

# Maria Blanca Sanchez

## List of Publications by Year in descending order

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Version: 2024-02-01

32  
papers

2,582  
citations

361413

20  
h-index

414414

32  
g-index

33  
all docs

33  
docs citations

33  
times ranked

3323  
citing authors

#	ARTICLE	IF	CITATIONS
1	Making Waves: Collaboration in the time of SARS-CoV-2 - rapid development of an international co-operation and wastewater surveillance database to support public health decision-making. <i>Water Research</i> , 2021, 199, 117167.	11.3	48
2	The Acquisition of Colistin Resistance Is Associated to the Amplification of a Large Chromosomal Region in <i>Klebsiella pneumoniae</i> kp52145. <i>International Journal of Molecular Sciences</i> , 2021, 22, 649.	4.1	2
3	Evolutionary landscapes of <i>Pseudomonas aeruginosa</i> towards ribosome-targeting antibiotic resistance depend on selection strength. <i>International Journal of Antimicrobial Agents</i> , 2020, 55, 105965.	2.5	16
4	The intrinsic resistome of <i>Klebsiella pneumoniae</i> . <i>International Journal of Antimicrobial Agents</i> , 2019, 53, 29-33.	2.5	20
5	Overexpression of the Efflux Pumps SmeVWX and SmeDEF Is a Major Cause of Resistance to Co-trimoxazole in <i>Stenotrophomonas maltophilia</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	3.2	24
6	Vitamin K <sub>3</sub> Induces the Expression of the <i>Stenotrophomonas maltophilia</i> SmeVWX Multidrug Efflux Pump. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.2	19
7	Characterization of the biosynthetic gene cluster (ata) for the A201A aminonucleoside antibiotic from <i>Saccharothrix mutabilis</i> subsp. <i>capreolus</i> . <i>Journal of Antibiotics</i> , 2017, 70, 404-413.	2.0	10
8	Bacterial Multidrug Efflux Pumps: Much More Than Antibiotic Resistance Determinants. <i>Microorganisms</i> , 2016, 4, 14.	3.6	486
9	Multidrug efflux pumps as main players in intrinsic and acquired resistance to antimicrobials. <i>Drug Resistance Updates</i> , 2016, 28, 13-27.	14.4	139
10	Use of phenotype microarrays to study the effect of acquisition of resistance to antimicrobials in bacterial physiology. <i>Research in Microbiology</i> , 2016, 167, 723-730.	2.1	5
11	The analysis of the antibiotic resistome offers new opportunities for therapeutic intervention. <i>Future Medicinal Chemistry</i> , 2016, 8, 1133-1151.	2.3	17
12	Antibiotic resistance in the opportunistic pathogen <i>Stenotrophomonas maltophilia</i> . <i>Frontiers in Microbiology</i> , 2015, 6, 658.	3.5	178
13	The inactivation of RNase G reduces the <i>Stenotrophomonas maltophilia</i> susceptibility to quinolones by triggering the heat shock response. <i>Frontiers in Microbiology</i> , 2015, 6, 1068.	3.5	17
14	Predictive Studies Suggest that the Risk for the Selection of Antibiotic Resistance by Biocides Is Likely Low in <i>Stenotrophomonas maltophilia</i> . <i>PLoS ONE</i> , 2015, 10, e0132816.	2.5	21
15	Regulation of <i>Smqnr</i> expression by <i>SmqnrR</i> is strain-specific in <i>Stenotrophomonas maltophilia</i> : Table 1.. <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 2913-2914.	3.0	7
16	The Efflux Pump SmeDEF Contributes to Trimethoprim-Sulfamethoxazole Resistance in <i>Stenotrophomonas maltophilia</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 4347-4348.	3.2	56
17	High-level quinolone resistance is associated with the overexpression of smeVWX in <i>Stenotrophomonas maltophilia</i> clinical isolates. <i>Clinical Microbiology and Infection</i> , 2015, 21, 464-467.	6.0	44
18	Interplay between intrinsic and acquired resistance to quinolones in <i>Stenotrophomonas maltophilia</i> . <i>Environmental Microbiology</i> , 2014, 16, 1282-1296.	3.8	60

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19	The DSF Quorum Sensing System Controls the Positive Influence of <i>Stenotrophomonas maltophilia</i> on Plants. PLoS ONE, 2013, 8, e67103.	2.5	51
20	The intrinsic resistome of bacterial pathogens. <i>Frontiers in Microbiology</i> , 2013, 4, 103.	3.5	137
21	Whole-Genome Sequence of <i>Stenotrophomonas maltophilia</i> D457, a Clinical Isolate and a Model Strain. <i>Journal of Bacteriology</i> , 2012, 194, 3563-3564.	2.2	41
22	The Inactivation of Intrinsic Antibiotic Resistance Determinants Widens the Mutant Selection Window for Quinolones in <i>Stenotrophomonas maltophilia</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 6397-6399.	3.2	12
23	Metagenomics and antibiotics. <i>Clinical Microbiology and Infection</i> , 2012, 18, 27-31.	6.0	45
24	Differential Epigenetic Compatibility of qnr Antibiotic Resistance Determinants with the Chromosome of <i>Escherichia coli</i> . PLoS ONE, 2012, 7, e35149.	2.5	24
25	Quinolone Resistance: Much More than Predicted. <i>Frontiers in Microbiology</i> , 2011, 2, 22.	3.5	113
26	SmQnr Contributes to Intrinsic Resistance to Quinolones in <i>Stenotrophomonas maltophilia</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2010, 54, 580-581.	3.2	75
27	Polymorphic Mutation Frequencies of Clinical and Environmental <i>Stenotrophomonas maltophilia</i> Populations. <i>Applied and Environmental Microbiology</i> , 2010, 76, 1746-1758.	3.1	55
28	A global view of antibiotic resistance. <i>FEMS Microbiology Reviews</i> , 2009, 33, 44-65.	8.6	271
29	Functional role of bacterial multidrug efflux pumps in microbial natural ecosystems. <i>FEMS Microbiology Reviews</i> , 2009, 33, 430-449.	8.6	384
30	<i>Stenotrophomonas maltophilia</i> drug resistance. <i>Future Microbiology</i> , 2009, 4, 655-660.	2.0	98
31	Predictive analysis of transmissible quinolone resistance indicates <i>Stenotrophomonas maltophilia</i> as a potential source of a novel family of Qnr determinants. <i>BMC Microbiology</i> , 2008, 8, 148.	3.3	104
32	The pur3 gene from the pur cluster encodes a monophosphatase essential for puromycin biosynthesis in <i>Streptomyces</i> . <i>FEBS Letters</i> , 2006, 580, 1807-1811.	2.8	1