Sara Hernando-Amado

List of Publications by Year
in descending order

33 papers	2,456 citations	361045 20 h-index	414034 32 g-index
36 all docs	36 docs citations	36 times ranked	3314 citing authors

#	Article	IF	Citations
1	Defining and combating antibiotic resistance from One Health and Global Health perspectives. Nature Microbiology, 2019, 4, 1432-1442.	5.9	614
2	Bacterial Multidrug Efflux Pumps: Much More Than Antibiotic Resistance Determinants. Microorganisms, 2016, 4, 14.	1.6	486
3	Multidrug Efflux Pumps at the Crossroad between Antibiotic Resistance and Bacterial Virulence. Frontiers in Microbiology, 2016, 7, 1483.	1.5	180
4	Multidrug efflux pumps as main players in intrinsic and acquired resistance to antimicrobials. Drug Resistance Updates, 2016, 28, 13-27.	6.5	139
5	Prediction of the intestinal resistome by a three-dimensional structure-based method. Nature Microbiology, 2019, 4, 112-123.	5.9	129
6	Mutation-Driven Evolution of Pseudomonas aeruginosa in the Presence of either Ceftazidime or Ceftazidime-Avibactam. Antimicrobial Agents and Chemotherapy, 2018, 62, .	1.4	83
7	A Function of SmeDEF, the Major Quinolone Resistance Determinant of Stenotrophomonas maltophilia, Is the Colonization of Plant Roots. Applied and Environmental Microbiology, 2014, 80, 4559-4565.	1.4	75
8	Antibiotic Resistance: Moving From Individual Health Norms to Social Norms in One Health and Global Health. Frontiers in Microbiology, 2020, 11, 1914.	1.5	64
9	Fitness costs associated with the acquisition of antibiotic resistance. Essays in Biochemistry, 2017, 61, 37-48.	2.1	62
10	The family of DOF transcription factors in Brachypodium distachyon: phylogenetic comparison with rice and barley DOFs and expression profiling. BMC Plant Biology, 2012, 12, 202.	1.6	54
11	Mutational Evolution of Pseudomonas aeruginosa Resistance to Ribosome-Targeting Antibiotics. Frontiers in Genetics, 2018, 9, 451.	1.1	52
12	Structure, expression profile and subcellular localisation of four different sucrose synthase genes from barley. Planta, 2011, 234, 391-403.	1.6	45
13	Antibiotic Resistance Evolution Is Contingent on the Quorum-Sensing Response in Pseudomonas aeruginosa. Molecular Biology and Evolution, 2019, 36, 2238-2251.	3.5	40
14	Naringenin Inhibition of the Pseudomonas aeruginosa Quorum Sensing Response Is Based on Its Time-Dependent Competition With N-(3-Oxo-dodecanoyl)-L-homoserine Lactone for LasR Binding. Frontiers in Molecular Biosciences, 2020, 7, 25.	1.6	40
15	Pseudomonas aeruginosa: an antibiotic resilient pathogen with environmental origin. Current Opinion in Microbiology, 2021, 64, 125-132.	2.3	38
16	Rapid and robust evolution of collateral sensitivity in <i>Pseudomonas aeruginosa</i> antibiotic-resistant mutants. Science Advances, 2020, 6, eaba5493.	4.7	33
17	Coming from the Wild: Multidrug Resistant Opportunistic Pathogens Presenting a Primary, Not Human-Linked, Environmental Habitat. International Journal of Molecular Sciences, 2021, 22, 8080.	1.8	33
18	Antimicrobial resistance: A multifaceted problem with multipronged solutions. MicrobiologyOpen, 2019, 8, e945.	1.2	32

#	Article	IF	Citations
19	The development of efflux pump inhibitors to treat Gram-negative infections. Expert Opinion on Drug Discovery, 2018, 13, 919-931.	2.5	30
20	Characterization of a novel Zn2+-dependent intrinsic imipenemase from Pseudomonas aeruginosa. Journal of Antimicrobial Chemotherapy, 2014, 69, 2972-2978.	1.3	26
21	Wildlife and Antibiotic Resistance. Frontiers in Cellular and Infection Microbiology, 2022, 12, .	1.8	23
22	Evolution under low antibiotic concentrations: a risk for the selection of <i>Pseudomonas aeruginosa</i> multidrugâ€resistant mutants in nature. Environmental Microbiology, 2022, 24, 1279-1293.	1.8	22
23	Novel Inducers of the Expression of Multidrug Efflux Pumps That Trigger<i>Pseudomonas aeruginosa</i>Transient Antibiotic Resistance. Antimicrobial Agents and Chemotherapy, 2019, 63, .	1.4	20
24	Convergent phenotypic evolution towards fosfomycin collateral sensitivity of <i>Pseudomonasâ€‰aeruginosa</i> antibioticâ€resistant mutants. Microbial Biotechnology, 2022, 15, 613-629.	2.0	19
25	Mutational background influences<i>P. aeruginosa</i>ciprofloxacin resistance evolution but preserves collateral sensitivity robustness. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2109370119.	3.3	18
26	The analysis of the antibiotic resistome offers new opportunities for therapeutic intervention. Future Medicinal Chemistry, 2016, 8, 1133-1151.	1.1	17
27	Analysis of the Pseudomonas aeruginosa Aminoglycoside Differential Resistomes Allows Defining Genes Simultaneously Involved in Intrinsic Antibiotic Resistance and Virulence. Antimicrobial Agents and Chemotherapy, 2019, 63, .	1.4	17
28	Evolutionary landscapes of Pseudomonas aeruginosa towards ribosome-targeting antibiotic resistance depend on selection strength. International Journal of Antimicrobial Agents, 2020, 55, 105965.	1.1	16
29	Discovery of inhibitors of <scp><i>Pseudomonas aeruginosa</i></scp> virulence through the search for naturalâ€like compounds with a dual role as inducers and substrates of efflux pumps. Environmental Microbiology, 2021, 23, 7396-7411.	1.8	16
30	Rapid Decline of Ceftazidime Resistance in Antibiotic-Free and Sublethal Environments Is Contingent on Genetic Background. Molecular Biology and Evolution, 2022, 39, .	3.5	16
31	Evolution of Habitat-Dependent Antibiotic Resistance in Pseudomonas aeruginosa. Microbiology Spectrum, 2022, 10, .	1.2	11
32	Use of phenotype microarrays to study the effect of acquisition of resistance to antimicrobials in bacterial physiology. Research in Microbiology, 2016, 167, 723-730.	1.0	5
33	Emergence of intrinsically resistant Gram-negative bacteria with an environmental primary habitat. International Journal of Antimicrobial Agents, 2021, 58, 21002296.	1.1	0