Ana UsiÃ© Chimenos

List of Publications by Year
in descending order

16 papers	260 citations	1307594 7 h-index	1125743 13 g-index
17 all docs	17 docs citations	17 times ranked	389 citing authors

#	Article	IF	Citations
1	Ovine footrot in Southern Portugal: Detection of Dichelobacter nodosus and Fusobacterium necrophorum in sheep with different lesion scores. Veterinary Microbiology, 2022, 266, 109339.	1.9	3
2	Kinship Analysis and Pedigree Reconstruction of a Natural Regenerated Cork Oak (Quercus suber) Population. Forests, 2022, 13, 226.	2.1	3
3	Quercus suber Transcriptome Analyses: Identification of Genes and SNPs Related to Cork Quality. , 2022, 11, .		2
4	The Crown Pearl: a draft genome assembly of the European freshwater pearl mussel<i>Margaritifera margaritifera</i>(Linnaeus, 1758). DNA Research, 2021, 28, .	3.4	15
5	Transcriptome Characterization of Different Tissues of Stone Pine (Pinus pinea L.): De Novo Assembly. , 2021, 11, .		0
6	Comparative Transcriptomic Response of Two Pinus Species to Infection with the Pine Wood Nematode Bursaphelenchus xylophilus. Forests, 2020, 11, 204.	2.1	19
7	Characterization of the cork formation and production transcriptome in Quercus cerris‰Ã—‰suber hybrids. Physiology and Molecular Biology of Plants, 2018, 24, 535-549.	3.1	9
8	ChIP-Seq reveals that QsMYB1 directly targets genes involved in lignin and suberin biosynthesis pathways in cork oak (Quercus suber). BMC Plant Biology, 2018, 18, 198.	3.6	50
9	The draft genome sequence of cork oak. Scientific Data, 2018, 5, 180069.	5.3	98
10	Expression Profiling in Pinus pinaster in Response to Infection with the Pine Wood Nematode Bursaphelenchus xylophilus. Forests, 2017, 8, 279.	2.1	22
11	Comprehensive Analysis of the Cork Oak (Quercus suber) Transcriptome Involved in the Regulation of Bud Sprouting. Forests, 2017, 8, 486.	2.1	6
12	Database Constraints Applied to Metabolic Pathway Reconstruction Tools. Scientific World Journal, The, 2014, 2014, 1-12.	2.1	1
13	CheNER: chemical named entity recognizer. Bioinformatics, 2014, 30, 1039-1040.	4.1	15
14	Biblio-MetReS for user-friendly mining of genes and biological processes in scientific documents. PeerJ, 2014, 2, e276.	2.0	4
15	P-Biblio-MetReS, a parallel data mining tool for the reconstruction of molecular networks. , 2013, , .		0
16	Methods for and results from the study of design principles in molecular systems. Mathematical Biosciences, 2011, 231, 3-18.	1.9	13