Juan JosÃ© R Coque

List of Publications by Year
in descending order

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45 papers	1,458 citations	361413 20 h-index	330143 37 g-index
45 all docs	45 docs citations	45 times ranked	1453 citing authors

#	Article	IF	Citations
1	First Report of Pleurostoma richardsiae Associated with Twig and Branch Dieback of Olive Trees in Spain. Plant Disease, 2022, 106, 1981.	1.4	2
2	The Grapevine Microbiome to the Rescue: Implications for the Biocontrol of Trunk Diseases. Plants, 2022, 11, 840.	3.5	17
3	Using Rhizosphere Phosphate Solubilizing Bacteria to Improve Barley (Hordeum vulgare) Plant Productivity. Microorganisms, 2021, 9, 1619.	3.6	15
4	Advances in the control of phytopathogenic fungi that infect crops through their root system. Advances in Applied Microbiology, 2020, 111, 123-170.	2.4	18
5	Developing tools for evaluating inoculation methods of biocontrol Streptomyces sp. strains into grapevine plants. PLoS ONE, 2019, 14, e0211225.	2.5	20
6	Necrotic and Cytolytic Activity on Grapevine Leaves Produced by Nep1-Like Proteins of Diplodia seriata. Frontiers in Plant Science, 2019, 10, 1282.	3.6	13
7	Use of Endophytic and Rhizosphere Actinobacteria from Grapevine Plants To Reduce Nursery Fungal Graft Infections That Lead to Young Grapevine Decline. Applied and Environmental Microbiology, 2017, 83, .	3.1	83
8	Effects of liming on soil properties, leaf tissue cation composition and grape yield in a moderately acid vineyard soil. Influence on must and wine quality. Oeno One, 2017, 51, 343.	1.4	10
9	Selection of Saccharomyces cerevisiae Strains Applied to the Production of Prieto Picudo RosÃ© Wines with a Different Aromatic Profile. South African Journal of Enology and Viticulture, 2016, 35, .	0.4	6
10	Determining optimum harvest time under Mediterranean conditions: developing a new model for measuring L-malic acid concentration in red grapes. Australian Journal of Grape and Wine Research, 2016, 22, 232-239.	2.1	3
11	Effectiveness of Natural Antifungal Compounds in Controlling Infection by Grapevine Trunk Disease Pathogens through Pruning Wounds. Applied and Environmental Microbiology, 2015, 81, 6474-6483.	3.1	37
12	Manganese transporter protein MntH is required for virulence ofXylophilus ampelinus, the causal agent of bacterial necrosis in grapevine. Australian Journal of Grape and Wine Research, 2014, 20, 442-450.	2.1	2
13	Sensory and chemical characterisation of the aroma of Prieto Picudo rosÃ© wines: The differential role of autochthonous yeast strains on aroma profiles. Food Chemistry, 2012, 133, 284-292.	8.2	50
14	Destruction of Chloroanisoles by Using a Hydrogen Peroxide Activated Method and Its Application To Remove Chloroanisoles from Cork Stoppers. Journal of Agricultural and Food Chemistry, 2011, 59, 12589-12597.	5.2	16
15	Cytoplasmic- and extracellular-proteome analysis of Diplodia seriata: a phytopathogenic fungus involved in grapevine decline. Proteome Science, 2010, 8, 46.	1.7	38
16	Characterization of a novel 2,4,6-trichlorophenol-inducible gene encoding chlorophenol O-methyltransferase from Trichoderma longibrachiatum responsible for the formation of chloroanisoles and detoxification of chlorophenols. Fungal Genetics and Biology, 2010, 47, 458-467.	2.1	16
17	The analysis of natural cork stoppers in transversal sections as an effective tool to determine the origin of the taint by 2,4,6-trichloroanisole. European Food Research and Technology, 2009, 230, 135-143.	3.3	11
18	Two overlapping antiparallel genes encoding the iron regulator DmdR1 and the Adm proteins control sidephore and antibiotic biosynthesis in Streptomycesâ€ƒcoelicolor A3(2). FEBS Journal, 2009, 276, 4814-4827.	4.7	46

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19	Biodegradation of 2,4,6â€TCA by the whiteâ€rot fungus Phlebia radiata is initiated by a phase I (Oâ€demethylation)â€“phase II (Oâ€conjugation) reactions system: implications for the chlorine cycle. Environmental Microbiology, 2009, 11, 99-110.	3.8	20
20	Environmental significance of O-demethylation of chloroanisoles by soil bacterial isolates as a mechanism that improves the overall biodegradation of chlorophenols. Environmental Microbiology, 2007, 9, 2512-2521.	3.8	21
21	Transcriptional regulation of the desferrioxamine gene cluster ofStreptomyces coelicoloris mediated by binding of DmdR1 to an iron box in the promoter of thedesAgene. FEBS Journal, 2007, 274, 1110-1122.	4.7	54
22	Functional analysis of two divalent metal-dependent regulatory genes dmdR1 and dmdR2 in Streptomyces coelicolor and proteome changes in deletion mutants. FEBS Journal, 2005, 272, 725-735.	4.7	27
23	Polyphasic identification of yeasts isolated from bark of cork oak during the manufacturing process of cork stoppers. FEMS Yeast Research, 2004, 4, 745-750.	2.3	23
24	Degradation of vanillic acid and production of guaiacol by microorganisms isolated from cork samples. FEMS Microbiology Letters, 2003, 220, 49-55.	1.8	76
25	Characterization of an Inducible Chlorophenol O -Methyltransferase from Trichoderma longibrachiatum Involved in the Formation of Chloroanisoles and Determination of Its Role in Cork Taint of Wines. Applied and Environmental Microbiology, 2003, 69, 5089-5095.	3.1	59
26	Cork Taint of Wines: Role of the Filamentous Fungi Isolated from Cork in the Formation of 2,4,6-Trichloroanisole by O Methylation of 2,4,6-Trichlorophenol. Applied and Environmental Microbiology, 2002, 68, 5860-5869.	3.1	132
27	Sequencing of a 4.3 kbp region of chromosome 2 ofCandida albicans reveals the presence of homologues ofSHE9 fromSaccharomyces cerevisiae and of bacterial phosphatidylinositol-phospholipase C. Yeast, 2001, 18, 711-721.	1.7	15
28	Isoform-specific insertion near the Grb2-binding domain modulates the intrinsic guanine nucleotide exchange activity of hSos1. Oncogene, 1999, 18, 1651-1661.	5.9	13
29	Cell cycle regulation of a DNA ligase-encoding gene (CaLIG4) fromCandida albicans. Yeast, 1999, 15, 1199-1210.	1.7	14
30	Biochemical characterization of the SecA protein of Streptomyces lividans . Interaction with nucleotides, binding to membrane vesicles and in vitro translocation of proAmy protein. FEBS Journal, 1998, 257, 472-478.	0.2	11
31	The Nine Genes of the Nocardia lactamdurans Cephamycin Cluster Are Transcribed into Large mRNAs from Three Promoters, Two of Them Located in a Bidirectional Promoter Region. Journal of Bacteriology, 1998, 180, 5489-5494.	2.2	19
32	The Folate Branch of the Methionine Biosynthesis Pathway in Streptomyces lividans : Disruption of the 5,10-Methylenetetrahydrofolate Reductase Gene Leads to Methionine Auxotrophy. Journal of Bacteriology, 1998, 180, 1586-1591.	2.2	17
33	The bla gene of the cephamycin cluster of Streptomyces clavuligerus encodes a class A beta-lactamase of low enzymatic activity. Journal of Bacteriology, 1997, 179, 6035-6040.	2.2	44
34	Cloning, expression in Streptomyces lividans and biochemical characterization of a thermostable endo-Î²-1,4-xylanase of Thermomonospora alba ULâ€ŠJB1 with cellulose-binding ability. Applied Microbiology and Biotechnology, 1997, 48, 208-217.	3.6	53
35	Characterization of the secA gene of Streptomyces lividans encoding a protein translocase which complements an Escherichia coli mutant defective in the ATPase activity of SecA. Gene, 1996, 176, 61-65.	2.2	12
36	Overexpression of the Nocardia lactamduransalpha-Aminoadipyl-Cysteinyl-Valine Synthetase in Streptomyces lividans. The Purified Multienzyme Uses Cystathionine and 6-Oxopiperidine 2-Carboxylate as Substrates for Synthesis of the Tripeptide. FEBS Journal, 1996, 242, 264-270.	0.2	23

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37	Isolated Sos1 PH Domain Exhibits Germinal Vesicle Breakdown-inducing Activity in Oocytes. Journal of Biological Chemistry, 1996, 271, 18272-18276.	3.4	10
38	A two-protein component 7 alpha-cephem-methoxylase encoded by two genes of the cephamycin C cluster converts cephalosporin C to 7-methoxycephalosporin C. Journal of Bacteriology, 1995, 177, 2230-2235.	2.2	54
39	Characterization of the cmcH genes of Nocardia lactamdurans and streptomyces clavuligerus encoding a functional 3'-hydroxymethylcephem O-carbamoyltransferase for cephamycin biosynthesis. Gene, 1995, 162, 21-27.	2.2	54
40	Interdependence of Gene Expression for Early Steps of Cephalosporin Synthesis in Streptomyces clavuligerus. Annals of the New York Academy of Sciences, 1994, 721, 117-122.	3.8	2
41	Efficient Transformation of the Cephamycin C Producer Nocardia lactamdurans and Development of Shuttle and Promoter-Probe Cloning Vectors. Applied and Environmental Microbiology, 1994, 60, 4086-4093.	3.1	52
42	Characterization and expression in Streptomyces lividans of cefD and cefE genes from Nocardia lactamdurans: the organization of the cephamycin gene cluster differs from that in Streptomyces clavuligerus. Molecular Genetics and Genomics, 1993, 236-236, 453-458.	2.4	46
43	Analysis of the codon usage of the cephamycin C producerNocardia lactamdurans. FEMS Microbiology Letters, 1993, 110, 91-95.	1.8	10
44	A gene encoding lysine 6-aminotransferase, which forms the beta-lactam precursor alpha-aminoadipic acid, is located in the cluster of cephamycin biosynthetic genes in Nocardia lactamdurans. Journal of Bacteriology, 1991, 173, 6258-6264.	2.2	69
45	The cephamycin biosynthetic genes pcbAB, encoding a large multidomain peptide synthetase, and pcbC of Nocardia lactamdurans are clustered together in an organization different from the same genes in Acremonium chrysogenum and Penicillium chrysogenum. Molecular Microbiology, 1991, 5, 1125-1133.	2.5	125