You-Liang Peng

List of Publications by Year
in descending order

77 papers	3,065 citations	186209 28 h-index	175177 52 g-index
78 all docs	78 docs citations	78 times ranked	3127 citing authors

#	Article	IF	Citations
1	Specific adaptation of Ustilaginoidea virens in occupying host florets revealed by comparative and functional genomics. Nature Communications, 2014, 5, 3849.	5.8	202
2	A novel wall-associated receptor-like protein kinase gene, OsWAK1, plays important roles in rice blast disease resistance. Plant Molecular Biology, 2009, 69, 337-346.	2.0	195
3	Different Chitin Synthase Genes Are Required for Various Developmental and Plant Infection Processes in the Rice Blast Fungus Magnaporthe oryzae. PLoS Pathogens, 2012, 8, e1002526.	2.1	177
4	Comparative Analysis of the Genomes of Two Field Isolates of the Rice Blast Fungus Magnaporthe oryzae. PLoS Genetics, 2012, 8, e1002869.	1.5	167
5	Characterization of debilitation-associated mycovirus infecting the plant-pathogenic fungus Sclerotinia sclerotiorum. Journal of General Virology, 2006, 87, 241-249.	1.3	159
6	<i>N</i>-Glycosylation of Effector Proteins by an Î±-1,3-Mannosyltransferase Is Required for the Rice Blast Fungus to Evade Host Innate Immunity Â. Plant Cell, 2014, 26, 1360-1376.	3.1	146
7	A Novel Protein Com1 Is Required for Normal Conidium Morphology and Full Virulence in <i>Magnaporthe oryzae</i>. Molecular Plant-Microbe Interactions, 2010, 23, 112-123.	1.4	135
8	Temporal sequence of cytological events in rice leaves infected with <i>Pyricularia oryzae</i>. Canadian Journal of Botany, 1988, 66, 730-735.	1.2	110
9	The Dawn of Fungal Pathogen Genomics. Annual Review of Phytopathology, 2006, 44, 337-366.	3.5	95
10	Species of Botryosphaeriaceae involved in grapevine dieback in China. Fungal Diversity, 2013, 61, 221-236.	4.7	95
11	Specific recognition of two MAX effectors by integrated HMA domains in plant immune receptors involves distinct binding surfaces. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 11637-11642.	3.3	94
12	MoSnt2-dependent deacetylation of histone H3 mediates MoTor-dependent autophagy and plant infection by the rice blast fungus <i>Magnaporthe oryzae</i>. Autophagy, 2018, 14, 1543-1561.	4.3	89
13	Rice false smut fungus hijacks the rice nutrients supply by blocking and mimicking the fertilization of rice ovary. Environmental Microbiology, 2016, 18, 3840-3849.	1.8	75
14	Diverse species of Colletotrichum associated with grapevine anthracnose in China. Fungal Diversity, 2015, 71, 233-246.	4.7	64
15	Revealing Shared and Distinct Gene Network Organization in Arabidopsis Immune Responses by Integrative Analysis. Plant Physiology, 2015, 167, 1186-1203.	2.3	62
16	Structural basis of dimerization and dual W-box DNA recognition by rice WRKY domain. Nucleic Acids Research, 2019, 47, 4308-4318.	6.5	56
17	The essential effector SCRE1 in <i>Ustilaginoidea virens</i> suppresses rice immunity via a small peptide region. Molecular Plant Pathology, 2020, 21, 445-459.	2.0	54
18	Proteomic studies of phytopathogenic fungi, oomycetes and their interactions with hosts. European Journal of Plant Pathology, 2010, 126, 81-95.	0.8	53

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19	Advances in fungal proteomics. Microbiological Research, 2007, 162, 193-200.	2.5	52
20	A positiveâ€charged patch and stabilized hydrophobic core are essential for avirulence function of AvrPib in the rice blast fungus. Plant Journal, 2018, 96, 133-146.	2.8	49
21	A designer rice NLR immune receptor confers resistance to the rice blast fungus carrying noncorresponding avirulence effectors. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	48
22	MoCAP proteins regulated by MoArk1-mediated phosphorylation coordinate endocytosis and actin dynamics to govern development and virulence of Magnaporthe oryzae. PLoS Genetics, 2017, 13, e1006814.	1.5	46
23	Large-Scale Insertional Mutagenesis in Magnaporthe oryzae by Agrobacterium tumefaciens-Mediated Transformation. Methods in Molecular Biology, 2011, 722, 213-224.	0.4	45
24	The Nep1-like protein family of Magnaporthe oryzae is dispensable for the infection of rice plants. Scientific Reports, 2017, 7, 4372.	1.6	43
25	Global analysis of sumoylation function reveals novel insights into development and appressoriumâ€mediated infection of the rice blast fungus. New Phytologist, 2018, 219, 1031-1047.	3.5	43
26	<i>ZNF1</i> Encodes a Putative C2H2 Zinc-Finger Protein Essential for Appressorium Differentiation by the Rice Blast Fungus <i>Magnaporthe oryzae</i>. Molecular Plant-Microbe Interactions, 2016, 29, 22-35.	1.4	38
27	A serine/threonine-protein phosphatase PP2A catalytic subunit is essential for asexual development and plant infection in Magnaporthe oryzae. Current Genetics, 2013, 59, 33-41.	0.8	35
28	Glutamate synthase MoGlt1â€mediated glutamate homeostasis is important for autophagy, virulence and conidiation in the rice blast fungus. Molecular Plant Pathology, 2018, 19, 564-578.	2.0	35
29	OsNBL3, a mitochondrionâ€localized pentatricopeptide repeat protein, is involved in splicing <i>nad5</i> intron 4 and its disruption causes lesion mimic phenotype with enhanced resistance to biotic and abiotic stresses. Plant Biotechnology Journal, 2021, 19, 2277-2290.	4.1	28
30	The Y137H mutation of VvCYP51 gene confers the reduced sensitivity to tebuconazole in Villosiclava virens. Scientific Reports, 2015, 5, 17575.	1.6	27
31	Iron Response Regulator Protein IrrB in Magnetospirillum gryphiswaldense MSR-1 Helps Control the Iron/Oxygen Balance, Oxidative Stress Tolerance, and Magnetosome Formation. Applied and Environmental Microbiology, 2015, 81, 8044-8053.	1.4	26
32	Molecular cloning and differential expression of an Î³-aminobutyrate transaminase gene, OsGABA-T, in rice (Oryza sativa) leaves infected with blast fungus. Journal of Plant Research, 2006, 119, 663-669.	1.2	24
33	A carnitineâ€"acylcarnitine carrier protein, MoCrc1, is essential for pathogenicity in Magnaporthe oryzae. Current Genetics, 2012, 58, 139-148.	0.8	24
34	A Putative Zn2Cys6 Transcription Factor Is Associated With Isoprothiolane Resistance in Magnaporthe oryzae. Frontiers in Microbiology, 2018, 9, 2608.	1.5	24
35	Activation of Mst11 and Feedback Inhibition of Germ Tube Growth in <i>Magnaporthe oryzae</i>. Molecular Plant-Microbe Interactions, 2015, 28, 881-891.	1.4	22
36	Phosphorylation-mediated Regulatory Networks in Mycelia of Pyricularia oryzae Revealed by Phosphoproteomic Analyses. Molecular and Cellular Proteomics, 2017, 16, 1669-1682.	2.5	21

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37	A glycine-rich protein MoGrp1 functions as a novel splicing factor to regulate fungal virulence and growth in Magnaporthe oryzae. Phytopathology Research, 2019, 1, .	0.9	20
38	Structure-guided analysis of Arabidopsis JASMONATE-INDUCED OXYGENASE (JOX) 2 reveals key residues for recognition of jasmonic acid substrate by plant JOXs. Molecular Plant, 2021, 14, 820-828.	3.9	20
39	Physiological characteristics of Magnetospirillum gryphiswaldense MSR-1 that control cell growth under high-iron and low-oxygen conditions. Scientific Reports, 2017, 7, 2800.	1.6	19
40	GPI7â€mediated glycosylphosphatidylinositol anchoring regulates appressorial penetration and immune evasion during infection of <scp><i>Magnaporthe oryzae</i></scp>. Environmental Microbiology, 2020, 22, 2581-2595.	1.8	19
41	Structural basis of DNA recognition by PCG2 reveals a novel DNA binding mode for winged helix-turn-helix domains. Nucleic Acids Research, 2015, 43, 1231-1240.	6.5	18
42	Substitution of tryptophan 89 with tyrosine switches the DNA binding mode of PC4. Scientific Reports, 2015, 5, 8789.	1.6	17
43	An LRRâ€only protein promotes NLPâ€triggered cell death and disease susceptibility by facilitating oligomerization of NLP in Arabidopsis. New Phytologist, 2021, 232, 1808-1822.	3.5	17
44	A spindle pole antigen gene MoSPA2 is important for polar cell growth of vegetative hyphae and conidia, but is dispensable for pathogenicity in Magnaporthe oryzae. Current Genetics, 2014, 60, 255-263.	0.8	16
45	Evolutionary and genomic comparisons of hybrid uninucleate and nonhybrid Rhizoctonia fungi. Communications Biology, 2021, 4, 201.	2.0	16
46	MoCps1 is important for conidiation, conidial morphology and virulence in Magnaporthe oryzae. Current Genetics, 2016, 62, 861-871.	0.8	13
47	The cyclin dependent kinase subunit Cks1 is required for infectionâ€associated development of the rice blast fungus <i>Magnaporthe oryzae</i>. Environmental Microbiology, 2017, 19, 3959-3981.	1.8	13
48	A novel glycine-rich domain protein, GRDP1, functions as a critical feedback regulator for controlling cell death and disease resistance in rice. Journal of Experimental Botany, 2021, 72, 608-622.	2.4	13
49	Elucidation of ustilaginoidin biosynthesis reveals a previously unrecognised class of ene-reductases. Chemical Science, 2021, 12, 14883-14892.	3.7	12
50	Molecular cloning and differential expression of an aldehyde dehydrogenase gene in rice leaves in response to infection by blast fungus. Biologia (Poland), 2007, 62, 523-528.	0.8	11
51	Large-scale identification of lysine acetylated proteins in vegetative hyphae of the rice blast fungus. Scientific Reports, 2017, 7, 15316.	1.6	11
52	Prp19â€associated splicing factor Cwf15 regulates fungal virulence and development in the rice blast fungus. Environmental Microbiology, 2021, 23, 5901-5916.	1.8	11
53	Ubiquitination in the rice blast fungus Magnaporthe oryzae: from development and pathogenicity to stress responses. Phytopathology Research, 2022, 4, .	0.9	11
54	Induced expression of oryzain Î± gene encoding a cysteine proteinase under stress conditions. Journal of Plant Research, 2007, 120, 465-469.	1.2	10

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55	Optimization of a protein extraction technique for fungal proteomics. Indian Journal of Microbiology, 2010, 50, 127-131.	1.5	10
56	Loss and Natural Variations of Blast Fungal Avirulence Genes Breakdown Rice Resistance Genes in the Sichuan Basin of China. Frontiers in Plant Science, 2022, 13, 788876.	1.7	9
57	Crystal structures of <i>Magnaporthe oryzae</i> trehalose-6-phosphate synthase (MoTps1) suggest a model for catalytic process of Tps1. Biochemical Journal, 2019, 476, 3227-3240.	1.7	8
58	Pseudomonas bacteriocin syringacin M released upon desiccation suppresses the growth of sensitive bacteria in plant necrotic lesions. Microbial Biotechnology, 2020, 13, 134-147.	2.0	7
59	Genome Sequence of <i>Magnaporthe oryzae</i> EA18 Virulent to Multiple Widely Used Rice Varieties. Molecular Plant-Microbe Interactions, 2022, 35, 727-730.	1.4	7
60	Antimicrobial Phenolic Compounds from Anabasis Aphylla L. Natural Product Communications, 2009, 4, 1934578X0900400.	0.2	6
61	Expression, purification, crystallization and preliminary X-ray diffraction analysis of the effector-interaction domain of the resistance protein RGA5-A from<i>Oryza sativa</i>L.<i>japonica</i>. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 171-174.	0.4	6
62	Genetic Interaction between Arabidopsis Qpm3.1 Locus and Bacterial Effector Gene hopW1-1 Underlies Natural Variation in Quantitative Disease Resistance to Pseudomonas Infection. Frontiers in Plant Science, 2017, 8, 695.	1.7	6
63	Crystallization of the rice immune receptor RGA5A_S with the rice blast fungus effector AVR1-CO39 prepared<i>via</i>mixture and tandem strategies. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 262-267.	0.4	6
64	Comparative Secretome Analysis of Magnaporthe oryzae Identified Proteins Involved in Virulence and Cell Wall Integrity. Genomics, Proteomics and Bioinformatics, 2022, 20, 728-746.	3.0	5
65	MoTlg2, a t-SNARE component is important for formation of the SpitzenkÃ¶rper and polar deposition of chitin in Magnaporthe oryzae. Physiological and Molecular Plant Pathology, 2014, 87, 9-18.	1.3	4
66	Structure based function-annotation of hypothetical protein MGG_01005 from Magnaporthe oryzae reveals it is the dynein light chain orthologue of dynlt1/3. Scientific Reports, 2018, 8, 3952.	1.6	4
67	OsNBL1, a Multi-Organelle Localized Protein, Plays Essential Roles in Rice Senescence, Disease Resistance, and Salt Tolerance. Rice, 2021, 14, 10.	1.7	4
68	First Report of Didymella glomerata Causing Didymella Leaf Blight on Maize in China. Plant Disease, 2022, , .	0.7	4
69	Fungal oxysterol-binding protein-related proteins promote pathogen virulence and activate plant immunity. Journal of Experimental Botany, 2022, 73, 2125-2141.	2.4	4
70	Molecular Genetics of Anthracnose Resistance in Maize. Journal of Fungi (Basel, Switzerland), 2022, 8, 540.	1.5	4
71	Transcriptional Landscapes of Long Non-coding RNAs and Alternative Splicing in Pyricularia oryzae Revealed by RNA-Seq. Frontiers in Plant Science, 2021, 12, 723636.	1.7	3
72	Two distinct nucleic acid binding surfaces of Cdc5 regulate development. Biochemical Journal, 2019, 476, 3355-3368.	1.7	3

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73	The Rice Malectin Regulates Plant Cell Death and Disease Resistance by Participating in Glycoprotein Quality Control. International Journal of Molecular Sciences, 2022, 23, 5819.	1.8	3
74	Characterization of a Novel RING Finger Gene <i>OsRFP1</i>, which is Induced by Ethylene, Salicylic Acid and Blast Fungus Infection in Rice. Journal of Phytopathology, 2008, 156, 396-402.	0.5	2
75	Expression Profile During the Development of Appressoria Induced by Hydrophobic Surfaces in<i>Magnaporthe grisea</i>Y34. Journal of Phytopathology, 2010, 158, 143-153.	0.5	2
76	Rice blast fungus proteomics. Archives of Phytopathology and Plant Protection, 2010, 43, 149-153.	0.6	0
77	A report on the 10th International Congress of Plant Pathology. Food Security, 2013, 5, 895-898.	2.4	0