	Genome Sequence Resource of Phomopsis longicolla YC2-1, a Fungal Pathogen Causing Phomopsis Stem Blight in Soybean. Molecular Plant-Microbe Interactions, 2021, 34, 842-844.	1.4	6
20	A CRISPR/Cas9â€mediated in situ complementation method for Phytophthora sojae mutants. Molecular Plant Pathology, 2021, 22, 373-381.	2.0	25
21	Specific interaction of an RNA-binding protein with the 3â€²-UTR of its target mRNA is critical to oomycete sexual reproduction. PLoS Pathogens, 2021, 17, e1010001.	2.1	13
22	Identification and characterization of L-type lectin receptor-like kinases involved in Glycine maxâ€“Phytophthora sojae interaction. Planta, 2021, 254, 128.	1.6	2
23	An atypical Phytophthora sojae RxLR effector manipulates host vesicle trafficking to promote infection. PLoS Pathogens, 2021, 17, e1010104.	2.1	9
24	The Mevalonate Pathway Is Important for Growth, Spore Production, and the Virulence of Phytophthora sojae. Frontiers in Microbiology, 2021, 12, .	1.5	5
25	An Improved Method for the Identification of Soybean Resistance to Phytophthora sojae Applied to Germplasm Resources from the Huanghuaihai and Dongbei Regions of China. Plant Disease, 2020, 104, 408-413.	0.7	5
26	N - glycosylation shields Phytophthora sojae apoplastic effector PsXEG1 from a specific host aspartic protease. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 27685-27693.	3.3	51
27	A LAMP-assay-based specific microbiota analysis reveals community dynamics and potential interactions of 13 major soybean root pathogens. Journal of Integrative Agriculture, 2020, 19, 2056-2063.	1.7	7
28	Conserved Subgroups of the Plant-Specific RWP-RK Transcription Factor Family Are Present in Oomycete Pathogens. Frontiers in Microbiology, 2020, 11, 1724.	1.5	11
29	Prediction and Characterization of RXLR Effectors in Pythium Species. Molecular Plant-Microbe Interactions, 2020, 33, 1046-1058.	1.4	34
30	Identification of Resistance Genes to Phytophthora sojae in Domestic Soybean Cultivars from China Using Particle Bombardment. Plant Disease, 2020, 104, 1888-1893.	0.7	3
31	G protein Î± subunit suppresses sporangium formation through a serine/threonine protein kinase in Phytophthora sojae. PLoS Pathogens, 2020, 16, e1008138.	2.1	13
32	Pathogenicity and fungicide sensitivity of Pythium and Phytopythium spp. associated with soybean in the Huangâ€Huai region of China. Plant Pathology, 2020, 69, 1083-1092.	1.2	14
33	Chitin synthase is involved in vegetative growth, asexual reproduction and pathogenesis of Phytophthora capsici and Phytophthora sojae. Environmental Microbiology, 2019, 21, 4537-4547.	1.8	25
34	Wheat Straw Return Influences Nitrogen-Cycling and Pathogen Associated Soil Microbiota in a Wheatâ€“Soybean Rotation System. Frontiers in Microbiology, 2019, 10, 1811.	1.5	36
35	A loop-mediated isothermal amplification assay can rapidly diagnose soybean root-rot and damping-off diseases caused by Pythium spinosum. Australasian Plant Pathology, 2019, 48, 553-562.	0.5	4
36	Polymorphism in natural alleles of the avirulence gene Avr1c is associated with the host adaptation of Phytophthora sojae. Phytopathology Research, 2019, 1, .	0.9	8

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37	Phytophthora sojae Effector PsAvh240 Inhibits Host Aspartic Protease Secretion to Promote Infection. Molecular Plant, 2019, 12, 552-564.	3.9	60
38	The WY domain in the Phytophthora effector PSR 1 is required for infection and RNA silencing suppression activity. New Phytologist, 2019, 223, 839-852.	3.5	31
39	Structural analysis of Phytophthora suppressor of RNA silencing 2 (PSR2) reveals a conserved modular fold contributing to virulence. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 8054-8059.	3.3	46
40	A Phytophthora Effector Suppresses Trans-Kingdom RNAi to Promote Disease Susceptibility. Cell Host and Microbe, 2019, 25, 153-165.e5.	5.1	173
41	The Phytophthora sojae <scp>RXLR</scp> effector Avh238 destabilizes soybean Type2 Gm<scp>ACS</scp>s to suppress ethylene biosynthesis and promote infection. New Phytologist, 2019, 222, 425-437.	3.5	63
42	Rapid diagnosis of rice bakanae caused by Fusarium fujikuroi and F. proliferatum using loopâ€mediated isothermal amplification assays. Journal of Phytopathology, 2018, 166, 283-290.	0.5	11
43	Leucine-rich repeat receptor-like gene screen reveals that Nicotiana RXEG1 regulates glycoside hydrolase 12 MAMP detection. Nature Communications, 2018, 9, 594.	5.8	142
44	EumicrobeDBLite: a lightweight genomic resource and analytic platform for draft oomycete genomes. Molecular Plant Pathology, 2018, 19, 227-237.	2.0	24
45	The MADS-box Transcription Factor PsMAD1 Is Involved in Zoosporogenesis and Pathogenesis of Phytophthora sojae. Frontiers in Microbiology, 2018, 9, 2259.	1.5	26
46	Phytophthora methylomes are modulated by 6mA methyltransferases and associated with adaptive genome regions. Genome Biology, 2018, 19, 181.	3.8	61
47	Genomeâ€wide identification of long nonâ€coding RNAs suggests a potential association with effector gene transcription in Phytophthora sojae. Molecular Plant Pathology, 2018, 19, 2177-2186.	2.0	49
48	Endophytic fungal communities associated with field-grown soybean roots and seeds in the Huang-Huai region of China. PeerJ, 2018, 6, e4713.	0.9	35
49	A Phytophthora effector recruits a host cytoplasmic transacetylase into nuclear speckles to enhance plant susceptibility. ELife, 2018, 7, .	2.8	60
50	Distinct regions of the Phytophthora essential effector Avh238 determine its function in cell death activation and plant immunity suppression. New Phytologist, 2017, 214, 361-375.	3.5	67
51	A paralogous decoy protects Phytophthora sojae apoplastic effector PsXEG1 from a host inhibitor. Science, 2017, 355, 710-714.	6.0	236
52	Rapid diagnosis of wheat head blight caused by Fusarium asiaticum using a loop-mediated isothermal amplification assay. Australasian Plant Pathology, 2017, 46, 261-266.	0.5	11
53	Rapid Diagnosis of Soya Bean Root Rot Caused by Fusarium culmorum Using a Loopâ€Mediated Isothermal Amplification Assay. Journal of Phytopathology, 2017, 165, 249-256.	0.5	15
54	A Phytophthora Effector Manipulates Host Histone Acetylation and Reprograms Defense Gene Expression to Promote Infection. Current Biology, 2017, 27, 981-991.	1.8	120

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55	A Puf RNA-binding protein encoding gene PIM90 regulates the sexual and asexual life stages of the litchi downy blight pathogen Peronophythora litchii. Fungal Genetics and Biology, 2017, 98, 39-45.	0.9	28
56	Rapid detection of Colletotrichum gloeosporioides using a loop-mediated isothermal amplification assay. Australasian Plant Pathology, 2017, 46, 493-498.	0.5	12
57	An oomycete plant pathogen reprograms host pre-mRNA splicing to subvert immunity. Nature Communications, 2017, 8, 2051.	5.8	84
58	Pythium cedri sp. nov. (Pythiaceae, Pythiales) from southern China based on morphological and molecular characters. Phytotaxa, 2017, 309, 135.	0.1	11
59	Comparative Genomic Analysis among Four Representative Isolates of Phytophthora sojae Reveals Genes under Evolutionary Selection. Frontiers in Microbiology, 2016, 7, 1547.	1.5	20
60	<scp>P</scp>s<scp>H</scp>int1, associated with the <scp>G</scp>â€protein Î± subunit <scp>PsGPA1</scp>, is required for the chemotaxis and pathogenicity of <scp>P</scp>hytophthora sojae. Molecular Plant Pathology, 2016, 17, 272-285.	2.0	29
61	Sequencing of the Litchi Downy Blight Pathogen Reveals It Is a Phytophthora Species With Downy Mildew-Like Characteristics. Molecular Plant-Microbe Interactions, 2016, 29, 573-583.	1.4	73
62	A Phytophthora sojae effector suppresses endoplasmic reticulum stress-mediated immunity by stabilizing plant Binding immunoglobulin Proteins. Nature Communications, 2016, 7, 11685.	5.8	119
63	Filamentous pathogen effectors interfering with small RNA silencing in plant hosts. Current Opinion in Microbiology, 2016, 32, 1-6.	2.3	26
64	Bioinformatics Analysis Reveals Abundant Short Alpha-Helices as a Common Structural Feature of Oomycete RxLR Effector Proteins. PLoS ONE, 2015, 10, e0135240.	1.1	16
65	Differential regulation of defense-related proteins in soybean during compatible and incompatible interactions between Phytophthora sojae and soybean by comparative proteomic analysis. Plant Cell Reports, 2015, 34, 1263-1280.	2.8	15
66	<scp>PsMPK7</scp>, a stressâ€associated mitogenâ€activated protein kinase (<scp>MAPK</scp>) in <scp>P</scp>hytophthora sojae, is required for stress tolerance, reactive oxygenated species detoxification, cyst germination, sexual reproduction and infection of soybean. Molecular Plant Pathology, 2015, 16, 61-70.	2.0	38
67	Global Genome and Transcriptome Analyses of Magnaporthe oryzae Epidemic Isolate 98-06 Uncover Novel Effectors and Pathogenicity-Related Genes, Revealing Gene Gain and Lose Dynamics in Genome Evolution. PLoS Pathogens, 2015, 11, e1004801.	2.1	148
68	A Phytophthora sojae Glycoside Hydrolase 12 Protein Is a Major Virulence Factor during Soybean Infection and Is Recognized as a PAMP. Plant Cell, 2015, 27, 2057-2072.	3.1	335
69	The heat shock transcription factor <scp>P</scp>s<scp>HSF</scp>1 of <scp>P</scp>hytophthora sojae is required for oxidative stress tolerance and detoxifying the plant oxidative burst. Environmental Microbiology, 2015, 17, 1351-1364.	1.8	32
70	The Activation of Phytophthora Effector Avr3b by Plant Cyclophilin is Required for the Nudix Hydrolase Activity of Avr3b. PLoS Pathogens, 2015, 11, e1005139.	2.1	66
71	Pleiotropic Function of the Putative Zinc-Finger Protein MoMsn2 in Magnaporthe oryzae. Molecular Plant-Microbe Interactions, 2014, 27, 446-460.	1.4	56
72	Phytophthora Suppressor of RNA Silencing 2 Is a Conserved RxLR Effector that Promotes Infection in Soybean and Arabidopsis thaliana. Molecular Plant-Microbe Interactions, 2014, 27, 1379-1389.	1.4	101

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73	Computational identification of novel microRNAs and targets in Glycine max. Molecular Biology Reports, 2014, 41, 4965-4975.	1.0	7
74	PsMPK1, an SLT2-type mitogen-activated protein kinase, is required for hyphal growth, zoosporogenesis, cell wall integrity, and pathogenicity in Phytophthora sojae. Fungal Genetics and Biology, 2014, 65, 14-24.	0.9	35
75	Phylogenetic and transcriptional analysis of an expanded bZIP transcription factor family in Phytophthora sojae. BMC Genomics, 2013, 14, 839.	1.2	30
76	Gene Duplication and Fragment Recombination Drive Functional Diversification of a Superfamily of Cytoplasmic Effectors in Phytophthora sojae. PLoS ONE, 2013, 8, e70036.	1.1	46
77	The RxLR effector Avh241 from Phytophthora sojae requires plasma membrane localization to induce plant cell death. New Phytologist, 2012, 196, 247-260.	3.5	151
78	A Myb Transcription Factor of Phytophthora sojae, Regulated by MAP Kinase PsSAK1, Is Required for Zoospore Development. PLoS ONE, 2012, 7, e40246.	1.1	33
79	Development of a loop-mediated isothermal amplification assay for detection of Phytophthora sojae. FEMS Microbiology Letters, 2012, 334, 27-34.	0.7	83
80	Characterization of intronic structures and alternative splicing in Phytophthora sojae by comparative analysis of expressed sequence tags and genomic sequences. Canadian Journal of Microbiology, 2011, 57, 84-90.	0.8	19
81	Microarray profiling reveals microRNAs involving soybean resistance to Phytophthora sojae. Genome, 2011, 54, 954-958.	0.9	56
82	Genome-wide identification of Phytophthora sojae SNARE genes and functional characterization of the conserved SNARE PsYKT6. Fungal Genetics and Biology, 2011, 48, 241-251.	0.9	27
83	Transcriptional Programming and Functional Interactions within the Phytophthora sojae RXLR Effector Repertoire Â Â. Plant Cell, 2011, 23, 2064-2086.	3.1	455
84	Two Host Cytoplasmic Effectors Are Required for Pathogenesis of Phytophthora sojae by Suppression of Host Defenses Â Â. Plant Physiology, 2011, 155, 490-501.	2.3	100
85	Digital Gene Expression Profiling of the Phytophthora sojae Transcriptome. Molecular Plant-Microbe Interactions, 2011, 24, 1530-1539.	1.4	119