

Yong-Hwan Lee

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104
papers

6,893
citations

36
h-index

82
g-index

107
ext. papers

8,781
ext. citations

6.6
avg. IF

5.21
L-index

#	Paper	IF	Citations
104	The genome sequence of the rice blast fungus <i>Magnaporthe grisea</i> . <i>Nature</i> , 2005 , 434, 980-6	50.4	1202
103	Comparative genomics reveals mobile pathogenicity chromosomes in <i>Fusarium</i> . <i>Nature</i> , 2010 , 464, 367-73	50.4	1085
102	Genome sequence of the hot pepper provides insights into the evolution of pungency in <i>Capsicum</i> species. <i>Nature Genetics</i> , 2014 , 46, 270-8	36.3	594
101	Lifestyle transitions in plant pathogenic <i>Colletotrichum</i> fungi deciphered by genome and transcriptome analyses. <i>Nature Genetics</i> , 2012 , 44, 1060-5	36.3	564
100	GH3-mediated auxin homeostasis links growth regulation with stress adaptation response in <i>Arabidopsis</i> . <i>Journal of Biological Chemistry</i> , 2007 , 282, 10036-10046	5.4	346
99	Insight into trade-off between wood decay and parasitism from the genome of a fungal forest pathogen. <i>New Phytologist</i> , 2012 , 194, 1001-1013	9.8	168
98	Homeobox transcription factors are required for conidiation and appressorium development in the rice blast fungus <i>Magnaporthe oryzae</i> . <i>PLoS Genetics</i> , 2009 , 5, e1000757	6	143
97	A novel pathogenicity gene is required in the rice blast fungus to suppress the basal defenses of the host. <i>PLoS Pathogens</i> , 2009 , 5, e1000401	7.6	143
96	New reference genome sequences of hot pepper reveal the massive evolution of plant disease-resistance genes by retroduplication. <i>Genome Biology</i> , 2017 , 18, 210	18.3	142
95	Fungal secretome database: integrated platform for annotation of fungal secretomes. <i>BMC Genomics</i> , 2010 , 11, 105	4.5	128
94	A Quick and Safe Method for Fungal DNA Extraction. <i>Plant Pathology Journal</i> , 2009 , 25, 108-111	2.5	121
93	FTFD: an informatics pipeline supporting phylogenomic analysis of fungal transcription factors. <i>Bioinformatics</i> , 2008 , 24, 1024-5	7.2	119
92	Systematic functional profiling of transcription factor networks in <i>Cryptococcus neoformans</i> . <i>Nature Communications</i> , 2015 , 6, 6757	17.4	99
91	Fungal cytochrome P450 database. <i>BMC Genomics</i> , 2008 , 9, 402	4.5	96
90	Kingdom-Wide Analysis of Fungal Small Secreted Proteins (SSPs) Reveals their Potential Role in Host Association. <i>Frontiers in Plant Science</i> , 2016 , 7, 186	6.2	96
89	Insights on the evolution of mycoparasitism from the genome of <i>Clonostachys rosea</i> . <i>Genome Biology and Evolution</i> , 2015 , 7, 465-80	3.9	93
88	Systematic functional analysis of kinases in the fungal pathogen <i>Cryptococcus neoformans</i> . <i>Nature Communications</i> , 2016 , 7, 12766	17.4	79

87	Genome-wide profiling of DNA methylation provides insights into epigenetic regulation of fungal development in a plant pathogenic fungus, <i>Magnaporthe oryzae</i> . <i>Scientific Reports</i> , 2015 , 5, 8567	4.9	76
86	Genome-wide analysis of T-DNA integration into the chromosomes of <i>Magnaporthe oryzae</i> . <i>Molecular Microbiology</i> , 2007 , 66, 371-82	4.1	69
85	Secret lifestyles of <i>Neurospora crassa</i> . <i>Scientific Reports</i> , 2014 , 4, 5135	4.9	60
84	Genome Sequence of <i>Striga asiatica</i> Provides Insight into the Evolution of Plant Parasitism. <i>Current Biology</i> , 2019 , 29, 3041-3052.e4	6.3	59
83	Cyber infrastructure for <i>Fusarium</i> : three integrated platforms supporting strain identification, phylogenetics, comparative genomics and knowledge sharing. <i>Nucleic Acids Research</i> , 2011 , 39, D640-6	20.1	56
82	Rice blast fungus (<i>Magnaporthe oryzae</i>) infects <i>Arabidopsis</i> via a mechanism distinct from that required for the infection of rice. <i>Plant Physiology</i> , 2009 , 149, 474-86	6.6	54
81	Gapless genome assembly of <i>Colletotrichum higginsianum</i> reveals chromosome structure and association of transposable elements with secondary metabolite gene clusters. <i>BMC Genomics</i> , 2017 , 18, 667	4.5	53
80	Phytophthora Database: A Forensic Database Supporting the Identification and Monitoring of <i>Phytophthora</i> . <i>Plant Disease</i> , 2008 , 92, 966-972	1.5	51
79	Fungal plant cell wall-degrading enzyme database: a platform for comparative and evolutionary genomics in fungi and Oomycetes. <i>BMC Genomics</i> , 2013 , 14 Suppl 5, S7	4.5	49
78	Vegetative Compatibility Groups and Pathogenicity Among Isolates of <i>Fusarium oxysporum</i> f. sp. <i>cucumerinum</i> . <i>Plant Disease</i> , 1998 , 82, 244-246	1.5	48
77	Integrative structural annotation of de novo RNA-Seq provides an accurate reference gene set of the enormous genome of the onion (<i>Allium cepa</i> L.). <i>DNA Research</i> , 2015 , 22, 19-27	4.5	47
76	Global expression profiling of transcription factor genes provides new insights into pathogenicity and stress responses in the rice blast fungus. <i>PLoS Pathogens</i> , 2013 , 9, e1003350	7.6	43
75	Histone acetylation in fungal pathogens of plants. <i>Plant Pathology Journal</i> , 2014 , 30, 1-9	2.5	43
74	Systematic characterization of the peroxidase gene family provides new insights into fungal pathogenicity in <i>Magnaporthe oryzae</i> . <i>Scientific Reports</i> , 2015 , 5, 11831	4.9	40
73	CFGP 2.0: a versatile web-based platform for supporting comparative and evolutionary genomics of fungi and Oomycetes. <i>Nucleic Acids Research</i> , 2013 , 41, D714-9	20.1	40
72	The PEX7-mediated peroxisomal import system is required for fungal development and pathogenicity in <i>Magnaporthe oryzae</i> . <i>PLoS ONE</i> , 2011 , 6, e28220	3.7	40
71	Phylogenomic Analysis of a 55.1-kb 19-Genes Dataset Resolves a Monophyletic that Includes the Species Complex. <i>Phytopathology</i> , 2021 , 111, 1064-1079	3.8	39
70	Domestication of <i>Oryza</i> species eco-evolutionarily shapes bacterial and fungal communities in rice seed. <i>Microbiome</i> , 2020 , 8, 20	16.6	38

69	fPoxDB: fungal peroxidase database for comparative genomics. <i>BMC Microbiology</i> , 2014 , 14, 117	4.5	37
68	<i>Agrobacterium tumefaciens</i> -mediated transformation of the lichen fungus, <i>Umbilicaria muehlenbergii</i> . <i>PLoS ONE</i> , 2013 , 8, e83896	3.7	35
67	Systematic characterization of the bZIP transcription factor gene family in the rice blast fungus, <i>Magnaporthe oryzae</i> . <i>Environmental Microbiology</i> , 2015 , 17, 1425-43	5.2	34
66	Transcriptome Analysis of Early Responsive Genes in Rice during <i>Magnaporthe oryzae</i> Infection. <i>Plant Pathology Journal</i> , 2014 , 30, 343-54	2.5	34
65	Functional analysis of MCNA, a gene encoding a catalytic subunit of calcineurin, in the rice blast fungus <i>magnaporthe oryzae</i> . <i>Journal of Microbiology and Biotechnology</i> , 2009 , 19, 11-6	3.3	33
64	Two conidiation-related Zn(II)2Cys6 transcription factor genes in the rice blast fungus. <i>Fungal Genetics and Biology</i> , 2013 , 61, 133-41	3.9	32
63	<i>Pseudomonas</i> sp. LSW25R, antagonistic to plant pathogens, promoted plant growth, and reduced blossom-end rot of tomato fruits in a hydroponic system. <i>European Journal of Plant Pathology</i> , 2010 , 126, 1-11	2.1	28
62	Regulation of cAMP-dependent protein kinase during appressorium formation in <i>Magnaporthe grisea</i> . <i>FEMS Microbiology Letters</i> , 1999 , 170, 419-423	2.9	28
61	Role of the MoYAK1 protein kinase gene in <i>Magnaporthe oryzae</i> development and pathogenicity. <i>Environmental Microbiology</i> , 2015 , 17, 4672-89	5.2	26
60	Comparative functional analysis of the velvet gene family reveals unique roles in fungal development and pathogenicity in <i>Magnaporthe oryzae</i> . <i>Fungal Genetics and Biology</i> , 2014 , 66, 33-43	3.9	26
59	Gene expression profiling during conidiation in the rice blast pathogen <i>Magnaporthe oryzae</i> . <i>PLoS ONE</i> , 2012 , 7, e43202	3.7	26
58	The Rice Microbiome: A Model Platform for Crop Holobiome. <i>Phytobiomes Journal</i> , 2020 , 4, 5-18	4.8	23
57	Whole genome sequence and genome annotation of <i>Colletotrichum acutatum</i> , causal agent of anthracnose in pepper plants in South Korea. <i>Genomics Data</i> , 2016 , 8, 45-6		20
56	The cell cycle gene MoCDC15 regulates hyphal growth, asexual development and plant infection in the rice blast pathogen <i>Magnaporthe oryzae</i> . <i>Fungal Genetics and Biology</i> , 2011 , 48, 784-92	3.9	19
55	Roles of Forkhead-box Transcription Factors in Controlling Development, Pathogenicity, and Stress Response in <i>Magnaporthe oryzae</i> . <i>Plant Pathology Journal</i> , 2014 , 30, 136-50	2.5	17
54	Genome-Wide Analysis of Hypoxia-Responsive Genes in the Rice Blast Fungus, <i>Magnaporthe oryzae</i> . <i>PLoS ONE</i> , 2015 , 10, e0134939	3.7	16
53	Transcriptome Profiling of the Rice Blast Fungus and Its Host During Infection. <i>Molecular Plant-Microbe Interactions</i> , 2020 , 33, 141-144	3.6	16
52	Role of MoAND1-mediated nuclear positioning in morphogenesis and pathogenicity in the rice blast fungus, <i>Magnaporthe oryzae</i> . <i>Fungal Genetics and Biology</i> , 2014 , 69, 43-51	3.9	15

51	Two nuclear effectors of the rice blast fungus modulate host immunity via transcriptional reprogramming. <i>Nature Communications</i> , 2020 , 11, 5845	17.4	15
50	Global DNA Methylation in the Chestnut Blight Fungus and Genome-Wide Changes in DNA Methylation Accompanied with Sectorization. <i>Frontiers in Plant Science</i> , 2018 , 9, 103	6.2	14
49	Identification of a Gene Involved in Early Senescence and Defense Response in Rice. <i>Frontiers in Plant Science</i> , 2018 , 9, 1274	6.2	14
48	Genome wide analysis of the transition to pathogenic lifestyles in Magnaporthales fungi. <i>Scientific Reports</i> , 2018 , 8, 5862	4.9	13
47	Role of the Histone Acetyltransferase Rtt109 in Development and Pathogenicity of the Rice Blast Fungus. <i>Molecular Plant-Microbe Interactions</i> , 2018 , 31, 1200-1210	3.6	12
46	SUMOylation is required for fungal development and pathogenicity in the rice blast fungus <i>Magnaporthe oryzae</i> . <i>Molecular Plant Pathology</i> , 2018 , 19, 2134-2148	5.7	11
45	A MYST family histone acetyltransferase, MoSAS3, is required for development and pathogenicity in the rice blast fungus. <i>Molecular Plant Pathology</i> , 2019 , 20, 1491-1505	5.7	11
44	Hypoxia: A Double-Edged Sword During Fungal Pathogenesis?. <i>Frontiers in Microbiology</i> , 2020 , 11, 1920	5.7	11
43	A Small GTPase RHO2 Plays an Important Role in Pre-infection Development in the Rice Blast Pathogen. <i>Plant Pathology Journal</i> , 2018 , 34, 470-479	2.5	10
42	ER retention receptor, MoERR1 is required for fungal development and pathogenicity in the rice blast fungus, <i>Magnaporthe oryzae</i> . <i>Scientific Reports</i> , 2017 , 7, 1259	4.9	9
41	Potential roles of laccases on virulence of <i>Heterobasidion annosum</i> s.s. <i>Microbial Pathogenesis</i> , 2015 , 81, 16-21	3.8	9
40	A High-Quality Draft Genome Sequence of <i>Colletotrichum gloeosporioides</i> sensu stricto SMCG1#C, a Causal Agent of Anthracnose on <i>Cunninghamia lanceolata</i> in China. <i>Molecular Plant-Microbe Interactions</i> , 2019 , 32, 139-141	3.6	9
39	Evolution of the Genes Encoding Effector Candidates Within Multiple Pathotypes of. <i>Frontiers in Microbiology</i> , 2019 , 10, 2575	5.7	9
38	dbHiMo: a web-based epigenomics platform for histone-modifying enzymes. <i>Database: the Journal of Biological Databases and Curation</i> , 2015 , 2015, bav052	5	9
37	Regulation of cellular diacylglycerol through lipid phosphate phosphatases is required for pathogenesis of the rice blast fungus, <i>Magnaporthe oryzae</i> . <i>PLoS ONE</i> , 2014 , 9, e100726	3.7	9
36	Use of <i>Colletotrichum graminicola</i> KA001 to Control Barnyard Grass. <i>Plant Disease</i> , 2000 , 84, 55-59	1.5	9
35	Molecular characterization of a cDNA for a cysteine-rich antifungal protein from <i>Capsicum annuum</i> 2004 , 47, 375-382		8
34	Crystal structure and functional analysis of isocitrate lyases from <i>Magnaporthe oryzae</i> and <i>Fusarium graminearum</i> . <i>Journal of Structural Biology</i> , 2016 , 194, 395-403	3.4	8

33	Draft Genome Sequence of an Endophytic Fungus, sp. Strain JS-464, Isolated from a Reed Plant., <i>Genome Announcements</i> , 2017 , 5,		7
32	Genome Sequence of an Endophytic Fungus, JS-169, Which Has Antifungal Activity. <i>Genome Announcements</i> , 2017 , 5,		7
31	, Encoding a Histone Demethylase Containing JmjC Domain, Is Required for Pathogenic Development of the Rice Blast Fungus,. <i>Plant Pathology Journal</i> , 2017 , 33, 193-205	2.5	7
30	Genome-wide functional analysis of phosphatases in the pathogenic fungus <i>Cryptococcus neoformans</i> . <i>Nature Communications</i> , 2020 , 11, 4212	17.4	7
29	Distinct roles of the YPEL gene family in development and pathogenicity in the ascomycete fungus <i>Magnaporthe oryzae</i> . <i>Scientific Reports</i> , 2018 , 8, 14461	4.9	7
28	Draft Genome Sequence of JS-1675, an Endophytic Fungus from. <i>Microbiology Resource Announcements</i> , 2019 , 8,	1.3	6
27	The complete mitochondrial genome sequence of the ascomycete plant pathogen <i>Colletotrichum acutatum</i> . <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016 , 27, 4547-4548	1.3	6
26	F-box only and CUE proteins are crucial ubiquitination-associated components for conidiation and pathogenicity in the rice blast fungus, <i>Magnaporthe oryzae</i> . <i>Fungal Genetics and Biology</i> , 2020 , 144, 103473	2.9	6
25	Lyso-phosphatidylethanolamine primes the plant immune system and promotes basal resistance against hemibiotrophic pathogens. <i>BMC Biotechnology</i> , 2021 , 21, 12	3.5	6
24	Genomic comparisons of the laurel wilt pathogen, <i>Raffaelea lauricola</i> , and related tree pathogens highlight an arsenal of pathogenicity related genes. <i>Fungal Genetics and Biology</i> , 2019 , 125, 84-92	3.9	5
23	TGFam-Finder: a novel solution for target-gene family annotation in plants. <i>New Phytologist</i> , 2020 , 227, 1568-1581	9.8	5
22	Homeobox Transcription Factors Are Required for Fungal Development and the Suppression of Host Defense Mechanisms in the -Pepper Pathosystem. <i>MBio</i> , 2021 , 12, e0162021	7.8	5
21	A novel approach to investigate hypoxic microenvironment during rice colonization by <i>Magnaporthe oryzae</i> . <i>Environmental Microbiology</i> , 2019 , 21, 1151-1169	5.2	4
20	A quick and accurate screening method for fungal gene-deletion mutants by direct, priority-based, and inverse PCRs. <i>Journal of Microbiological Methods</i> , 2014 , 105, 39-41	2.8	4
19	Analysis of in planta Expressed Orphan Genes in the Rice Blast Fungus <i>Magnaporthe oryzae</i> . <i>Plant Pathology Journal</i> , 2014 , 30, 367-74	2.5	4
18	Genome-wide analysis of T-DNA integration into the chromosomes of <i>Magnaporthe oryzae</i> . <i>Molecular Microbiology</i> , 2007 , 66, 826-826	4.1	3
17	A rice gene encoding glycosyl hydrolase plays contrasting roles in immunity depending on the type of pathogens. <i>Molecular Plant Pathology</i> , 2021 ,	5.7	3
16	Comparative Analysis of the Korean Population of <i>Magnaporthe oryzae</i> by Multilocus Microsatellite Typing. <i>Plant Pathology Journal</i> , 2013 , 29, 435-9	2.5	3

15	Spatiotemporal Assembly of Bacterial and Fungal Communities of Seed-Seedling-Adult in Rice. <i>Frontiers in Microbiology</i> , 2021 , 12, 708475	5.7	3
14	Draft Genome Sequence of JS-1345, an Endophytic Fungus Isolated from Stem Tissue of Korean Fir. <i>Microbiology Resource Announcements</i> , 2020 , 9,	1.3	2
13	Draft Genome Sequence of <i>Aspergillus oryzae</i> BP2-1, Isolated from Traditional Malted Rice in South Korea. <i>Microbiology Resource Announcements</i> , 2020 , 9,	1.3	2
12	Comparative Genomics Platform and Phylogenetic Analysis of Fungal Laccases and Multi-Copper Oxidases. <i>Mycobiology</i> , 2020 , 48, 373-382	1.7	2
11	The Membrane-Bound Protein, MoAfo1, Is Involved in Sensing Diverse Signals from Different Surfaces in the Rice Blast Fungus. <i>Plant Pathology Journal</i> , 2021 , 37, 87-98	2.5	2
10	Draft Genome Sequence of <i>Alternaria alternata</i> JS-1623, a Fungal Endophyte of <i>Abies koreana</i> . <i>Mycobiology</i> , 2020 , 48, 240-244	1.7	1
9	In silico sequence analysis reveals new characteristics of fungal NADPH oxidase genes. <i>Mycobiology</i> , 2014 , 42, 241-8	1.7	1
8	Characterization of the MYB Genes Reveals Insights Into Their Evolutionary Conservation, Structural Diversity, and Functional Roles in .. <i>Frontiers in Microbiology</i> , 2021 , 12, 721530	5.7	1
7	Harnessing Chemical Ecology for Environment-Friendly Crop Protection. <i>Phytopathology</i> , 2021 , PHYTO012110035RVW	12.1	1
6	Characterization of a <i>Heterobasidion irregulare</i> endo-rhamnogalacturonase that mediate growth on pectin. <i>Journal of Phytopathology</i> , 2018 , 166, 34-43	1.8	1
5	Alternative splicing diversifies the transcriptome and proteome of the rice blast fungus during host infection.. <i>RNA Biology</i> , 2022 , 19, 373-385	4.8	1
4	ROS homeostasis mediated by MPK4 and SUMM2 determines synergid cell death.. <i>Nature Communications</i> , 2022 , 13, 1746	17.4	1
3	Compositional Shift of Bacterial, Archaeal, and Fungal Communities Is Dependent on Trophic Lifestyles in Rice Paddy Soil. <i>Frontiers in Microbiology</i> , 2021 , 12, 719486	5.7	0
2	Genome-wide profiling of long non-coding RNA of the rice blast fungus <i>Magnaporthe oryzae</i> during infection.. <i>BMC Genomics</i> , 2022 , 23, 132	4.5	0
1	Draft Genome Sequence of EL000614, a Strain Producing Grammicin, a Potent Nematicidal Compound. <i>Mycobiology</i> , 2021 , 49, 294-296	1.7	