

Jose Luis Martinez

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

233
papers

17,101
citations

65
h-index

127
g-index

265
ext. papers

20,584
ext. citations

6.9
avg, IF

7.42
L-index

#	Paper	IF	Citations
233	Mutational background influences 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	11.5	1
232	Evolution under low antibiotic concentrations: a risk for the selection of <i>Pseudomonas aeruginosa</i> multidrug-resistant mutants in nature. <i>Environmental Microbiology</i> , 2021 ,	5.2	3
231	Allogenuous Selection of Mutational Collateral Resistance: Old Drugs Select for New Resistance Within Antibiotic Families. <i>Frontiers in Microbiology</i> , 2021 , 12, 757833	5.7	0
230	<i>Pseudomonas aeruginosa</i> : an antibiotic resilient pathogen with environmental origin. <i>Current Opinion in Microbiology</i> , 2021 , 64, 125-132	7.9	4
229	The Origin of Niches and Species in the Bacterial World. <i>Frontiers in Microbiology</i> , 2021 , 12, 657986	5.7	12
228	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 ,	5.2	5
227	Convergent phenotypic evolution towards fosfomycin collateral sensitivity of <i>Pseudomonas aeruginosa</i> antibiotic-resistant mutants. <i>Microbial Biotechnology</i> , 2021 ,	6.3	7
226	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	3.9	1
225	Evolutionary Pathways and Trajectories in Antibiotic Resistance. <i>Clinical Microbiology Reviews</i> , 2021 , e0005019	34	17
224	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	2.6	1
223	Antibiotic resistance: Time of synthesis in a post-genomic age. <i>Computational and Structural Biotechnology Journal</i> , 2021 , 19, 3110-3124	6.8	6
222	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,	6.3	4
221	Explorative assessment of coronavirus-like short sequences from host-associated and environmental metagenomes. <i>Science of the Total Environment</i> , 2021 , 793, 148494	10.2	
220	Metagenomic analysis of an urban resistome before and after wastewater treatment. <i>Scientific Reports</i> , 2020 , 10, 8174	4.9	28
219	The Importance of Abdominal Wall Closure After Definitive Surgery for Enterocutaneous Fistula. <i>World Journal of Surgery</i> , 2020 , 44, 3333-3340	3.3	1
218	The Inactivation of Enzymes Belonging to the Central Carbon Metabolism Is a Novel Mechanism of Developing Antibiotic Resistance. <i>MSystems</i> , 2020 , 5,	7.6	6
217	Environmental remodeling of human gut microbiota and antibiotic resistome in livestock farms. <i>Nature Communications</i> , 2020 , 11, 1427	17.4	57

216	Antibiotic Resistance in the Environment: Expert Perspectives. <i>Handbook of Environmental Chemistry</i> , 2020 , 1-18	0.8	3
215	Naringenin Inhibition of the Quorum Sensing Response Is Based on Its Time-Dependent Competition With γ -(3-Oxo-dodecanoyl)-L-homoserine Lactone for LasR Binding. <i>Frontiers in Molecular Biosciences</i> , 2020 , 7, 25	5.6	13
214	Mechanisms of antimicrobial resistance in : a review of current knowledge. <i>Expert Review of Anti-Infective Therapy</i> , 2020 , 18, 335-347	5.5	24
213	Antibiotic residues in final effluents of European wastewater treatment plants and their impact on the aquatic environment. <i>Environment International</i> , 2020 , 140, 105733	12.9	124
212	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	14.3	5
211	Antimicrobial Peptide Exposure Selects for Resistant and Fit <i>Stenotrophomonas maltophilia</i> Mutants That Show Cross-Resistance to Antibiotics. <i>MSphere</i> , 2020 , 5,	5	2
210	Hydrocarbon Degradars as Pathogens 2020 , 267-281		
209	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	2.2	2
208	Rapid and robust evolution of collateral sensitivity in antibiotic-resistant mutants. <i>Science Advances</i> , 2020 , 6, eaba5493	14.3	16
207	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	5.2	10
206	Antibiotic Resistance: Moving From Individual Health Norms to Social Norms in One Health and Global Health. <i>Frontiers in Microbiology</i> , 2020 , 11, 1914	5.7	24
205	Mechanisms of Action and of Resistance to Quinolones 2019 , 39-55		7
204	Novel Inducers of the Expression of Multidrug Efflux Pumps That Trigger Transient Antibiotic Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2019 , 63,	5.9	9
203	Antibiotic Resistance Evolution Is Contingent on the Quorum-Sensing Response in <i>Pseudomonas aeruginosa</i> . <i>Molecular Biology and Evolution</i> , 2019 , 36, 2238-2251	8.3	23
202	Hydrocarbon Degradars as Pathogens 2019 , 1-15		
201	Involvement of the RND efflux pump transporter SmeH in the acquisition of resistance to ceftazidime in <i>Stenotrophomonas maltophilia</i> . <i>Scientific Reports</i> , 2019 , 9, 4917	4.9	20
200	Antibiotic resistance in European wastewater treatment plants mirrors the pattern of clinical antibiotic resistance prevalence. <i>Science Advances</i> , 2019 , 5, eaau9124	14.3	184
199	Analysis of the Aminoglycoside Differential Resistomes Allows Defining Genes Simultaneously Involved in Intrinsic Antibiotic Resistance and Virulence. <i>Antimicrobial Agents and Chemotherapy</i> , 2019 , 63,	5.9	9

198	Defining and combating antibiotic resistance from One Health and Global Health perspectives. <i>Nature Microbiology</i> , 2019 , 4, 1432-1442	26.6	264
197	Mechanisms and phenotypic consequences of acquisition of tigecycline resistance by <i>Stenotrophomonas maltophilia</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2019 , 74, 3221-3230	5.1	8
196	Man-made microbial resistances in built environments. <i>Nature Communications</i> , 2019 , 10, 968	17.4	78
195	Ecology and Evolution of Chromosomal Gene Transfer between Environmental Microorganisms and Pathogens 2019 , 139-160		0
194	Antimicrobial resistance: A multifaceted problem with multipronged solutions. <i>MicrobiologyOpen</i> , 2019 , 8, e945	3.4	15
193	Gene Transmission in the One Health Microbiosphere and the Channels of Antimicrobial Resistance. <i>Frontiers in Microbiology</i> , 2019 , 10, 2892	5.7	28
192	The intrinsic resistome of <i>Klebsiella pneumoniae</i> . <i>International Journal of Antimicrobial Agents</i> , 2019 , 53, 29-33	14.3	9
191	Prediction of the intestinal resistome by a three-dimensional structure-based method. <i>Nature Microbiology</i> , 2019 , 4, 112-123	26.6	72
190	The global regulator Crc orchestrates the metabolic robustness underlying oxidative stress resistance in <i>Pseudomonas aeruginosa</i> . <i>Environmental Microbiology</i> , 2019 , 21, 898-912	5.2	17
189	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,	5.9	17
188	Ecology and Evolution of Chromosomal Gene Transfer between Environmental Microorganisms and Pathogens. <i>Microbiology Spectrum</i> , 2018 , 6,	8.9	34
187	Methods for Measuring the Production of Quorum Sensing Signal Molecules. <i>Methods in Molecular Biology</i> , 2018 , 1736, 1-15	1.4	1
186	In-depth resistome analysis by targeted metagenomics. <i>Microbiome</i> , 2018 , 6, 11	16.6	73
185	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,	5.9	50
184	Biolog Phenotype Microarray Is a Tool for the Identification of Multidrug Resistance Efflux Pump Inducers. <i>Antimicrobial Agents and Chemotherapy</i> , 2018 , 62,	5.9	12
183	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	12.9	63
182	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	4.9	15
181	Role of the Multidrug Resistance Efflux Pump MexCD-OprJ in the Quorum Sensing Response. <i>Frontiers in Microbiology</i> , 2018 , 9, 2752	5.7	27

180	Mutational Evolution of Resistance to Ribosome-Targeting Antibiotics. <i>Frontiers in Genetics</i> , 2018 , 9, 451	4.5	34
179	The development of efflux pump inhibitors to treat Gram-negative infections. <i>Expert Opinion on Drug Discovery</i> , 2018 , 13, 919-931	6.2	16
178	Vitamin K Induces the Expression of the <i>Stenotrophomonas maltophilia</i> SmeVWX Multidrug Efflux Pump. <i>Antimicrobial Agents and Chemotherapy</i> , 2017 , 61,	5.9	13
177	The Evolution of Antibiotic Resistance 2017 , 257-284		2
176	Effect of antibiotics on bacterial populations: a multi-hierarchical selection process. <i>F1000Research</i> , 2017 , 6, 51	3.6	34
175	Draft Genome Sequences of Four Isolates Obtained from Patients with Chronic Obstructive Pulmonary Disease. <i>Genome Announcements</i> , 2017 , 5,		1
174	Interventions on Metabolism: Making Antibiotic-Susceptible Bacteria. <i>MBio</i> , 2017 , 8,	7.8	10
173	When Pathogens and Environmental Organisms Meet 2017 , 15-33		0
172	Genomic and metagenomic technologies to explore the antibiotic resistance mobilome. <i>Annals of the New York Academy of Sciences</i> , 2017 , 1388, 26-41	6.5	30
171	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	4.9	5
170	Fitness costs associated with the acquisition of antibiotic resistance. <i>Essays in Biochemistry</i> , 2017 , 61, 37-48	7.6	34
169	Double-Face Meets the Bacterial World: The Opportunistic Pathogen. <i>Frontiers in Microbiology</i> , 2017 , 8, 2190	5.7	42
168	Metabolic Compensation of Fitness Costs Is a General Outcome for Antibiotic-Resistant Mutants Overexpressing Efflux Pumps. <i>MBio</i> , 2017 , 8,	7.8	37
167	Multiple adaptive routes of <i>Salmonella enterica</i> Typhimurium to biocide and antibiotic exposure. <i>BMC Genomics</i> , 2016 , 17, 491	4.5	24
166	Antimicrobial Drug Efflux Pumps in <i>Stenotrophomonas maltophilia</i> 2016 , 401-416		
165	Multilevel selection of bcrABDR-mediated bacitracin resistance in <i>Enterococcus faecalis</i> from chicken farms. <i>Scientific Reports</i> , 2016 , 6, 34895	4.9	16
164	The analysis of the antibiotic resistome offers new opportunities for therapeutic intervention. <i>Future Medicinal Chemistry</i> , 2016 , 8, 1133-51	4.1	14
163	Draft Genome Sequences of Two <i>Ralstonia pickettii</i> Strains with Different Aminoglycoside Resistance Phenotypes. <i>Genome Announcements</i> , 2016 , 4,		4

162	Antiviral effects of green tea (<i>Camellia sinensis</i>) against pathogenic viruses in human and animals (a mini-review). <i>Tropical Journal of Obstetrics and Gynaecology</i> , 2016 , 13, 176	0.3	15
161	Bacterial Multidrug Efflux Pumps: Much More Than Antibiotic Resistance Determinants. <i>Microorganisms</i> , 2016 , 4,	4.9	294
160	Dissemination of Novel Antimicrobial Resistance Mechanisms through the Insertion Sequence Mediated Spread of Metabolic Genes. <i>Frontiers in Microbiology</i> , 2016 , 7, 1008	5.7	23
159	Multidrug Efflux Pumps at the Crossroad between Antibiotic Resistance and Bacterial Virulence. <i>Frontiers in Microbiology</i> , 2016 , 7, 1483	5.7	103
158	Multidrug efflux pumps as main players in intrinsic and acquired resistance to antimicrobials. <i>Drug Resistance Updates</i> , 2016 , 28, 13-27	23.2	87
157	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	4	2
156	The fungal resistome: a risk and an opportunity for the development of novel antifungal therapies. <i>Future Medicinal Chemistry</i> , 2016 , 8, 1503-20	4.1	6
155	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	5.7	62
154	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, 352-64	3.9	18
153	Regulation of Smqnr expression by SmqnrR is strain-specific in <i>Stenotrophomonas maltophilia</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2015 , 70, 2913-4	5.1	6
152	Prioritizing risks of antibiotic resistance genes in all metagenomes. <i>Nature Reviews Microbiology</i> , 2015 , 13, 396	22.2	37
151	The efflux pump SmeDEF contributes to trimethoprim-sulfamethoxazole resistance in <i>Stenotrophomonas maltophilia</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2015 , 59, 4347-8	5.9	32
150	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, 464-7	9.5	31
149	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, 3413-23	5.9	27
148	Tackling antibiotic resistance: the environmental framework. <i>Nature Reviews Microbiology</i> , 2015 , 13, 310-7	22.2	1092
147	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, 450-3	1.2	3
146	What is a resistance gene? Ranking risk in resistomes. <i>Nature Reviews Microbiology</i> , 2015 , 13, 116-23	22.2	483
145	The Plasmidome of Firmicutes: Impact on the Emergence and the Spread of Resistance to Antimicrobials. <i>Microbiology Spectrum</i> , 2015 , 3, PLAS-0039-2014	8.9	66

144	Draft Genome Sequence of Antarctic <i>Pseudomonas</i> sp. Strain KG01 with Full Potential for Biotechnological Applications. <i>Genome Announcements</i> , 2015 , 3,		4
143	Significant Differences Characterise the Correlation Coefficients between Biocide and Antibiotic Susceptibility Profiles in <i>Staphylococcus aureus</i> . <i>Current Pharmaceutical Design</i> , 2015 , 21, 2054-7	3.3	29
142	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	5.7	13
141	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	3.7	12
140	Antibiotic-resistant <i>Klebsiella pneumoniae</i> and <i>Escherichia coli</i> high-risk clones and an IncFII(k) mosaic plasmid hosting Tn1 (bla _{TEM} -4) in isolates from 1990 to 2004. <i>Antimicrobial Agents and Chemotherapy</i> , 2015 , 59, 2904-8	5.9	7
139	General principles of antibiotic resistance in bacteria. <i>Drug Discovery Today: Technologies</i> , 2014 , 11, 33-97.1	7.1	91
138	Interplay between intrinsic and acquired resistance to quinolones in <i>Stenotrophomonas maltophilia</i> . <i>Environmental Microbiology</i> , 2014 , 16, 1282-96	5.2	48
137	Characterization of a novel Zn ²⁺ -dependent intrinsic imipenemase from <i>Pseudomonas aeruginosa</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2014 , 69, 2972-8	5.1	14
136	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, 3904-13	5.9	33
135	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, 4559-65	4.8	56
134	Evolution of Bacterial Opportunistic Pathogens 2014 , 85-91		
133	Emergence and spread of antibiotic resistance: setting a parameter space. <i>Upsala Journal of Medical Sciences</i> , 2014 , 119, 68-77	2.8	86
132	Short-sighted evolution of bacterial opportunistic pathogens with an environmental origin. <i>Frontiers in Microbiology</i> , 2014 , 5, 239	5.7	14
131	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	3.7	103
130	Characterization of the polymyxin B resistome of <i>Pseudomonas aeruginosa</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2013 , 57, 110-9	5.9	100
129	Bacterial pathogens: from natural ecosystems to human hosts. <i>Environmental Microbiology</i> , 2013 , 15, 325-33	5.2	54
128	Phenotypic Resistance to Antibiotics. <i>Antibiotics</i> , 2013 , 2, 237-55	4.9	78
127	The DSF quorum sensing system controls the positive influence of <i>Stenotrophomonas maltophilia</i> on plants. <i>PLoS ONE</i> , 2013 , 8, e67103	3.7	46

126	Normal mutation rate variants arise in a Mutator (Mut S) Escherichia coli population. <i>PLoS ONE</i> , 2013 , 8, e72963	3.7	28
125	RND multidrug efflux pumps: what are they good for?. <i>Frontiers in Microbiology</i> , 2013 , 4, 7	5.7	126
124	The intrinsic resistome of bacterial pathogens. <i>Frontiers in Microbiology</i> , 2013 , 4, 103	5.7	92
123	The use of machine learning methodologies to analyse antibiotic and biocide susceptibility in Staphylococcus aureus. <i>PLoS ONE</i> , 2013 , 8, e55582	3.7	24
122	Overproduction of the multidrug efflux pump MexEF-OprN does not impair Pseudomonas aeruginosa fitness in competition tests, but produces specific changes in bacterial regulatory networks. <i>Environmental Microbiology</i> , 2012 , 14, 1968-81	5.2	81
121	Metagenomics and antibiotics. <i>Clinical Microbiology and Infection</i> , 2012 , 18 Suppl 4, 27-31	9.5	25
120	The antibiotic resistome: challenge and opportunity for therapeutic intervention. <i>Future Medicinal Chemistry</i> , 2012 , 4, 347-59	4.1	22
119	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 Staphylococcus aureus. <i>International Journal of Antimicrobial Agents</i> , 2012 , 40, 210-20	14.3	74
118	Differential epigenetic compatibility of qnr antibiotic resistance determinants with the chromosome of Escherichia coli. <i>PLoS ONE</i> , 2012 , 7, e35149	3.7	20
117	Whole-genome sequence of Stenotrophomonas maltophilia D457, a clinical isolate and a model strain. <i>Journal of Bacteriology</i> , 2012 , 194, 3563-4	3.5	34
116	Lack of evidence for reduced fitness of clinical Staphylococcus aureus isolates with reduced susceptibility to triclosan. <i>Antimicrobial Agents and Chemotherapy</i> , 2012 , 56, 6068-9; author reply 6072	5.9	6
115	The Inactivation of intrinsic antibiotic resistance determinants widens the mutant selection window for quinolones in Stenotrophomonas maltophilia. <i>Antimicrobial Agents and Chemotherapy</i> , 2012 , 56, 6397-9	5.9	12
114	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	5.7	532
113	Efflux pumps as an important mechanism for quinolone resistance. <i>Advances in Enzymology and Related Areas of Molecular Biology</i> , 2011 , 77, 167-235		12
112	Beyond serial passages: new methods for predicting the emergence of resistance to novel antibiotics. <i>Current Opinion in Pharmacology</i> , 2011 , 11, 439-45	5.1	65
111	Ecological and temporal constraints in the evolution of bacterial genomes. <i>Genes</i> , 2011 , 2, 804-28	4.2	15
110	Quinolone resistance: much more than predicted. <i>Frontiers in Microbiology</i> , 2011 , 2, 22	5.7	93
109	Environmental Pollution by Antibiotic Resistance Genes 2011 , 149-172		1

108	Metabolic regulation of antibiotic resistance. <i>FEMS Microbiology Reviews</i> , 2011 , 35, 768-89	15.1	153
107	The Evolution of Antibiotic Resistance 2011 , 305-337		3
106	The intrinsic resistome of <i>Pseudomonas aeruginosa</i> to β -lactams. <i>Virulence</i> , 2011 , 2, 144-6	4.7	68
105	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	7.6	77
104	Bottlenecks in the transferability of antibiotic resistance from natural ecosystems to human bacterial pathogens. <i>Frontiers in Microbiology</i> , 2011 , 2, 265	5.7	59
103	The global regulator Crc modulates metabolism, susceptibility to antibiotics and virulence in <i>Pseudomonas aeruginosa</i> . <i>Environmental Microbiology</i> , 2010 , 12, 3196-212	5.2	106
102	SmQnr contributes to intrinsic resistance to quinolones in <i>Stenotrophomonas maltophilia</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2010 , 54, 580-1	5.9	59
101	Genetic determinants involved in the susceptibility of <i>Pseudomonas aeruginosa</i> to beta-lactam antibiotics. <i>Antimicrobial Agents and Chemotherapy</i> , 2010 , 54, 4159-67	5.9	111
100	Polymorphic mutation frequencies of clinical and environmental <i>Stenotrophomonas maltophilia</i> populations. <i>Applied and Environmental Microbiology</i> , 2010 , 76, 1746-58	4.8	49
99	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, 14428-38	5.4	37
98	A global view of antibiotic resistance. <i>FEMS Microbiology Reviews</i> , 2009 , 33, 44-65	15.1	226
97	Functional role of bacterial multidrug efflux pumps in microbial natural ecosystems. <i>FEMS Microbiology Reviews</i> , 2009 , 33, 430-49	15.1	308
96	Towards an ecological approach to antibiotics and antibiotic resistance genes. <i>Clinical Microbiology and Infection</i> , 2009 , 15 Suppl 1, 14-6	9.5	30
95	Environmental pollution by antibiotics and by antibiotic resistance determinants. <i>Environmental Pollution</i> , 2009 , 157, 2893-902	9.3	1116
94	<i>Stenotrophomonas maltophilia</i> drug resistance. <i>Future Microbiology</i> , 2009 , 4, 655-60	2.9	75
93	Antibiotics and the Evolution of Antibiotic Resistance 2009 ,		3
92	Ecology and evolution of antibiotic resistance. <i>Environmental Microbiology Reports</i> , 2009 , 1, 469-76	3.7	103
91	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, 2521-30	4.4	310

90	Dictyostelium transcriptional responses to Pseudomonas aeruginosa: common and specific effects from PAO1 and PA14 strains. <i>BMC Microbiology</i> , 2008 , 8, 109	4.5	34
89	Predictive analysis of transmissible quinolone resistance indicates Stenotrophomonas maltophilia as a potential source of a novel family of Qnr determinants. <i>BMC Microbiology</i> , 2008 , 8, 148	4.5	95
88	The neglected intrinsic resistome of bacterial pathogens. <i>PLoS ONE</i> , 2008 , 3, e1619	3.7	203
87	Antibiotics as signals that trigger specific bacterial responses. <i>Current Opinion in Microbiology</i> , 2008 , 11, 161-7	7.9	240
86	Antibiotics and antibiotic resistance genes in natural environments. <i>Science</i> , 2008 , 321, 365-7	33.3	1122
85	Chronic Pseudomonas aeruginosa infection in chronic obstructive pulmonary disease. <i>Clinical Infectious Diseases</i> , 2008 , 47, 1526-33	11.6	162
84	Antibiotics and antibiotic resistance in water environments. <i>Current Opinion in Biotechnology</i> , 2008 , 19, 260-5	11.4	1260
83	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	3	48
82	Predicting antibiotic resistance. <i>Nature Reviews Microbiology</i> , 2007 , 5, 958-65	22.2	255
81	Mutation rate is reduced by increased dosage of mutL gene in Escherichia coli K-12. <i>FEMS Microbiology Letters</i> , 2007 , 275, 263-9	2.9	14
80	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, 13728-31	11.5	26
79	Contribution of a new mutation in parE to quinolone resistance in extended-spectrum-beta-lactamase-producing Escherichia coli isolates. <i>Journal of Clinical Microbiology</i> , 2007 , 45, 2740-2	9.7	49
78	Antibiotics as intermicrobial signaling agents instead of weapons. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 19484-9	11.5	479
77	Crosstalk between antibiotic resistance and virulence in Pseudomonas aeruginosa. <i>Reviews in Medical Microbiology</i> , 2005 , 16, 155-161	1.1	2
76	A molecular biological protocol to distinguish potentially human pathogenic Stenotrophomonas maltophilia from plant-associated Stenotrophomonas rhizophila. <i>Environmental Microbiology</i> , 2005 , 7, 1853-8	5.2	31
75	The biocide triclosan selects Stenotrophomonas maltophilia mutants that overproduce the SmeDEF multidrug efflux pump. <i>Antimicrobial Agents and Chemotherapy</i> , 2005 , 49, 781-2	5.9	90
74	Increased mutation frequencies in Escherichia coli isolates harboring extended-spectrum beta-lactamases. <i>Antimicrobial Agents and Chemotherapy</i> , 2005 , 49, 4754-6	5.9	34
73	Overexpression of the multidrug efflux pumps MexCD-OprJ and MexEF-OprN is associated with a reduction of type III secretion in Pseudomonas aeruginosa. <i>Journal of Bacteriology</i> , 2005 , 187, 1384-91	3.5	124

72	Role of Non-clinical Environments in the Selection of Virulence and Antibiotic Resistance Determinants in Pathogenic Bacteria. <i>Journal of Biological Sciences</i> , 2005 , 6, 1-8	0.4	7
71	Multi-resistant Enterobacteriaceae in Hospital Practice 2004 , 205-243		
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