MÃ³nica Sebastiana

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Transcriptional and metabolic profiling of grape (Vitis vinifera L.) leaves unravel possible innate resistance against pathogenic fungi. Journal of Experimental Botany, 2008, 59, 3371-3381.	4.8	141
2	Subtilisin-like proteases in plantââ,¬â€œpathogen recognition and immune priming: a perspective. Frontiers in Plant Science, 2014, 5, 739.	3.6	135
3	Reference Gene Selection and Validation for the Early Responses to Downy Mildew Infection in Susceptible and Resistant Vitis vinifera Cultivars. PLoS ONE, 2013, 8, e72998.	2.5	78
4	Castanea root transcriptome in response to Phytophthora cinnamomi challenge. Tree Genetics and Genomes, 2015, 11, 1.	1.6	72
5	A comprehensive assessment of the transcriptome of cork oak (Quercus suber) through EST sequencing. BMC Genomics, 2014, 15, 371.	2.8	53
6	Oak Root Response to Ectomycorrhizal Symbiosis Establishment: RNA-Seq Derived Transcript Identification and Expression Profiling. PLoS ONE, 2014, 9, e98376.	2.5	45
7	Ectomycorrhizal inoculation with Pisolithus tinctorius increases the performance of Quercus suber L. (cork oak) nursery and field seedlings. New Forests, 2013, 44, 937-949.	1.7	42
8	Specific adjustments in grapevine leaf proteome discriminating resistant and susceptible grapevine genotypes to Plasmopara viticola. Journal of Proteomics, 2017, 152, 48-57.	2.4	41
9	Ectomycorrhizal inoculation with Pisolithus tinctorius reduces stress induced by drought in cork oak. Mycorrhiza, 2018, 28, 247-258.	2.8	40
10	Metabolite extraction for high-throughput FTICR-MS-based metabolomics of grapevine leaves. EuPA Open Proteomics, 2016, 12, 4-9.	2.5	35
11	First clues on a jasmonic acid role in grapevine resistance against the biotrophic fungus Plasmopara viticola. European Journal of Plant Pathology, 2015, 142, 645-652.	1.7	33
12	The leaf lipid composition of ectomycorrhizal oak plants shows a drought-tolerance signature. Plant Physiology and Biochemistry, 2019, 144, 157-165.	5.8	29
13	Oak protein profile alterations upon root colonization by an ectomycorrhizal fungus. Mycorrhiza, 2017, 27, 109-128.	2.8	25
14	Identification of plant genes involved on the initial contact between ectomycorrhizal symbionts (Castanea sativa – European chestnut and Pisolithus tinctorius). European Journal of Soil Biology, 2009, 45, 275-282.	3.2	23
15	Tracking cashew economically important diseases in the West African region using metagenomics. Frontiers in Plant Science, 2015, 6, 482.	3.6	21
16	Fungal Transcript Pattern During the Preinfection Stage (12Âh) of Ectomycorrhiza Formed Between Pisolithus tinctorius and Castanea sativa Roots, Identified Using cDNA Microarrays. Current Microbiology, 2008, 57, 620-625.	2.2	19
17	Organogenic nodule development in hop (Humulus lupulus L.): Transcript and metabolic responses. BMC Genomics, 2008, 9, 445.	2.8	17
18	First Insights into the Effect of Mycorrhizae on the Expression of Pathogen Effectors during the Infection of Grapevine with Plasmopara viticola. Sustainability, 2021, 13, 1226.	3.2	17

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#	Article	IF	CITATIONS
19	A possible approach for gel-based proteomic studies in recalcitrant woody plants. SpringerPlus, 2013, 2, 210.	1.2	13
20	Labellum transcriptome reveals alkene biosynthetic genes involved in orchid sexual deception and pollination-induced senescence. Functional and Integrative Genomics, 2012, 12, 693-703.	3.5	11
21	Genomic study of the mammary gland in bovines acclimated to a tropical environment. South African Journal of Animal Sciences, 2016, 46, 1.	0.5	3
22	A genomic study on mammary gland acclimatization to tropical environment in the Holstein cattle. Tropical Animal Health and Production, 2018, 50, 187-195.	1.4	3
23	Pisolithus. , 2020, , 707-726.		1