

# Maria Blanca Sanchez

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4889701/publications.pdf>

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	Bacterial Multidrug Efflux Pumps: Much More Than Antibiotic Resistance Determinants. <i>Microorganisms</i> , 2016, 4, 14.	3.6	486
2	Functional role of bacterial multidrug efflux pumps in microbial natural ecosystems. <i>FEMS Microbiology Reviews</i> , 2009, 33, 430-449.	8.6	384
3	A global view of antibiotic resistance. <i>FEMS Microbiology Reviews</i> , 2009, 33, 44-65.	8.6	271
4	Antibiotic resistance in the opportunistic pathogen <i>Stenotrophomonas maltophilia</i> . <i>Frontiers in Microbiology</i> , 2015, 6, 658.	3.5	178
5	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
6	The intrinsic resistome of bacterial pathogens. <i>Frontiers in Microbiology</i> , 2013, 4, 103.	3.5	137
7	Quinolone Resistance: Much More than Predicted. <i>Frontiers in Microbiology</i> , 2011, 2, 22.	3.5	113
8	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
9	<i>Stenotrophomonas maltophilia</i> drug resistance. <i>Future Microbiology</i> , 2009, 4, 655-660.	2.0	98
10	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
11	Interplay between intrinsic and acquired resistance to quinolones in <i>Stenotrophomonas maltophilia</i> . <i>Environmental Microbiology</i> , 2014, 16, 1282-1296.	3.8	60
12	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
13	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
14	The DSF Quorum Sensing System Controls the Positive Influence of <i>Stenotrophomonas maltophilia</i> on Plants. <i>PLoS ONE</i> , 2013, 8, e67103.	2.5	51
15	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
16	Metagenomics and antibiotics. <i>Clinical Microbiology and Infection</i> , 2012, 18, 27-31.	6.0	45
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	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

#	ARTICLE	IF	CITATIONS
19	Differential Epigenetic Compatibility of qnr Antibiotic Resistance Determinants with the Chromosome of Escherichia coli. PLoS ONE, 2012, 7, e35149.	2.5	24
20	Overexpression of the Efflux Pumps SmeVWX and SmeDEF Is a Major Cause of Resistance to Co-trimoxazole in Stenotrophomonas maltophilia. Antimicrobial Agents and Chemotherapy, 2018, 62, .	3.2	24
21	Predictive Studies Suggest that the Risk for the Selection of Antibiotic Resistance by Biocides Is Likely Low in Stenotrophomonas maltophilia. PLoS ONE, 2015, 10, e0132816.	2.5	21
22	The intrinsic resistome of Klebsiella pneumoniae. International Journal of Antimicrobial Agents, 2019, 53, 29-33.	2.5	20
23	Vitamin K <sub>3</sub> Induces the Expression of the Stenotrophomonas maltophilia SmeVWX Multidrug Efflux Pump. Antimicrobial Agents and Chemotherapy, 2017, 61, .	3.2	19
24	The inactivation of RNase G reduces the Stenotrophomonas maltophilia susceptibility to quinolones by triggering the heat shock response. Frontiers in Microbiology, 2015, 6, 1068.	3.5	17
25	The analysis of the antibiotic resistome offers new opportunities for therapeutic intervention. Future Medicinal Chemistry, 2016, 8, 1133-1151.	2.3	17
26	Evolutionary landscapes of Pseudomonas aeruginosa towards ribosome-targeting antibiotic resistance depend on selection strength. International Journal of Antimicrobial Agents, 2020, 55, 105965.	2.5	16
27	The Inactivation of Intrinsic Antibiotic Resistance Determinants Widens the Mutant Selection Window for Quinolones in Stenotrophomonas maltophilia. Antimicrobial Agents and Chemotherapy, 2012, 56, 6397-6399.	3.2	12
28	Characterization of the biosynthetic gene cluster (ata) for the A201A aminonucleoside antibiotic from Saccharothrix mutabilis subsp. capreolus. Journal of Antibiotics, 2017, 70, 404-413.	2.0	10
29	Regulation of Sm <i>qnr</i> expression by Sm <i>qnrR</i> is strain-specific in <i>Stenotrophomonas maltophilia</i> : Table 1.. Journal of Antimicrobial Chemotherapy, 2015, 70, 2913-2914.	3.0	7
30	Use of phenotype microarrays to study the effect of acquisition of resistance to antimicrobials in bacterial physiology. Research in Microbiology, 2016, 167, 723-730.	2.1	5
31	The Acquisition of Colistin Resistance Is Associated to the Amplification of a Large Chromosomal Region in Klebsiella pneumoniae kp52145. International Journal of Molecular Sciences, 2021, 22, 649.	4.1	2
32	The pur3 gene from the pur cluster encodes a monophosphatase essential for puromycin biosynthesis in Streptomyces. FEBS Letters, 2006, 580, 1807-1811.	2.8	1