

# Jose Luis Martinez

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1827374/publications.pdf>

Version: 2024-02-01

238  
papers

23,864  
citations

10389

72  
h-index

8630

146  
g-index

265  
all docs

265  
docs citations

265  
times ranked

22332  
citing authors

#	ARTICLE	IF	CITATIONS
1	Convergent phenotypic evolution towards fosfomycin collateral sensitivity of <i>Pseudomonas aeruginosa</i> antibiotic-resistant mutants. <i>Microbial Biotechnology</i> , 2022, 15, 613-629.	4.2	19
2	Evolution under low antibiotic concentrations: a risk for the selection of <i>Pseudomonas aeruginosa</i> multidrug-resistant mutants in nature. <i>Environmental Microbiology</i> , 2022, 24, 1279-1293.	3.8	22
3	Fosfomycin Resistance Evolutionary Pathways of <i>Stenotrophomonas maltophilia</i> in Different Growing Conditions. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1132.	4.1	5
4	The Antibiotic Fosfomycin Mimics the Effects of the Intermediate Metabolites Phosphoenolpyruvate and Glyceraldehyde-3-Phosphate on the <i>Stenotrophomonas maltophilia</i> Transcriptome. <i>International Journal of Molecular Sciences</i> , 2022, 23, 159.	4.1	4
5	Rapid Decline of Ceftazidime Resistance in Antibiotic-Free and Sublethal Environments Is Contingent on Genetic Background. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	16
6	Mutational background influences <i>P. aeruginosa</i> ciprofloxacin resistance evolution but preserves collateral sensitivity robustness. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2109370119.	7.1	18
7	Glucose-6-phosphate Reduces Fosfomycin Activity Against <i>Stenotrophomonas maltophilia</i> . <i>Frontiers in Microbiology</i> , 2022, 13, .	3.5	2
8	Wildlife and Antibiotic Resistance. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, .	3.9	23
9	Evolution of Habitat-Dependent Antibiotic Resistance in <i>Pseudomonas aeruginosa</i> . <i>Microbiology Spectrum</i> , 2022, 10, .	3.0	11
10	The MexJK Multidrug Efflux Pump Is Not Involved in Acquired or Intrinsic Antibiotic Resistance in <i>Pseudomonas aeruginosa</i> , but Modulates the Bacterial Quorum Sensing Response. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7492.	4.1	6
11	Point-of-care ultrasound by the pediatrician in the diagnosis and follow-up of community-acquired pneumonia. <i>Jornal De Pediatria</i> , 2021, 97, 13-21.	2.0	3
12	Antibiotic resistance: Time of synthesis in a post-genomic age. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 3110-3124.	4.1	28
13	The Origin of Niches and Species in the Bacterial World. <i>Frontiers in Microbiology</i> , 2021, 12, 657986.	3.5	56
14	Discovery of inhibitors of <i>Pseudomonas aeruginosa</i> virulence through the search for natural-like compounds with a dual role as inducers and substrates of efflux pumps. <i>Environmental Microbiology</i> , 2021, 23, 7396-7411.	3.8	16
15	A wide-ranging <i>Pseudomonas aeruginosa</i> PeptideAtlas build: A useful proteomic resource for a versatile pathogen. <i>Journal of Proteomics</i> , 2021, 239, 104192.	2.4	7
16	Metagenomics Analysis Reveals an Extraordinary Inner Bacterial Diversity in Anisakids (Nematoda:). <i>Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50</i>	3.6	4
17	Evolutionary Pathways and Trajectories in Antibiotic Resistance. <i>Clinical Microbiology Reviews</i> , 2021, 34, e0005019.	13.6	71
18	Coming from the Wild: Multidrug Resistant Opportunistic Pathogens Presenting a Primary, Not Human-Linked, Environmental Habitat. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8080.	4.1	33

#	ARTICLE	IF	CITATIONS
19	Explorative assessment of coronavirus-like short sequences from host-associated and environmental metagenomes. <i>Science of the Total Environment</i> , 2021, 793, 148494.	8.0	0
20	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
21	Allogeneous Selection of Mutational Collateral Resistance: Old Drugs Select for New Resistance Within Antibiotic Families. <i>Frontiers in Microbiology</i> , 2021, 12, 757833.	3.5	15
22	<i>Pseudomonas aeruginosa</i> : an antibiotic resilient pathogen with environmental origin. <i>Current Opinion in Microbiology</i> , 2021, 64, 125-132.	5.1	38
23	Rapid and robust evolution of collateral sensitivity in <i>Pseudomonas aeruginosa</i> antibiotic-resistant mutants. <i>Science Advances</i> , 2020, 6, eaba5493.	10.3	33
24	The impaired quorum sensing response of <i>Pseudomonas aeruginosa</i> MexAB-OprM efflux pump overexpressing mutants is not due to non-physiological efflux of 3-oxo-C12-HSL. <i>Environmental Microbiology</i> , 2020, 22, 5167-5188.	3.8	24
25	Antibiotic Resistance: Moving From Individual Health Norms to Social Norms in One Health and Global Health. <i>Frontiers in Microbiology</i> , 2020, 11, 1914.	3.5	64
26	Metagenomic analysis of an urban resistome before and after wastewater treatment. <i>Scientific Reports</i> , 2020, 10, 8174.	3.3	58
27	The Importance of Abdominal Wall Closure After Definitive Surgery for Enterocutaneous Fistula. <i>World Journal of Surgery</i> , 2020, 44, 3333-3340.	1.6	2
28	The Inactivation of Enzymes Belonging to the Central Carbon Metabolism Is a Novel Mechanism of Developing Antibiotic Resistance. <i>MSystems</i> , 2020, 5, .	3.8	16
29	Environmental remodeling of human gut microbiota and antibiotic resistome in livestock farms. <i>Nature Communications</i> , 2020, 11, 1427.	12.8	133
30	Antibiotic Resistance in the Environment: Expert Perspectives. <i>Handbook of Environmental Chemistry</i> , 2020, , 1-18.	0.4	5
31	Naringenin Inhibition of the <i>Pseudomonas aeruginosa</i> Quorum Sensing Response Is Based on Its Time-Dependent Competition With N-(3-Oxo-dodecanoyl)-L-homoserine Lactone for LasR Binding. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 25.	3.5	40
32	Mechanisms of antimicrobial resistance in <i>Stenotrophomonas maltophilia</i> : a review of current knowledge. <i>Expert Review of Anti-Infective Therapy</i> , 2020, 18, 335-347.	4.4	73
33	Antibiotic residues in final effluents of European wastewater treatment plants and their impact on the aquatic environment. <i>Environment International</i> , 2020, 140, 105733.	10.0	338
34	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
35	<i>Pseudomonas fildesensis</i> sp. nov., a psychrotolerant bacterium isolated from Antarctic soil of King George Island, South Shetland Islands. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 3255-3263.	1.7	15
36	Antimicrobial Peptide Exposure Selects for Resistant and Fit <i>Stenotrophomonas maltophilia</i> Mutants That Show Cross-Resistance to Antibiotics. <i>MSphere</i> , 2020, 5, .	2.9	9

#	ARTICLE	IF	CITATIONS
37	Hydrocarbon Degraders as Pathogens. , 2020, , 267-281.		0
38	Defining and combating antibiotic resistance from One Health and Global Health perspectives. Nature Microbiology, 2019, 4, 1432-1442.	13.3	614
39	Mechanisms and phenotypic consequences of acquisition of tigecycline resistance by <i>Stenotrophomonas maltophilia</i> . Journal of Antimicrobial Chemotherapy, 2019, 74, 3221-3230.	3.0	14
40	Novel Inducers of the Expression of Multidrug Efflux Pumps That Trigger <i>Pseudomonas aeruginosa</i> Transient Antibiotic Resistance. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	20
41	Antibiotic Resistance Evolution Is Contingent on the Quorum-Sensing Response in <i>Pseudomonas aeruginosa</i> . Molecular Biology and Evolution, 2019, 36, 2238-2251.	8.9	40
42	Hydrocarbon Degraders as Pathogens. , 2019, , 1-15.		0
43	Involvement of the RND efflux pump transporter SmeH in the acquisition of resistance to ceftazidime in <i>Stenotrophomonas maltophilia</i> . Scientific Reports, 2019, 9, 4917.	3.3	31
44	Antibiotic resistance in European wastewater treatment plants mirrors the pattern of clinical antibiotic resistance prevalence. Science Advances, 2019, 5, eaau9124.	10.3	346
45	Analysis of the <i>Pseudomonas aeruginosa</i> Aminoglycoside Differential Resistomes Allows Defining Genes Simultaneously Involved in Intrinsic Antibiotic Resistance and Virulence. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	17
46	Man-made microbial resistances in built environments. Nature Communications, 2019, 10, 968.	12.8	128
47	Ecology and Evolution of Chromosomal Gene Transfer between Environmental Microorganisms and Pathogens. , 2019, , 139-160.		1
48	Antimicrobial resistance: A multifaceted problem with multipronged solutions. MicrobiologyOpen, 2019, 8, e945.	3.0	32
49	Gene Transmission in the One Health Microbiosphere and the Channels of Antimicrobial Resistance. Frontiers in Microbiology, 2019, 10, 2892.	3.5	66
50	The intrinsic resistome of <i>Klebsiella pneumoniae</i> . International Journal of Antimicrobial Agents, 2019, 53, 29-33.	2.5	20
51	Prediction of the intestinal resistome by a three-dimensional structure-based method. Nature Microbiology, 2019, 4, 112-123.	13.3	129
52	The global regulator Crc orchestrates the metabolic robustness underlying oxidative stress resistance in <i>Pseudomonas aeruginosa</i> . Environmental Microbiology, 2019, 21, 898-912.	3.8	27
53	Overexpression of the Efflux Pumps SmeVWX and SmeDEF Is a Major Cause of Resistance to Co-trimoxazole in <i>Stenotrophomonas maltophilia</i> . Antimicrobial Agents and Chemotherapy, 2018, 62, .	3.2	24
54	Ecology and Evolution of Chromosomal Gene Transfer between Environmental Microorganisms and Pathogens. Microbiology Spectrum, 2018, 6, .	3.0	48

#	ARTICLE	IF	CITATIONS
55	Methods for Measuring the Production of Quorum Sensing Signal Molecules. <i>Methods in Molecular Biology</i> , 2018, 1736, 1-15.	0.9	2
56	The development of a new parameter for tracking post-transcriptional regulation allows the detailed map of the <i>Pseudomonas aeruginosa</i> Crc regulon. <i>Scientific Reports</i> , 2018, 8, 16793.	3.3	30
57	Role of the Multidrug Resistance Efflux Pump MexCD-OprJ in the <i>Pseudomonas aeruginosa</i> Quorum Sensing Response. <i>Frontiers in Microbiology</i> , 2018, 9, 2752.	3.5	53
58	Mutational Evolution of <i>Pseudomonas aeruginosa</i> Resistance to Ribosome-Targeting Antibiotics. <i>Frontiers in Genetics</i> , 2018, 9, 451.	2.3	52
59	The development of efflux pump inhibitors to treat Gram-negative infections. <i>Expert Opinion on Drug Discovery</i> , 2018, 13, 919-931.	5.0	30
60	In-depth resistome analysis by targeted metagenomics. <i>Microbiome</i> , 2018, 6, 11.	11.1	115
61	Mutation-Driven Evolution of <i>Pseudomonas aeruginosa</i> in the Presence of either Ceftazidime or Ceftazidime-Avibactam. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	3.2	83
62	Biolog Phenotype Microarray Is a Tool for the Identification of Multidrug Resistance Efflux Pump Inducers. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	3.2	24
63	Bacterial lineages putatively associated with the dissemination of antibiotic resistance genes in a full-scale urban wastewater treatment plant. <i>Environment International</i> , 2018, 118, 179-188.	10.0	93
64	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
65	The Evolution of Antibiotic Resistance. , 2017, , 257-284.		3
66	Draft Genome Sequences of Four <i>Pseudomonas aeruginosa</i> Isolates Obtained from Patients with Chronic Obstructive Pulmonary Disease. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
67	Interventions on Metabolism: Making Antibiotic-Susceptible Bacteria. <i>MBio</i> , 2017, 8, .	4.1	19
68	Genomic and metagenomic technologies to explore the antibiotic resistance mobilome. <i>Annals of the New York Academy of Sciences</i> , 2017, 1388, 26-41.	3.8	43
69	Genome-wide analysis shows that RNase G plays a global role in the stability of mRNAs in <i>Stenotrophomonas maltophilia</i> . <i>Scientific Reports</i> , 2017, 7, 16016.	3.3	6
70	Fitness costs associated with the acquisition of antibiotic resistance. <i>Essays in Biochemistry</i> , 2017, 61, 37-48.	4.7	62
71	Editorial: A Multidisciplinary Look at <i>Stenotrophomonas maltophilia</i> : An Emerging Multi-Drug-Resistant Global Opportunistic Pathogen. <i>Frontiers in Microbiology</i> , 2017, 8, 1511.	3.5	58
72	Double-Face Meets the Bacterial World: The Opportunistic Pathogen <i>Stenotrophomonas maltophilia</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 2190.	3.5	66

#	ARTICLE	IF	CITATIONS
73	Effect of antibiotics on bacterial populations: a multi-hierarchical selection process. <i>F1000Research</i> , 2017, 6, 51.	1.6	75
74	Metabolic Compensation of Fitness Costs Is a General Outcome for Antibiotic-Resistant <i>Pseudomonas aeruginosa</i> Mutants Overexpressing Efflux Pumps. <i>MBio</i> , 2017, 8, .	4.1	61
75	Draft Genome Sequences of Two <i>Ralstonia pickettii</i> Strains with Different Aminoglycoside Resistance Phenotypes. <i>Genome Announcements</i> , 2016, 4, .	0.8	4
76	Antiviral effects of green tea (&lt;i>Camellia sinensis&lt;/i>) against pathogenic viruses in human and animals (a mini-review). <i>Tropical Journal of Obstetrics and Gynaecology</i> , 2016, 13, 176.	0.3	24
77	Bacterial Multidrug Efflux Pumps: Much More Than Antibiotic Resistance Determinants. <i>Microorganisms</i> , 2016, 4, 14.	3.6	486
78	Dissemination of Novel Antimicrobial Resistance Mechanisms through the Insertion Sequence Mediated Spread of Metabolic Genes. <i>Frontiers in Microbiology</i> , 2016, 7, 1008.	3.5	40
79	Multidrug Efflux Pumps at the Crossroad between Antibiotic Resistance and Bacterial Virulence. <i>Frontiers in Microbiology</i> , 2016, 7, 1483.	3.5	180
80	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
81	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
82	The fungal resistome: a risk and an opportunity for the development of novel antifungal therapies. <i>Future Medicinal Chemistry</i> , 2016, 8, 1503-1520.	2.3	9
83	Multiple adaptive routes of <i>Salmonella enterica</i> Typhimurium to biocide and antibiotic exposure. <i>BMC Genomics</i> , 2016, 17, 491.	2.8	39
84	Multilevel selection of bcrABDR-mediated bacitracin resistance in <i>Enterococcus faecalis</i> from chicken farms. <i>Scientific Reports</i> , 2016, 6, 34895.	3.3	20
85	The analysis of the antibiotic resistome offers new opportunities for therapeutic intervention. <i>Future Medicinal Chemistry</i> , 2016, 8, 1133-1151.	2.3	17
86	The Plasmidome of Firmicutes: Impact on the Emergence and the Spread of Resistance to Antimicrobials. <i>Microbiology Spectrum</i> , 2015, 3, PLAS-0039-2014.	3.0	83
87	Draft Genome Sequence of Antarctic <i>Pseudomonas</i> sp. Strain KG01 with Full Potential for Biotechnological Applications. <i>Genome Announcements</i> , 2015, 3, .	0.8	6
88	Significant Differences Characterise the Correlation Coefficients between Biocide and Antibiotic Susceptibility Profiles in <i>Staphylococcus aureus</i> . <i>Current Pharmaceutical Design</i> , 2015, 21, 2054-2057.	1.9	35
89	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
90	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

#	ARTICLE	IF	CITATIONS
91	Antibiotic-Resistant <i>Klebsiella pneumoniae</i> and <i>Escherichia coli</i> High-Risk Clones and an IncFII $\lambda$ Mosaic Plasmid Hosting Tn 1 ( $\lambda$ bla <sub>TEM-4</sub> ) in Isolates from 1990 to 2004. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 2904-2908.	3.2	9
92	Friends or foes: can we make a distinction between beneficial and harmful strains of the <i>Stenotrophomonas maltophilia</i> complex?. <i>Frontiers in Microbiology</i> , 2015, 6, 241.	3.5	95
93	Quantitative proteomics unravels that the post-transcriptional regulator Crc modulates the generation of vesicles and secreted virulence determinants of <i>Pseudomonas aeruginosa</i> . <i>Journal of Proteomics</i> , 2015, 127, 352-364.	2.4	26
94	Regulation of Sm <i>qnr</i> expression by Sm <i>qnrR</i> is strain-specific in <i>Stenotrophomonas maltophilia</i> : Table 1.. <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 2913-2914.	3.0	7
95	Prioritizing risks of antibiotic resistance genes in all metagenomes. <i>Nature Reviews Microbiology</i> , 2015, 13, 396-396.	28.6	45
96	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
97	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
98	Polymorphic Variation in Susceptibility and Metabolism of Triclosan-Resistant Mutants of <i>Escherichia coli</i> and <i>Klebsiella pneumoniae</i> Clinical Strains Obtained after Exposure to Biocides and Antibiotics. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 3413-3423.	3.2	41
99	Tackling antibiotic resistance: the environmental framework. <i>Nature Reviews Microbiology</i> , 2015, 13, 310-317.	28.6	1,612
100	Quantitative proteomics unravels that the post-transcriptional regulator Crc modulates the generation of vesicles and secreted virulence determinants of <i>Pseudomonas aeruginosa</i> . <i>Data in Brief</i> , 2015, 4, 450-453.	1.0	17
101	What is a resistance gene? Ranking risk in resistomes. <i>Nature Reviews Microbiology</i> , 2015, 13, 116-123.	28.6	698
102	Emergence and spread of antibiotic resistance: setting a parameter space. <i>Upsala Journal of Medical Sciences</i> , 2014, 119, 68-77.	0.9	120
103	Short-sighted evolution of bacterial opportunistic pathogens with an environmental origin. <i>Frontiers in Microbiology</i> , 2014, 5, 239.	3.5	21
104	Interkingdom signaling and its consequences for human health. <i>Virulence</i> , 2014, 5, 243-244.	4.4	9
105	General principles of antibiotic resistance in bacteria. <i>Drug Discovery Today: Technologies</i> , 2014, 11, 33-39.	4.0	157
106	Interplay between intrinsic and acquired resistance to quinolones in <i>Stenotrophomonas maltophilia</i> . <i>Environmental Microbiology</i> , 2014, 16, 1282-1296.	3.8	60
107	Characterization of a novel Zn <sup>2+</sup> -dependent intrinsic imipenemase from <i>Pseudomonas aeruginosa</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 2972-2978.	3.0	26
108	Metabolic Compensation of Fitness Costs Associated with Overexpression of the Multidrug Efflux Pump MexEF-OprN in <i>Pseudomonas aeruginosa</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 3904-3913.	3.2	42

#	ARTICLE	IF	CITATIONS
109	A Function of SmeDEF, the Major Quinolone Resistance Determinant of <i>Stenotrophomonas maltophilia</i> , Is the Colonization of Plant Roots. <i>Applied and Environmental Microbiology</i> , 2014, 80, 4559-4565.	3.1	75
110	Evaluation of Epidemiological Cut-Off Values Indicates that Biocide Resistant Subpopulations Are Uncommon in Natural Isolates of Clinically-Relevant Microorganisms. <i>PLoS ONE</i> , 2014, 9, e86669.	2.5	135
111	Characterization of the Polymyxin B Resistome of <i>Pseudomonas aeruginosa</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 110-119.	3.2	136
112	Bacterial pathogens: from natural ecosystems to human hosts. <i>Environmental Microbiology</i> , 2013, 15, 325-333.	3.8	68
113	Phenotypic Resistance to Antibiotics. <i>Antibiotics</i> , 2013, 2, 237-255.	3.7	134
114	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
115	Normal Mutation Rate Variants Arise in a Mutator (Mut S) <i>Escherichia coli</i> Population. <i>PLoS ONE</i> , 2013, 8, e72963.	2.5	37
116	RND multidrug efflux pumps: what are they good for?. <i>Frontiers in Microbiology</i> , 2013, 4, 7.	3.5	175
117	The intrinsic resistome of bacterial pathogens. <i>Frontiers in Microbiology</i> , 2013, 4, 103.	3.5	137
118	The Use of Machine Learning Methodologies to Analyse Antibiotic and Biocide Susceptibility in <i>Staphylococcus aureus</i> . <i>PLoS ONE</i> , 2013, 8, e55582.	2.5	40
119	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
120	Lack of Evidence for Reduced Fitness of Clinical <i>Staphylococcus aureus</i> Isolates with Reduced Susceptibility to Triclosan. <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 6068-6069.	3.2	8
121	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
122	Natural Antibiotic Resistance and Contamination by Antibiotic Resistance Determinants: The Two Ages in the Evolution of Resistance to Antimicrobials. <i>Frontiers in Microbiology</i> , 2012, 3, 1.	3.5	936
123	Metagenomics and antibiotics. <i>Clinical Microbiology and Infection</i> , 2012, 18, 27-31.	6.0	45
124	The antibiotic resistome: challenge and opportunity for therapeutic intervention. <i>Future Medicinal Chemistry</i> , 2012, 4, 347-359.	2.3	24
125	A novel resistance mechanism to triclosan that suggests horizontal gene transfer and demonstrates a potential selective pressure for reduced biocide susceptibility in clinical strains of <i>Staphylococcus aureus</i> . <i>International Journal of Antimicrobial Agents</i> , 2012, 40, 210-220.	2.5	92
126	Differential Epigenetic Compatibility of qnr Antibiotic Resistance Determinants with the Chromosome of <i>Escherichia coli</i> . <i>PLoS ONE</i> , 2012, 7, e35149.	2.5	24

#	ARTICLE	IF	CITATIONS
127	Overproduction of the multidrug efflux pump MexEFâ€œOprN does not impair <i>Pseudomonas aeruginosa</i> fitness in competition tests, but produces specific changes in bacterial regulatory networks. <i>Environmental Microbiology</i> , 2012, 14, 1968-1981.	3.8	100
128	The Evolution of Antibiotic Resistance. , 2011, , 305-337.		6
129	Efflux Pumps as an Important Mechanism for Quinolone Resistance. <i>Advances in Enzymology and Related Areas of Molecular Biology</i> , 2011, 77, 167-235.	1.3	16
130	Are nonlethal targets useful for developing novel antimicrobials?. <i>Future Microbiology</i> , 2011, 6, 605-607.	2.0	14
131	Beyond serial passages: new methods for predicting the emergence of resistance to novel antibiotics. <i>Current Opinion in Pharmacology</i> , 2011, 11, 439-445.	3.5	80
132	Ecological and Temporal Constraints in the Evolution of Bacterial Genomes. <i>Genes</i> , 2011, 2, 804-828.	2.4	17
133	Quinolone Resistance: Much More than Predicted. <i>Frontiers in Microbiology</i> , 2011, 2, 22.	3.5	113
134	Metabolic regulation of antibiotic resistance. <i>FEMS Microbiology Reviews</i> , 2011, 35, 768-789.	8.6	220
135	The intrinsic resistome of <i>Pseudomonas aeruginosa</i> to $\beta$ -lactams. <i>Virulence</i> , 2011, 2, 144-146.	4.4	93
136	The Binding of Triclosan to SmeT, the Repressor of the Multidrug Efflux Pump SmeDEF, Induces Antibiotic Resistance in <i>Stenotrophomonas maltophilia</i> . <i>PLoS Pathogens</i> , 2011, 7, e1002103.	4.7	94
137	Bottlenecks in the Transferability of Antibiotic Resistance from Natural Ecosystems to Human Bacterial Pathogens. <i>Frontiers in Microbiology</i> , 2011, 2, 265.	3.5	74
138	The global regulator Crc modulates metabolism, susceptibility to antibiotics and virulence in <i>Pseudomonas aeruginosa</i> . <i>Environmental Microbiology</i> , 2010, 12, 3196-3212.	3.8	133
139	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
140	Genetic Determinants Involved in the Susceptibility of <i>Pseudomonas aeruginosa</i> to $\beta$ -Lactam Antibiotics. <i>Antimicrobial Agents and Chemotherapy</i> , 2010, 54, 4159-4167.	3.2	149
141	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
142	Structural and Functional Analysis of SmeT, the Repressor of the <i>Stenotrophomonas maltophilia</i> Multidrug Efflux Pump SmeDEF. <i>Journal of Biological Chemistry</i> , 2009, 284, 14428-14438.	3.4	43
143	A global view of antibiotic resistance. <i>FEMS Microbiology Reviews</i> , 2009, 33, 44-65.	8.6	271
144	Functional role of bacterial multidrug efflux pumps in microbial natural ecosystems. <i>FEMS Microbiology Reviews</i> , 2009, 33, 430-449.	8.6	384

#	ARTICLE	IF	CITATIONS
145	Towards an ecological approach to antibiotics and antibiotic resistance genes. <i>Clinical Microbiology and Infection</i> , 2009, 15, 14-16.	6.0	46
146	Environmental pollution by antibiotics and by antibiotic resistance determinants. <i>Environmental Pollution</i> , 2009, 157, 2893-2902.	7.5	1,409
147	<i>Stenotrophomonas maltophilia</i> drug resistance. <i>Future Microbiology</i> , 2009, 4, 655-660.	2.0	98
148	Ecology and evolution of antibiotic resistance. <i>Environmental Microbiology Reports</i> , 2009, 1, 469-476.	2.4	123
149	The role of natural environments in the evolution of resistance traits in pathogenic bacteria. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2009, 276, 2521-2530.	2.6	387
150	Antibiotics and antibiotic resistance in water environments. <i>Current Opinion in Biotechnology</i> , 2008, 19, 260-265.	6.6	1,608
151	Dictyostelium transcriptional responses to <i>Pseudomonas aeruginosa</i> : common and specific effects from PAO1 and PA14 strains. <i>BMC Microbiology</i> , 2008, 8, 109.	3.3	46
152	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
153	The Neglected Intrinsic Resistome of Bacterial Pathogens. <i>PLoS ONE</i> , 2008, 3, e1619.	2.5	257
154	Antibiotics as signals that trigger specific bacterial responses. <i>Current Opinion in Microbiology</i> , 2008, 11, 161-167.	5.1	295
155	Antibiotics and Antibiotic Resistance Genes in Natural Environments. <i>Science</i> , 2008, 321, 365-367.	12.6	1,409
156	Chronic <i>Pseudomonas aeruginosa</i> Infection in Chronic Obstructive Pulmonary Disease. <i>Clinical Infectious Diseases</i> , 2008, 47, 1526-1533.	5.8	235
157	Clinical Impact of the Over-Expression of Efflux Pump in Nonfermentative Gram-Negative Bacilli, Development of Efflux Pump Inhibitors. <i>Current Drug Targets</i> , 2008, 9, 797-807.	2.1	60
158	Experimental validation of Haldane's hypothesis on the role of infection as an evolutionary force for Metazoans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 13728-13731.	7.1	33
159	Contribution of a New Mutation in <i>parE</i> to Quinolone Resistance in Extended-Spectrum- $\beta$ -Lactamase-Producing <i>Escherichia coli</i> Isolates. <i>Journal of Clinical Microbiology</i> , 2007, 45, 2740-2742.	3.9	57
160	P880 Single-step selection of double mutations leading to high antibiotic-resistance in hyper-mutable <i>Pseudomonas aeruginosa</i> . <i>International Journal of Antimicrobial Agents</i> , 2007, 29, S227-S228.	2.5	0
161	Predicting antibiotic resistance. <i>Nature Reviews Microbiology</i> , 2007, 5, 958-965.	28.6	305
162	Mutation rate is reduced by increased dosage of <i>mutL</i> gene in <i>Escherichia coli</i> K-12. <i>FEMS Microbiology Letters</i> , 2007, 275, 263-269.	1.8	18

#	ARTICLE	IF	CITATIONS
163	Antibiotics as intermicrobial signaling agents instead of weapons. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 19484-19489.	7.1	594
164	Growth of <i>Escherichia coli</i> in acetate as a sole carbon source is inhibited by ankyrin-like repeats present in the 2â€²,5â€²-linked oligoadenylate-dependent human RNase L enzyme. FEMS Microbiology Letters, 2006, 149, 107-113.	1.8	6
165	Crosstalk between antibiotic resistance and virulence in <i>Pseudomonas aeruginosa</i> . Reviews in Medical Microbiology, 2005, 16, 155-161.	0.9	2
166	A molecular biological protocol to distinguish potentially human pathogenic <i>Stenotrophomonas maltophilia</i> from plant-associated <i>Stenotrophomonas rhizophila</i> . Environmental Microbiology, 2005, 7, 1853-1858.	3.8	36
167	The Biocide Triclosan Selects <i>Stenotrophomonas maltophilia</i> Mutants That Overproduce the SmeDEF Multidrug Efflux Pump. Antimicrobial Agents and Chemotherapy, 2005, 49, 781-782.	3.2	108
168	Increased Mutation Frequencies in <i>Escherichia coli</i> Isolates Harboring Extended-Spectrum Î²-Lactamases. Antimicrobial Agents and Chemotherapy, 2005, 49, 4754-4756.	3.2	37
169	Overexpression of the Multidrug Efflux Pumps MexCD-OprJ and MexEF-OprN Is Associated with a Reduction of Type III Secretion in <i>Pseudomonas aeruginosa</i> . Journal of Bacteriology, 2005, 187, 1384-1391.	2.2	151
170	Role of Non-clinical Environments in the Selection of Virulence and Antibiotic Resistance Determinants in Pathogenic Bacteria. Journal of Biological Sciences, 2005, 6, 1-8.	0.3	10
171	Multi-resistant Enterobacteriaceae in Hospital Practice. , 2004, , 205-243.		0
172	Overexpression of the multidrug efflux pump SmeDEF impairs <i>Stenotrophomonas maltophilia</i> physiology. Journal of Antimicrobial Chemotherapy, 2004, 53, 432-434.	3.0	93
173	Regulatory Regions of smeDEF in <i>Stenotrophomonas maltophilia</i> Strains Expressing Different Amounts of the Multidrug Efflux Pump SmeDEF. Antimicrobial Agents and Chemotherapy, 2004, 48, 2274-2276.	3.2	37
174	Structure of <i>Pseudomonas aeruginosa</i> Populations Analyzed by Single Nucleotide Polymorphism and Pulsed-Field Gel Electrophoresis Genotyping. Journal of Bacteriology, 2004, 186, 4228-4237.	2.2	84
175	Polymorphic Mutation Frequencies in <i>Escherichia coli</i> : Emergence of Weak Mutators in Clinical Isolates. Journal of Bacteriology, 2004, 186, 5538-5542.	2.2	74
176	The <i>Pseudomonas putida</i> Crc Global Regulator Controls the Expression of Genes from Several Chromosomal Catabolic Pathways for Aromatic Compounds. Journal of Bacteriology, 2004, 186, 1337-1344.	2.2	114
177	Fosfomicin and Rifampin Disk Diffusion Tests for Detection of <i>Escherichia coli</i> Mutator Strains. Journal of Clinical Microbiology, 2004, 42, 4310-4312.	3.9	22
178	Differential interactions within the <i>Caenorhabditis elegans</i> <i>Pseudomonas aeruginosa</i> pathogenesis model. Journal of Theoretical Biology, 2003, 225, 469-476.	1.7	24
179	The efflux pump inhibitor Phe-Arg-beta-naphthylamide does not abolish the activity of the <i>Stenotrophomonas maltophilia</i> SmeDEF multidrug efflux pump. Journal of Antimicrobial Chemotherapy, 2003, 51, 1042-1045.	3.0	22
180	Cloning and Characterization of SmeT, a Repressor of the <i>Stenotrophomonas maltophilia</i> Multidrug Efflux Pump SmeDEF. Antimicrobial Agents and Chemotherapy, 2002, 46, 3386-3393.	3.2	89

#	ARTICLE	IF	CITATIONS
181	Interactions among Strategies Associated with Bacterial Infection: Pathogenicity, Epidemicity, and Antibiotic Resistance. <i>Clinical Microbiology Reviews</i> , 2002, 15, 647-679.	13.6	416
182	Fitness of in vitro selected <i>Pseudomonas aeruginosa</i> Δ <i>B</i> and <i>nfxB</i> multidrug resistant mutants. <i>Journal of Antimicrobial Chemotherapy</i> , 2002, 50, 657-664.	3.0	164
183	Transcriptional regulation of <i>mexR</i> , the repressor of <i>Pseudomonas aeruginosa</i> <i>mexAB-oprM</i> multidrug efflux pump. <i>FEMS Microbiology Letters</i> , 2002, 207, 63-68.	1.8	33
184	Environmental selection of antibiotic resistance genes. Minireview. <i>Environmental Microbiology</i> , 2001, 3, 1-9.	3.8	331
185	Expression of Multidrug Efflux Pump <i>SmeDEF</i> by Clinical Isolates of <i>Stenotrophomonas maltophilia</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2001, 45, 1879-1881.	3.2	105
186	<i>Stenotrophomonas maltophilia</i> D457R Contains a Cluster of Genes from Gram-Positive Bacteria Involved in Antibiotic and Heavy Metal Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2000, 44, 1778-1782.	3.2	126
187	Cloning and Characterization of <i>SmeDEF</i> , a Novel Multidrug Efflux Pump from <i>Stenotrophomonas maltophilia</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2000, 44, 3079-3086.	3.2	179
188	Mutation Frequencies and Antibiotic Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2000, 44, 1771-1777.	3.2	530
189	Biological Cost of <i>AmpC</i> Production for <i>Salmonella enterica</i> Serotype Typhimurium. <i>Antimicrobial Agents and Chemotherapy</i> , 2000, 44, 3137-3143.	3.2	90
190	Macrolide Resistance Genes in <i>Enterococcus</i> spp. <i>Antimicrobial Agents and Chemotherapy</i> , 2000, 44, 967-971.	3.2	195
191	Emergence of multidrug-resistant mutants is increased under antibiotic selective pressure in <i>Pseudomonas aeruginosa</i> . <i>Microbiology (United Kingdom)</i> , 1999, 145, 2857-2862.	1.8	96
192	Environmental and clinical isolates of <i>Pseudomonas aeruginosa</i> show pathogenic and biodegradative properties irrespective of their origin. <i>Environmental Microbiology</i> , 1999, 1, 421-430.	3.8	194
193	Detection of fungal spores from contaminated surfaces by the polymerase chain reaction. <i>World Journal of Microbiology and Biotechnology</i> , 1999, 15, 33-36.	3.6	4
194	Aminoglycoside resistance mediated by the bifunctional enzyme 6'-N-aminoglycoside acetyltransferase-2"-O-aminoglycoside phosphotransferase. <i>Frontiers in Bioscience - Landmark</i> , 1999, 4, d1.	3.0	41
195	Quinolone resistance by mutations in chromosomal gyrase genes. Just the tip of the iceberg?. <i>Journal of Antimicrobial Chemotherapy</i> , 1998, 42, 683-688.	3.0	68
196	Metal Accumulation and Vanadium-Induced Multidrug Resistance by Environmental Isolates of <i>Escherichia hermannii</i> and <i>Enterobacter cloacae</i> . <i>Applied and Environmental Microbiology</i> , 1998, 64, 4317-4320.	3.1	97
197	Growth of <i>Escherichia coli</i> in acetate as a sole carbon source is inhibited by ankyrin-like repeats present in the 2'5'-linked oligoadenylate-dependent human RNase L enzyme. <i>FEMS Microbiology Letters</i> , 1997, 149, 107-113.	1.8	10
198	H-NS and RpoS regulate emergence of Lac Ara+ mutants of <i>Escherichia coli</i> MCS2. <i>Journal of Bacteriology</i> , 1997, 179, 4620-4622.	2.2	44

#	ARTICLE	IF	CITATIONS
199	Multiple mechanisms of N-phosphonacetyl-L-aspartate resistance in human cell lines: Carbamyl-P synthetase/aspartate transcarbamylase/dihydro-orotase gene amplification is frequent only when chromosome 2 is rearranged. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 1816-1821.	7.1	22
200	Multiple antibiotic resistance in <i>Stenotrophomonas maltophilia</i> . Antimicrobial Agents and Chemotherapy, 1997, 41, 1140-1142.	3.2	152
201	Oleoylanilide, a possible causative agent of toxic oil syndrome, interferes with the cytoskeleton in a neuronal cell line. Neurotoxicology and Teratology, 1997, 19, 147-150.	2.4	2
202	IMMUNOBLOTTING TECHNIQUES. , 1996, , 537-554.		5
203	hns mutant unveils the presence of a latent haemolytic activity in <i>Escherichia coli</i> K-12. Molecular Microbiology, 1996, 19, 909-910.	2.5	18
204	Spread and evolution of natural plasmids harboring transposon Tn5. FEMS Microbiology Ecology, 1996, 19, 63-71.	2.7	12
205	pH modulation of aminoglycoside resistance in <i>Staphylococcus epidermidis</i> harbouring 6â€™-N-aminoglycoside acetyltransferase. Journal of Antimicrobial Chemotherapy, 1996, 37, 881-889.	3.0	7
206	Spread and evolution of natural plasmids harboring transposon Tn5. FEMS Microbiology Ecology, 1996, 19, 63-71.	2.7	1
207	Non-canonical mechanisms of antibiotic resistance. European Journal of Clinical Microbiology and Infectious Diseases, 1994, 13, 1015-1022.	2.9	17
208	The Organization of Intercistronic Regions of the Aerobactin Operon of pColV-K30 may Account for the Differential Expression of the iucABCD iutA Genes. Journal of Molecular Biology, 1994, 238, 288-293.	4.2	77
209	Bleomycin increases amikacin and streptomycin resistance in <i>Escherichia coli</i> harboring transposon Tn5. Antimicrobial Agents and Chemotherapy, 1993, 37, 1982-1985.	3.2	7
210	Factors determining resistance to Î²-lactam combined with Î²-lactamase inhibitors in <i>Escherichia coli</i> . Journal of Antimicrobial Chemotherapy, 1991, 27, 569-575.	3.0	102
211	Do bacteria have sex?. Nature, 1991, 352, 288-288.	27.8	2
212	Heavy Metals, Chlorine and Antibiotic Resistance in <i>Escherichia coli</i> Isolates from Ambulatory Patients. Journal of Chemotherapy, 1990, 2, 238-240.	1.5	1
213	Mechanisms of iron acquisition and bacterial virulence. FEMS Microbiology Letters, 1990, 75, 45-56.	1.8	81
214	Beta-lactam-fofomycin antagonism involving modification of penicillin-binding protein 3 in <i>Pseudomonas aeruginosa</i> . Antimicrobial Agents and Chemotherapy, 1990, 34, 2093-2096.	3.2	18
215	Epidemiology of antibiotic-inactivating enzymes and DNA probes: the problem of quantity. Journal of Antimicrobial Chemotherapy, 1990, 26, 301-303.	3.0	7
216	Cloning of the determinants for microcin D93 production and analysis of three different D-type microcin plasmids. Plasmid, 1990, 23, 216-225.	1.4	14

#	ARTICLE	IF	CITATIONS
217	Mechanisms of iron acquisition and bacterial virulence. FEMS Microbiology Letters, 1990, 75, 45-56.	1.8	100
218	Antibiotic inactivating enzymes from a clinical isolate of <i>Agrobacterium radiobacter</i> . Journal of Antimicrobial Chemotherapy, 1989, 23, 283-284.	3.0	23
219	Small plasmids are involved in amoxicillin-clavulanate resistance in <i>Escherichia coli</i> . Antimicrobial Agents and Chemotherapy, 1989, 33, 595.	3.2	46
220	Bleomycin-kanamycin resistance as a marker of the presence of transposon Tn5 in clinical strains of <i>Escherichia coli</i> . European Journal of Clinical Microbiology and Infectious Diseases, 1989, 8, 995-998.	2.9	6
221	Sewage dilution and loss of antibiotic resistance and virulence determinants in <i>E. coli</i> . FEMS Microbiology Letters, 1989, 59, 93-96.	1.8	17
222	Aerobactin production and plasmid distribution in <i>Escherichia coli</i> clinical isolates. FEMS Microbiology Letters, 1989, 60, 41-44.	1.8	3
223	Aerobactin production and plasmid distribution in <i>Escherichia coli</i> clinical isolates. FEMS Microbiology Letters, 1989, 60, 41-44.	1.8	4
224	<i>Shigella sonnei</i> bacteremia in an elderly diabetic patient. European Journal of Clinical Microbiology and Infectious Diseases, 1988, 7, 404-405.	2.9	7
225	Aerobactin production as a virulence factor: A reevaluation. European Journal of Clinical Microbiology and Infectious Diseases, 1988, 7, 621-629.	2.9	78
226	Synergistic effect of dosage and bacterial inoculum in TEM-1 mediated antibiotic resistance. European Journal of Clinical Microbiology and Infectious Diseases, 1988, 7, 778-779.	2.9	17
227	Aerobactin production linked to transferable antibiotic resistance in <i>Escherichia coli</i> strains isolated from sewage. FEMS Microbiology Letters, 1988, 50, 57-59.	1.8	13
228	Aerobactin-producing multi-resistance plasmids. Journal of Antimicrobial Chemotherapy, 1987, 19, 552-553.	3.0	14
229	Acquisition of antibiotic resistance plasmids in vivo by extraintestinal <i>Salmonella</i> spp.. Journal of Antimicrobial Chemotherapy, 1987, 20, 452-453.	3.0	17
230	RESISTANCE TO BETA-LACTAM/CLAVULANATE. Lancet, The, 1987, 330, 1473.	13.7	75
231	Incidence of aerobactin production in Gram-negative hospital isolates. FEMS Microbiology Letters, 1987, 43, 351-353.	1.8	29
232	Epidemiology of aerobactin production in Enterobacteriaceae. Annales De L'Institut Pasteur Microbiologie, 1986, 137, 297-303.	0.6	19
233	Isolation, characterization, and mode of action on <i>Escherichia coli</i> strains of microcin D93. Antimicrobial Agents and Chemotherapy, 1986, 29, 456-460.	3.2	15
234	Multifactorial determination of systemic invasivity in <i>Escherichia coli</i> . FEMS Microbiology Letters, 1986, 37, 259-261.	1.8	9

#	ARTICLE	IF	CITATIONS
235	Microcin-mediated Interactions Between <i>Klebsiella pneumoniae</i> and <i>Escherichia coli</i> Strains. <i>Microbiology (United Kingdom)</i> , 1984, 130, 391-400.	1.8	29
236	Microcin 15n: a second antibiotic from <i>Escherichia coli</i> LP15. <i>Journal of Antibiotics</i> , 1983, 36, 325-327.	2.0	10
237	Evolution of Bacterial Opportunistic Pathogens. , 0, , 85-91.		0
238	The Plasmidome of <i>Firmicutes</i> : Impact on the Emergence and the Spread of Resistance to Antimicrobials. , 0, , 379-419.		3