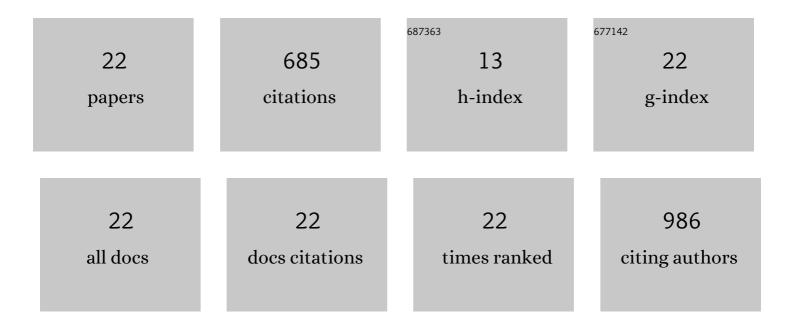
Yueqiang Leng

List of Publications by Year in descending order

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#	Article	lF	CITATIONS
1	Comparative Genome Structure, Secondary Metabolite, and Effector Coding Capacity across Cochliobolus Pathogens. PLoS Genetics, 2013, 9, e1003233.	3.5	232
2	Molecular mapping of QTL for Fusarium head blight resistance introgressed into durum wheat. Theoretical and Applied Genetics, 2018, 131, 1939-1951.	3.6	57
3	Sfpâ€type 4′â€phosphopantetheinyl transferase is required for lysine synthesis, tolerance to oxidative stress and virulence in the plant pathogenic fungus <i>Cochliobolus sativus</i> . Molecular Plant Pathology, 2012, 13, 375-387.	4.2	49
4	Functional characterization of the gene FoOCH1 encoding a putative α-1,6-mannosyltransferase in Fusarium oxysporum f. sp. cubense. Fungal Genetics and Biology, 2014, 65, 1-13.	2.1	40
5	The Role of Mitogen-Activated Protein (MAP) Kinase Signaling Components in the Fungal Development, Stress Response and Virulence of the Fungal Cereal Pathogen Bipolaris sorokiniana. PLoS ONE, 2015, 10, e0128291.	2.5	35
6	Sources and Genetics of Spot Blotch Resistance to a New Pathotype of <i>Cochliobolus sativus</i> in the USDA National Small Grains Collection. Plant Disease, 2016, 100, 1988-1993.	1.4	33
7	Molecular Mapping of Fusarium Head Blight Resistance in the Spring Wheat Line ND2710. Phytopathology, 2018, 108, 972-979.	2.2	32
8	RNAâ€mediated gene silencing in the cereal fungal pathogen <i>Cochliobolus sativus</i> . Molecular Plant Pathology, 2011, 12, 289-298.	4.2	25
9	Coordinated and independent functions of velvet-complex genes in fungal development and virulence of the fungal cereal pathogen Cochliobolus sativus. Fungal Biology, 2016, 120, 948-960.	2.5	25
10	RNA-Seq Revealed Differences in Transcriptomes between 3ADON and 15ADON Populations of Fusarium graminearum In Vitro and In Planta. PLoS ONE, 2016, 11, e0163803.	2.5	25
11	Identification and application of a unique genetic locus in diagnosis of <i>Fusarium oxysporum</i> f. sp. <i>cubense</i> tropical race 4. Canadian Journal of Plant Pathology, 2013, 35, 482-493.	1.4	21
12	The gene conferring susceptibility to spot blotch caused by Cochliobolus sativus is located at the Mla locus in barley cultivar Bowman. Theoretical and Applied Genetics, 2018, 131, 1531-1539.	3.6	21
13	Genome-wide association mapping of spot blotch resistance to three different pathotypes of Cochliobolus sativus in the USDA barley core collection. Molecular Breeding, 2017, 37, 1.	2.1	17
14	The regulatory gene VosA affects conidiogenesis and is involved in virulence of the fungal cereal pathogen Cochliobolus sativus. Fungal Biology, 2015, 119, 884-900.	2.5	13
15	<i>Brachypodium distachyon</i> – <i>Cochliobolus sativus</i> Pathosystem is a New Model for Studying Plant–Fungal Interactions in Cereal Crops. Phytopathology, 2015, 105, 482-489.	2.2	13
16	Fine mapping of a dominant gene conferring resistance to spot blotch caused by a new pathotype of Bipolaris sorokiniana in barley. Theoretical and Applied Genetics, 2019, 132, 41-51.	3.6	11
17	Molecular Mapping of Loci Conferring Susceptibility to Spot Blotch and Resistance to Powdery Mildew in Barley Using the Sequencing-Based Genotyping Approach. Phytopathology, 2020, 110, 440-446.	2.2	11
18	A conserved hypothetical gene is required but not sufficient for Ptr ToxC production in Pyrenophora tritici-repentis. Molecular Plant-Microbe Interactions, 2022, , .	2.6	11

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#	Article	IF	CITATIONS
19	Construction of Hairpin RNA-Expressing Vectors for RNA-Mediated Gene Silencing in Fungi. Methods in Molecular Biology, 2012, 835, 623-633.	0.9	6
20	Prevalence of inversion positive and inversion negative mating type (MAT) alleles andMATheterokaryons inSclerotinia sclerotiorumin the United States. Botany, 2015, 93, 497-505.	1.0	3
21	Molecular Mapping of Quantitative Trait Loci for Fusarium Head Blight Resistance in the Brazilian Spring Wheat Cultivar "Surpresa― Frontiers in Plant Science, 2021, 12, 778472.	3.6	3
22	Genome Sequence Resources for the Maize Pathogen <i>Fusarium temperatum</i> Isolated in Poland. Molecular Plant-Microbe Interactions, 2021, 34, 214-217.	2.6	2