Lamprinos Frantzeskakis

List of Publications by Year
in descending order

13	567	1040056 9	1125743 13
papers	citations	h-index	g-index

16	16	16	972
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The leucine-rich repeats in allelic barley MLA immune receptors define specificity towards sequence-unrelated powdery mildew avirulence effectors with a predicted common RNase-like fold. PLoS Pathogens, 2021, 17, e1009223.	4.7	50
2	First draft genome assemblies of Pleochaeta shiraiana and Phyllactinia moricola, two tree-parasitic powdery mildew fungi with hemiendophytic mycelia. Phytopathology, 2021, , .	2.2	3
3	Rapid evolution in plantâ€“microbe interactions â€“ a molecular genomics perspective. New Phytologist, 2020, 225, 1134-1142.	7.3	96
4	Ultraviolet Mutagenesis Coupled with Next-Generation Sequencing as a Method for Functional Interrogation of Powdery Mildew Genomes. Molecular Plant-Microbe Interactions, 2020, 33, 1008-1021.	2.6	7
5	Smut infection of perennial hosts: the genome and the transcriptome of the Brassicaceae smut fungus Thecaphora thlaspeos reveal functionally conserved and novel effectors. New Phytologist, 2019, 222, 1474-1492.	7.3	11
6	The need for speed: compartmentalized genome evolution in filamentous phytopathogens. Molecular Plant Pathology, 2019, 20, 3-7.	4.2	79
7	The Parauncinula polyspora Draft Genome Provides Insights into Patterns of Gene Erosion and Genome Expansion in Powdery Mildew Fungi. MBio, 2019, 10, .	4.1	18
8	Small RNAs from cereal powdery mildew pathogens may target host plant genes. Fungal Biology, 2018, 122, 1050-1063.	2.5	41
9	Signatures of host specialization and a recent transposable element burst in the dynamic one-speed genome of the fungal barley powdery mildew pathogen. BMC Genomics, 2018, 19, 381.	2.8	138
10	Rapid evolution in the tugâ€ofâ€war between microbes and plants. New Phytologist, 2018, 219, 12-14.	7.3	4
11	The Plant-Dependent Life Cycle of Thecaphora thlaspeos: A Smut Fungus Adapted to Brassicaceae. Molecular Plant-Microbe Interactions, 2017, 30, 271-282.	2.6	13
12	PCR amplification of repetitive DNA: a limitation to genome editing technologies and many other applications. Scientific Reports, 2014, 4, 5052.	3.3	92
13	Reevaluation of the Reliability and Usefulness of the Somatic Homologous Recombination Reporter Lines. Plant Cell, 2012, 24, 4314-4323.	6.6	5