

# Jose Luis Martinez

## List of Publications by Citations

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233  
papers

17,101  
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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	Antibiotics and antibiotic resistance in water environments. <i>Current Opinion in Biotechnology</i> , <b>2008</b> , 19, 260-5	11.4	1260
232	Antibiotics and antibiotic resistance genes in natural environments. <i>Science</i> , <b>2008</b> , 321, 365-7	33.3	1122
231	Environmental pollution by antibiotics and by antibiotic resistance determinants. <i>Environmental Pollution</i> , <b>2009</b> , 157, 2893-902	9.3	1116
230	Tackling antibiotic resistance: the environmental framework. <i>Nature Reviews Microbiology</i> , <b>2015</b> , 13, 310-7	22.2	1092
229	Natural antibiotic resistance and contamination by antibiotic resistance determinants: the two ages in the evolution of resistance to antimicrobials. <i>Frontiers in Microbiology</i> , <b>2012</b> , 3, 1	5.7	532
228	What is a resistance gene? Ranking risk in resistomes. <i>Nature Reviews Microbiology</i> , <b>2015</b> , 13, 116-23	22.2	483
227	Antibiotics as intermicrobial signaling agents instead of weapons. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2006</b> , 103, 19484-9	11.5	479
226	Mutation frequencies and antibiotic resistance. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2000</b> , 44, 1771-7	5.9	433
225	Interactions among strategies associated with bacterial infection: pathogenicity, epidemicity, and antibiotic resistance. <i>Clinical Microbiology Reviews</i> , <b>2002</b> , 15, 647-79	34	341
224	The role of natural environments in the evolution of resistance traits in pathogenic bacteria. <i>Proceedings of the Royal Society B: Biological Sciences</i> , <b>2009</b> , 276, 2521-30	4.4	310
223	Functional role of bacterial multidrug efflux pumps in microbial natural ecosystems. <i>FEMS Microbiology Reviews</i> , <b>2009</b> , 33, 430-49	15.1	308
222	Bacterial Multidrug Efflux Pumps: Much More Than Antibiotic Resistance Determinants. <i>Microorganisms</i> , <b>2016</b> , 4,	4.9	294
221	Environmental selection of antibiotic resistance genes. <i>Environmental Microbiology</i> , <b>2001</b> , 3, 1-9	5.2	281
220	Defining and combating antibiotic resistance from One Health and Global Health perspectives. <i>Nature Microbiology</i> , <b>2019</b> , 4, 1432-1442	26.6	264
219	Predicting antibiotic resistance. <i>Nature Reviews Microbiology</i> , <b>2007</b> , 5, 958-65	22.2	255
218	Antibiotics as signals that trigger specific bacterial responses. <i>Current Opinion in Microbiology</i> , <b>2008</b> , 11, 161-7	7.9	240
217	A global view of antibiotic resistance. <i>FEMS Microbiology Reviews</i> , <b>2009</b> , 33, 44-65	15.1	226

216	The neglected intrinsic resistome of bacterial pathogens. <i>PLoS ONE</i> , <b>2008</b> , 3, e1619	3.7	203
215	Antibiotic resistance in European wastewater treatment plants mirrors the pattern of clinical antibiotic resistance prevalence. <i>Science Advances</i> , <b>2019</b> , 5, eaau9124	14.3	184
214	Chronic <i>Pseudomonas aeruginosa</i> infection in chronic obstructive pulmonary disease. <i>Clinical Infectious Diseases</i> , <b>2008</b> , 47, 1526-33	11.6	162
213	Macrolide resistance genes in <i>Enterococcus</i> spp. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2000</b> , 44, 967-71	5.9	161
212	Environmental and clinical isolates of <i>Pseudomonas aeruginosa</i> show pathogenic and biodegradative properties irrespective of their origin. <i>Environmental Microbiology</i> , <b>1999</b> , 1, 421-30	5.2	161
211	Metabolic regulation of antibiotic resistance. <i>FEMS Microbiology Reviews</i> , <b>2011</b> , 35, 768-89	15.1	153
210	Cloning and characterization of SmeDEF, a novel multidrug efflux pump from <i>Stenotrophomonas maltophilia</i> . <i>Antimicrobial Agents and Chemotherapy</i> , <b>2000</b> , 44, 3079-86	5.9	146
209	Fitness of in vitro selected <i>Pseudomonas aeruginosa</i> nalB and nfxB multidrug resistant mutants. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2002</b> , 50, 657-64	5.1	138
208	Multiple antibiotic resistance in <i>Stenotrophomonas maltophilia</i> . <i>Antimicrobial Agents and Chemotherapy</i> , <b>1997</b> , 41, 1140-2	5.9	131
207	RND multidrug efflux pumps: what are they good for?. <i>Frontiers in Microbiology</i> , <b>2013</b> , 4, 7	5.7	126
206	Antibiotic residues in final effluents of European wastewater treatment plants and their impact on the aquatic environment. <i>Environment International</i> , <b>2020</b> , 140, 105733	12.9	124
205	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> . <i>Journal of Bacteriology</i> , <b>2005</b> , 187, 1384-91	3.5	124
204	Genetic determinants involved in the susceptibility of <i>Pseudomonas aeruginosa</i> to beta-lactam antibiotics. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2010</b> , 54, 4159-67	5.9	111
203	<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> , <b>2000</b> , 44, 1778-82	5.9	109
202	The <i>Pseudomonas putida</i> Crc global regulator controls the expression of genes from several chromosomal catabolic pathways for aromatic compounds. <i>Journal of Bacteriology</i> , <b>2004</b> , 186, 1337-44	3.5	107
201	The global regulator Crc modulates metabolism, susceptibility to antibiotics and virulence in <i>Pseudomonas aeruginosa</i> . <i>Environmental Microbiology</i> , <b>2010</b> , 12, 3196-212	5.2	106
200	Ecology and evolution of antibiotic resistance. <i>Environmental Microbiology Reports</i> , <b>2009</b> , 1, 469-76	3.7	103
199	Evaluation of epidemiological cut-off values indicates that biocide resistant subpopulations are uncommon in natural isolates of clinically-relevant microorganisms. <i>PLoS ONE</i> , <b>2014</b> , 9, e86669	3.7	103

198	Multidrug Efflux Pumps at the Crossroad between Antibiotic Resistance and Bacterial Virulence. <i>Frontiers in Microbiology</i> , <b>2016</b> , 7, 1483	5.7	103
197	Characterization of the polymyxin B resistome of <i>Pseudomonas aeruginosa</i> . <i>Antimicrobial Agents and Chemotherapy</i> , <b>2013</b> , 57, 110-9	5.9	100
196	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> , <b>2008</b> , 8, 148	4.5	95
195	Expression of multidrug efflux pump SmeDEF by clinical isolates of <i>Stenotrophomonas maltophilia</i> . <i>Antimicrobial Agents and Chemotherapy</i> , <b>2001</b> , 45, 1879-81	5.9	95
194	Quinolone resistance: much more than predicted. <i>Frontiers in Microbiology</i> , <b>2011</b> , 2, 22	5.7	93
193	The intrinsic resistome of bacterial pathogens. <i>Frontiers in Microbiology</i> , <b>2013</b> , 4, 103	5.7	92
192	General principles of antibiotic resistance in bacteria. <i>Drug Discovery Today: Technologies</i> , <b>2014</b> , 11, 33-9	7.1	91
191	Mechanisms of iron acquisition and bacterial virulence. <i>FEMS Microbiology Letters</i> , <b>1990</b> , 75, 45-56	2.9	91
190	The biocide triclosan selects <i>Stenotrophomonas maltophilia</i> mutants that overproduce the SmeDEF multidrug efflux pump. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2005</b> , 49, 781-2	5.9	90
189	Emergence of multidrug-resistant mutants is increased under antibiotic selective pressure in <i>Pseudomonas aeruginosa</i> . <i>Microbiology (United Kingdom)</i> , <b>1999</b> , 145 ( Pt 10), 2857-62	2.9	88
188	Factors determining resistance to beta-lactam combined with beta-lactamase inhibitors in <i>Escherichia coli</i> . <i>Journal of Antimicrobial Chemotherapy</i> , <b>1991</b> , 27, 569-75	5.1	87
187	Multidrug efflux pumps as main players in intrinsic and acquired resistance to antimicrobials. <i>Drug Resistance Updates</i> , <b>2016</b> , 28, 13-27	23.2	87
186	Emergence and spread of antibiotic resistance: setting a parameter space. <i>Upsala Journal of Medical Sciences</i> , <b>2014</b> , 119, 68-77	2.8	86
185	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> , <b>1998</b> , 64, 4317-20	4.8	85
184	Overproduction of the multidrug efflux pump MexEF-OprN does not impair <i>Pseudomonas aeruginosa</i> fitness in competition tests, but produces specific changes in bacterial regulatory networks. <i>Environmental Microbiology</i> , <b>2012</b> , 14, 1968-81	5.2	81
183	Overexpression of the multidrug efflux pump SmeDEF impairs <i>Stenotrophomonas maltophilia</i> physiology. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2004</b> , 53, 432-4	5.1	80
182	Phenotypic Resistance to Antibiotics. <i>Antibiotics</i> , <b>2013</b> , 2, 237-55	4.9	78
181	Man-made microbial resistances in built environments. <i>Nature Communications</i> , <b>2019</b> , 10, 968	17.4	78

180	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> , <b>2011</b> , 7, e1002103	7.6	77
179	Structure of <i>Pseudomonas aeruginosa</i> populations analyzed by single nucleotide polymorphism and pulsed-field gel electrophoresis genotyping. <i>Journal of Bacteriology</i> , <b>2004</b> , 186, 4228-37	3.5	77
178	<i>Stenotrophomonas maltophilia</i> drug resistance. <i>Future Microbiology</i> , <b>2009</b> , 4, 655-60	2.9	75
177	Biological cost of AmpC production for <i>Salmonella enterica</i> serotype Typhimurium. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2000</b> , 44, 3137-43	5.9	75
176	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> , <b>2012</b> , 40, 210-20	14.3	74
175	In-depth resistome analysis by targeted metagenomics. <i>Microbiome</i> , <b>2018</b> , 6, 11	16.6	73
174	Prediction of the intestinal resistome by a three-dimensional structure-based method. <i>Nature Microbiology</i> , <b>2019</b> , 4, 112-123	26.6	72
173	The intrinsic resistome of <i>Pseudomonas aeruginosa</i> to $\beta$ -lactams. <i>Virulence</i> , <b>2011</b> , 2, 144-6	4.7	68
172	Polymorphic mutation frequencies in <i>Escherichia coli</i> : emergence of weak mutators in clinical isolates. <i>Journal of Bacteriology</i> , <b>2004</b> , 186, 5538-42	3.5	68
171	The Plasmidome of Firmicutes: Impact on the Emergence and the Spread of Resistance to Antimicrobials. <i>Microbiology Spectrum</i> , <b>2015</b> , 3, PLAS-0039-2014	8.9	66
170	Beyond serial passages: new methods for predicting the emergence of resistance to novel antibiotics. <i>Current Opinion in Pharmacology</i> , <b>2011</b> , 11, 439-45	5.1	65
169	Cloning and characterization of SmeT, a repressor of the <i>Stenotrophomonas maltophilia</i> multidrug efflux pump SmeDEF. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2002</b> , 46, 3386-93	5.9	65
168	Bacterial lineages putatively associated with the dissemination of antibiotic resistance genes in a full-scale urban wastewater treatment plant. <i>Environment International</i> , <b>2018</b> , 118, 179-188	12.9	63
167	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> , <b>2015</b> , 6, 241	5.7	62
166	Aerobactin production as a virulence factor: a reevaluation. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , <b>1988</b> , 7, 621-9	5.3	60
165	SmQnr contributes to intrinsic resistance to quinolones in <i>Stenotrophomonas maltophilia</i> . <i>Antimicrobial Agents and Chemotherapy</i> , <b>2010</b> , 54, 580-1	5.9	59
164	Bottlenecks in the transferability of antibiotic resistance from natural ecosystems to human bacterial pathogens. <i>Frontiers in Microbiology</i> , <b>2011</b> , 2, 265	5.7	59
163	Environmental remodeling of human gut microbiota and antibiotic resistome in livestock farms. <i>Nature Communications</i> , <b>2020</b> , 11, 1427	17.4	57

162	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> , <b>2014</b> , 80, 4559-65	4.8	56
161	Quinolone resistance by mutations in chromosomal gyrase genes. Just the tip of the iceberg?. <i>Journal of Antimicrobial Chemotherapy</i> , <b>1998</b> , 42, 683-8	5.1	55
160	The organization of intercistronic regions of the aerobactin operon of pColV-K30 may account for the differential expression of the iucABCD iutA genes. <i>Journal of Molecular Biology</i> , <b>1994</b> , 238, 288-93	6.5	55
159	Bacterial pathogens: from natural ecosystems to human hosts. <i>Environmental Microbiology</i> , <b>2013</b> , 15, 325-33	5.2	54
158	Resistance to beta-lactam/clavulanate. <i>Lancet, The</i> , <b>1987</b> , 2, 1473	4.0	54
157	Mutation-Driven Evolution of <i>Pseudomonas aeruginosa</i> in the Presence of either Ceftazidime or Ceftazidime-Avibactam. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2018</b> , 62,	5.9	50
156	Mechanisms of iron acquisition and bacterial virulence. <i>FEMS Microbiology Letters</i> , <b>1990</b> , 6, 45-56	2.9	50
155	Polymorphic mutation frequencies of clinical and environmental <i>Stenotrophomonas maltophilia</i> populations. <i>Applied and Environmental Microbiology</i> , <b>2010</b> , 76, 1746-58	4.8	49
154	Contribution of a new mutation in parE to quinolone resistance in extended-spectrum-beta-lactamase-producing <i>Escherichia coli</i> isolates. <i>Journal of Clinical Microbiology</i> , <b>2007</b> , 45, 2740-2	9.7	49
153	Interplay between intrinsic and acquired resistance to quinolones in <i>Stenotrophomonas maltophilia</i> . <i>Environmental Microbiology</i> , <b>2014</b> , 16, 1282-96	5.2	48
152	Clinical impact of the over-expression of efflux pump in nonfermentative Gram-negative bacilli, development of efflux pump inhibitors. <i>Current Drug Targets</i> , <b>2008</b> , 9, 797-807	3	48
151	The DSF quorum sensing system controls the positive influence of <i>Stenotrophomonas maltophilia</i> on plants. <i>PLoS ONE</i> , <b>2013</b> , 8, e67103	3.7	46
150	Double-Face Meets the Bacterial World: The Opportunistic Pathogen. <i>Frontiers in Microbiology</i> , <b>2017</b> , 8, 2190	5.7	42
149	H-NS and RpoS regulate emergence of Lac Ara+ mutants of <i>Escherichia coli</i> MCS2. <i>Journal of Bacteriology</i> , <b>1997</b> , 179, 4620-2	3.5	42
148	Aminoglycoside resistance mediated by the bifunctional enzyme 6PN-aminoglycoside acetyltransferase-2"-O-aminoglycoside phosphotransferase. <i>Frontiers in Bioscience - Landmark</i> , <b>1999</b> , 4, D1-8	2.8	40
147	Prioritizing risks of antibiotic resistance genes in all metagenomes. <i>Nature Reviews Microbiology</i> , <b>2015</b> , 13, 396	22.2	37
146	Structural and functional analysis of SmeT, the repressor of the <i>Stenotrophomonas maltophilia</i> multidrug efflux pump SmeDEF. <i>Journal of Biological Chemistry</i> , <b>2009</b> , 284, 14428-38	5.4	37
145	Metabolic Compensation of Fitness Costs Is a General Outcome for Antibiotic-Resistant Mutants Overexpressing Efflux Pumps. <i>MBio</i> , <b>2017</b> , 8,	7.8	37

144	Effect of antibiotics on bacterial populations: a multi-hierarchical selection process. <i>F1000Research</i> , <b>2017</b> , 6, 51	3.6	34
143	Ecology and Evolution of Chromosomal Gene Transfer between Environmental Microorganisms and Pathogens. <i>Microbiology Spectrum</i> , <b>2018</b> , 6,	8.9	34
142	Fitness costs associated with the acquisition of antibiotic resistance. <i>Essays in Biochemistry</i> , <b>2017</b> , 61, 37-48	7.6	34
141	Whole-genome sequence of <i>Stenotrophomonas maltophilia</i> D457, a clinical isolate and a model strain. <i>Journal of Bacteriology</i> , <b>2012</b> , 194, 3563-4	3.5	34
140	Dictyostelium transcriptional responses to <i>Pseudomonas aeruginosa</i> : common and specific effects from PAO1 and PA14 strains. <i>BMC Microbiology</i> , <b>2008</b> , 8, 109	4.5	34
139	Increased mutation frequencies in <i>Escherichia coli</i> isolates harboring extended-spectrum beta-lactamases. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2005</b> , 49, 4754-6	5.9	34
138	Small plasmids are involved in amoxicillin-clavulanate resistance in <i>Escherichia coli</i> . <i>Antimicrobial Agents and Chemotherapy</i> , <b>1989</b> , 33, 595	5.9	34
137	Mutational Evolution of Resistance to Ribosome-Targeting Antibiotics. <i>Frontiers in Genetics</i> , <b>2018</b> , 9, 451	4.5	34
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> , <b>2014</b> , 58, 3904-13	5.9	33
135	The efflux pump SmeDEF contributes to trimethoprim-sulfamethoxazole resistance in <i>Stenotrophomonas maltophilia</i> . <i>Antimicrobial Agents and Chemotherapy</i> , <b>2015</b> , 59, 4347-8	5.9	32
134	Regulatory regions of smeDEF in <i>Stenotrophomonas maltophilia</i> strains expressing different amounts of the multidrug efflux pump SmeDEF. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2004</b> , 48, 2274-6	5.9	32
133	High-level quinolone resistance is associated with the overexpression of smeVWX in <i>Stenotrophomonas maltophilia</i> clinical isolates. <i>Clinical Microbiology and Infection</i> , <b>2015</b> , 21, 464-7	9.5	31
132	A molecular biological protocol to distinguish potentially human pathogenic <i>Stenotrophomonas maltophilia</i> from plant-associated <i>Stenotrophomonas rhizophila</i> . <i>Environmental Microbiology</i> , <b>2005</b> , 7, 1853-8	5.2	31
131	Genomic and metagenomic technologies to explore the antibiotic resistance mobilome. <i>Annals of the New York Academy of Sciences</i> , <b>2017</b> , 1388, 26-41	6.5	30
130	Towards an ecological approach to antibiotics and antibiotic resistance genes. <i>Clinical Microbiology and Infection</i> , <b>2009</b> , 15 Suppl 1, 14-6	9.5	30
129	Transcriptional regulation of mexR, the repressor of <i>Pseudomonas aeruginosa</i> mexAB-oprM multidrug efflux pump. <i>FEMS Microbiology Letters</i> , <b>2002</b> , 207, 63-8	2.9	30
128	Significant Differences Characterise the Correlation Coefficients between Biocide and Antibiotic Susceptibility Profiles in <i>Staphylococcus aureus</i> . <i>Current Pharmaceutical Design</i> , <b>2015</b> , 21, 2054-7	3.3	29
127	Metagenomic analysis of an urban resistome before and after wastewater treatment. <i>Scientific Reports</i> , <b>2020</b> , 10, 8174	4.9	28

126	Normal mutation rate variants arise in a Mutator (Mut S) Escherichia coli population. <i>PLoS ONE</i> , <b>2013</b> , 8, e72963	3.7	28
125	Gene Transmission in the One Health Microbiosphere and the Channels of Antimicrobial Resistance. <i>Frontiers in Microbiology</i> , <b>2019</b> , 10, 2892	5.7	28
124	Polymorphic variation in susceptibility and metabolism of triclosan-resistant mutants of Escherichia coli and Klebsiella pneumoniae clinical strains obtained after exposure to biocides and antibiotics. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2015</b> , 59, 3413-23	5.9	27
123	Incidence of aerobactin production in Gram-negative hospital isolates. <i>FEMS Microbiology Letters</i> , <b>1987</b> , 43, 351-353	2.9	27
122	Role of the Multidrug Resistance Efflux Pump MexCD-OprJ in the Quorum Sensing Response. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 2752	5.7	27
121	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> , <b>2007</b> , 104, 13728-31	11.5	26
120	Metagenomics and antibiotics. <i>Clinical Microbiology and Infection</i> , <b>2012</b> , 18 Suppl 4, 27-31	9.5	25
119	Mechanisms of antimicrobial resistance in : a review of current knowledge. <i>Expert Review of Anti-Infective Therapy</i> , <b>2020</b> , 18, 335-347	5.5	24
118	Multiple adaptive routes of Salmonella enterica Typhimurium to biocide and antibiotic exposure. <i>BMC Genomics</i> , <b>2016</b> , 17, 491	4.5	24
117	The use of machine learning methodologies to analyse antibiotic and biocide susceptibility in Staphylococcus aureus. <i>PLoS ONE</i> , <b>2013</b> , 8, e55582	3.7	24
116	Antibiotic Resistance: Moving From Individual Health Norms to Social Norms in One Health and Global Health. <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 1914	5.7	24
115	Antibiotic Resistance Evolution Is Contingent on the Quorum-Sensing Response in Pseudomonas aeruginosa. <i>Molecular Biology and Evolution</i> , <b>2019</b> , 36, 2238-2251	8.3	23
114	Antibiotic inactivating enzymes from a clinical isolate of Agrobacterium radiobacter. <i>Journal of Antimicrobial Chemotherapy</i> , <b>1989</b> , 23, 283-4	5.1	23
113	Dissemination of Novel Antimicrobial Resistance Mechanisms through the Insertion Sequence Mediated Spread of Metabolic Genes. <i>Frontiers in Microbiology</i> , <b>2016</b> , 7, 1008	5.7	23
112	The antibiotic resistome: challenge and opportunity for therapeutic intervention. <i>Future Medicinal Chemistry</i> , <b>2012</b> , 4, 347-59	4.1	22
111	Differential interactions within the Caenorhabditis elegans-Pseudomonas aeruginosa pathogenesis model. <i>Journal of Theoretical Biology</i> , <b>2003</b> , 225, 469-76	2.3	21
110	The efflux pump inhibitor Phe-Arg-beta-naphthylamide does not abolish the activity of the Stenotrophomonas maltophilia SmeDEF multidrug efflux pump. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2003</b> , 51, 1042-5	5.1	21
109	Involvement of the RND efflux pump transporter SmeH in the acquisition of resistance to ceftazidime in Stenotrophomonas maltophilia. <i>Scientific Reports</i> , <b>2019</b> , 9, 4917	4.9	20



108	Differential epigenetic compatibility of qnr antibiotic resistance determinants with the chromosome of Escherichia coli. <i>PLoS ONE</i> , <b>2012</b> , 7, e35149	3.7	20
107	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. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1997</b> , 94, 1816-21	11.5	20
106	Fosfomycin and rifampin disk diffusion tests for detection of Escherichia coli mutator strains. <i>Journal of Clinical Microbiology</i> , <b>2004</b> , 42, 4310-2	9.7	20
105	Microcin-mediated interactions between Klebsiella pneumoniae and Escherichia coli strains. <i>Microbiology (United Kingdom)</i> , <b>1984</b> , 130, 391-400	2.9	19
104	Quantitative proteomics unravels that the post-transcriptional regulator Crc modulates the generation of vesicles and secreted virulence determinants of Pseudomonas aeruginosa. <i>Journal of Proteomics</i> , <b>2015</b> , 127, 352-64	3.9	18
103	Overexpression of the Efflux Pumps SmeVWX and SmeDEF Is a Major Cause of Resistance to Co-trimoxazole in Stenotrophomonas maltophilia. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2018</b> , 62,	5.9	17
102	Evolutionary Pathways and Trajectories in Antibiotic Resistance. <i>Clinical Microbiology Reviews</i> , <b>2021</b> , e0005019	34	17
101	The global regulator Crc orchestrates the metabolic robustness underlying oxidative stress resistance in Pseudomonas aeruginosa. <i>Environmental Microbiology</i> , <b>2019</b> , 21, 898-912	5.2	17
100	Multilevel selection of bcrABDR-mediated bacitracin resistance in Enterococcus faecalis from chicken farms. <i>Scientific Reports</i> , <b>2016</b> , 6, 34895	4.9	16
99	Beta-lactam-fosfomycin antagonism involving modification of penicillin-binding protein 3 in Pseudomonas aeruginosa. <i>Antimicrobial Agents and Chemotherapy</i> , <b>1990</b> , 34, 2093-6	5.9	16
98	Acquisition of antibiotic resistance plasmids in vivo by extraintestinal Salmonella spp. <i>Journal of Antimicrobial Chemotherapy</i> , <b>1987</b> , 20, 452-3	5.1	16
97	Epidemiology of aerobactin production in Enterobacteriaceae. <i>Annales De L'Institut Pasteur Microbiologie</i> , <b>1986</b> , 137B, 297-303		16
96	Rapid and robust evolution of collateral sensitivity in antibiotic-resistant mutants. <i>Science Advances</i> , <b>2020</b> , 6, eaba5493	14.3	16
95	The development of efflux pump inhibitors to treat Gram-negative infections. <i>Expert Opinion on Drug Discovery</i> , <b>2018</b> , 13, 919-931	6.2	16
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