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List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Comparative genomics reveals high biological diversity and specific adaptations in the industrially and medically important fungal genus Aspergillus. Genome Biology, 2017, 18, 28.	8.8	417
2	Comparative genomics of citric-acid-producing <i>Aspergillus niger</i> ATCC 1015 versus enzyme-producing CBS 513.88. Genome Research, 2011, 21, 885-897.	5.5	329
3	Transcriptional Activation and Production of Tryptophan-Derived Secondary Metabolites in Arabidopsis Roots Contributes to the Defense against the Fungal Vascular Pathogen Verticillium longisporum. Molecular Plant, 2012, 5, 1389-1402.	8.3	120
4	<i><scp>V</scp>erticillium</i> transcription activator of adhesion <scp>V</scp> ta2 suppresses microsclerotia formation and is required for systemic infection of plant roots. New Phytologist, 2014, 202, 565-581.	7.3	92
5	Bacillus thuringiensis and Bacillus weihenstephanensis Inhibit the Growth of Phytopathogenic Verticillium Species. Frontiers in Microbiology, 2016, 7, 2171.	3.5	74
6	Silencing of Vlaro2 for chorismate synthase revealed that the phytopathogen Verticillium longisporum induces the cross-pathway control in the xylem. Applied Microbiology and Biotechnology, 2010, 85, 1961-1976.	3.6	62
7	The Plant Host <i>Brassica napus</i> Induces in the Pathogen <i>Verticillium longisporum</i> the Expression of Functional Catalase Peroxidase Which Is Required for the Late Phase of Disease. Molecular Plant-Microbe Interactions, 2012, 25, 569-581.	2.6	55
8	The Cpc1 Regulator of the Cross-Pathway Control of Amino Acid Biosynthesis Is Required for Pathogenicity of the Vascular Pathogen <i>Verticillium longisporum</i> . Molecular Plant-Microbe Interactions, 2013, 26, 1312-1324.	2.6	55
9	<i>Verticillium dahliae</i> transcription factors Som1 and Vta3 control microsclerotia formation and sequential steps of plant root penetration and colonisation to induce disease. New Phytologist, 2019, 221, 2138-2159.	7.3	50
10	Verticillium dahliae VdTHI4, involved in thiazole biosynthesis, stress response and DNA repair functions, is required for vascular disease induction in tomato. Environmental and Experimental Botany, 2014, 108, 14-22.	4.2	40
11	Infections with the vascular pathogens Verticillium longisporum and Verticillium dahliae induce distinct disease symptoms and differentially affect drought stress tolerance of Arabidopsis thaliana. Environmental and Experimental Botany, 2014, 108, 23-37.	4.2	38
12	Molecular diagnosis to discriminate pathogen and apathogen species of the hybrid Verticillium longisporum on the oilseed crop Brassica napus. Applied Microbiology and Biotechnology, 2013, 97, 4467-4483.	3.6	30
13	The velvet protein Vel1 controls initial plant root colonization and conidia formation for xylem distribution in Verticillium wilt. PLoS Genetics, 2021, 17, e1009434.	3.5	20
14	Verticillium longisporum Elicits Media-Dependent Secretome Responses With Capacity to Distinguish Between Plant-Related Environments. Frontiers in Microbiology, 2020, 11, 1876.	3.5	18
15	Fluorescent pseudomonads pursue media-dependent strategies to inhibit growth of pathogenic Verticillium fungi. Applied Microbiology and Biotechnology, 2018, 102, 817-831.	3.6	6
16	Pseudomonas Strains Induce Transcriptional and Morphological Changes and Reduce Root Colonization of Verticillium spp Frontiers in Microbiology, 2021, 12, 652468.	3.5	6
17	A 20â€kb lineageâ€specific genomic region tames virulence in pathogenic amphidiploid Verticillium longisporum. Molecular Plant Pathology, 2021, 22, 939-953.	4.2	6
18	Draft Genome Sequence of the Phenazine-Producing Pseudomonas fluorescens Strain 2-79. Genome Announcements, 2015, 3, .	0.8	5

#	Article	IF	CITATIONS
19	Draft Genome Sequence of the Beneficial Rhizobacterium Pseudomonas fluorescens DSM 8569, a Natural Isolate of Oilseed Rape (Brassica napus). Genome Announcements, 2015, 3, .	0.8	2