

Jose Luis Martinez

List of Publications by Year in descending order

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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	Tackling antibiotic resistance: the environmental framework. <i>Nature Reviews Microbiology</i> , 2015, 13, 310-317.	28.6	1,612
2	Antibiotics and antibiotic resistance in water environments. <i>Current Opinion in Biotechnology</i> , 2008, 19, 260-265.	6.6	1,608
3	Antibiotics and Antibiotic Resistance Genes in Natural Environments. <i>Science</i> , 2008, 321, 365-367.	12.6	1,409
4	Environmental pollution by antibiotics and by antibiotic resistance determinants. <i>Environmental Pollution</i> , 2009, 157, 2893-2902.	7.5	1,409
5	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
6	What is a resistance gene? Ranking risk in resistomes. <i>Nature Reviews Microbiology</i> , 2015, 13, 116-123.	28.6	698
7	Defining and combating antibiotic resistance from One Health and Global Health perspectives. <i>Nature Microbiology</i> , 2019, 4, 1432-1442.	13.3	614
8	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, 19484-19489.	7.1	594
9	Mutation Frequencies and Antibiotic Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2000, 44, 1771-1777.	3.2	530
10	Bacterial Multidrug Efflux Pumps: Much More Than Antibiotic Resistance Determinants. <i>Microorganisms</i> , 2016, 4, 14.	3.6	486
11	Interactions among Strategies Associated with Bacterial Infection: Pathogenicity, Epidemicity, and Antibiotic Resistance. <i>Clinical Microbiology Reviews</i> , 2002, 15, 647-679.	13.6	416
12	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
13	Functional role of bacterial multidrug efflux pumps in microbial natural ecosystems. <i>FEMS Microbiology Reviews</i> , 2009, 33, 430-449.	8.6	384
14	Antibiotic resistance in European wastewater treatment plants mirrors the pattern of clinical antibiotic resistance prevalence. <i>Science Advances</i> , 2019, 5, eaau9124.	10.3	346
15	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
16	Environmental selection of antibiotic resistance genes. Minireview. <i>Environmental Microbiology</i> , 2001, 3, 1-9.	3.8	331
17	Predicting antibiotic resistance. <i>Nature Reviews Microbiology</i> , 2007, 5, 958-965.	28.6	305
18	Antibiotics as signals that trigger specific bacterial responses. <i>Current Opinion in Microbiology</i> , 2008, 11, 161-167.	5.1	295

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19	A global view of antibiotic resistance. <i>FEMS Microbiology Reviews</i> , 2009, 33, 44-65.	8.6	271
20	The Neglected Intrinsic Resistome of Bacterial Pathogens. <i>PLoS ONE</i> , 2008, 3, e1619.	2.5	257
21	Chronic <i>Pseudomonas aeruginosa</i> Infection in Chronic Obstructive Pulmonary Disease. <i>Clinical Infectious Diseases</i> , 2008, 47, 1526-1533.	5.8	235
22	Metabolic regulation of antibiotic resistance. <i>FEMS Microbiology Reviews</i> , 2011, 35, 768-789.	8.6	220
23	Macrolide Resistance Genes in <i>Enterococcus</i> spp. <i>Antimicrobial Agents and Chemotherapy</i> , 2000, 44, 967-971.	3.2	195
24	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
25	Multidrug Efflux Pumps at the Crossroad between Antibiotic Resistance and Bacterial Virulence. <i>Frontiers in Microbiology</i> , 2016, 7, 1483.	3.5	180
26	Cloning and Characterization of SmeDEF, a Novel Multidrug Efflux Pump from <i>Stenotrophomonas maltophilia</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2000, 44, 3079-3086.	3.2	179
27	RND multidrug efflux pumps: what are they good for?. <i>Frontiers in Microbiology</i> , 2013, 4, 7.	3.5	175
28	Fitness of in vitro selected <i>Pseudomonas aeruginosa</i> Δ nalB and Δ nfxB multidrug resistant mutants. <i>Journal of Antimicrobial Chemotherapy</i> , 2002, 50, 657-664.	3.0	164
29	General principles of antibiotic resistance in bacteria. <i>Drug Discovery Today: Technologies</i> , 2014, 11, 33-39.	4.0	157
30	Multiple antibiotic resistance in <i>Stenotrophomonas maltophilia</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 1997, 41, 1140-1142.	3.2	152
31	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> , 2005, 187, 1384-1391.	2.2	151
32	Genetic Determinants Involved in the Susceptibility of <i>Pseudomonas aeruginosa</i> to β -Lactam Antibiotics. <i>Antimicrobial Agents and Chemotherapy</i> , 2010, 54, 4159-4167.	3.2	149
33	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
34	The intrinsic resistome of bacterial pathogens. <i>Frontiers in Microbiology</i> , 2013, 4, 103.	3.5	137
35	Characterization of the Polymyxin B Resistome of <i>Pseudomonas aeruginosa</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 110-119.	3.2	136
36	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

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37	Phenotypic Resistance to Antibiotics. <i>Antibiotics</i> , 2013, 2, 237-255.	3.7	134
38	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
39	Environmental remodeling of human gut microbiota and antibiotic resistome in livestock farms. <i>Nature Communications</i> , 2020, 11, 1427.	12.8	133
40	Prediction of the intestinal resistome by a three-dimensional structure-based method. <i>Nature Microbiology</i> , 2019, 4, 112-123.	13.3	129
41	Man-made microbial resistances in built environments. <i>Nature Communications</i> , 2019, 10, 968.	12.8	128
42	<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
43	Ecology and evolution of antibiotic resistance. <i>Environmental Microbiology Reports</i> , 2009, 1, 469-476.	2.4	123
44	Emergence and spread of antibiotic resistance: setting a parameter space. <i>Upsala Journal of Medical Sciences</i> , 2014, 119, 68-77.	0.9	120
45	In-depth resistome analysis by targeted metagenomics. <i>Microbiome</i> , 2018, 6, 11.	11.1	115
46	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> , 2004, 186, 1337-1344.	2.2	114
47	Quinolone Resistance: Much More than Predicted. <i>Frontiers in Microbiology</i> , 2011, 2, 22.	3.5	113
48	The Biocide Triclosan Selects <i>Stenotrophomonas maltophilia</i> Mutants That Overproduce the SmeDEF Multidrug Efflux Pump. <i>Antimicrobial Agents and Chemotherapy</i> , 2005, 49, 781-782.	3.2	108
49	Expression of Multidrug Efflux Pump SmeDEF by Clinical Isolates of <i>Stenotrophomonas maltophilia</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2001, 45, 1879-1881.	3.2	105
50	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
51	Factors determining resistance to β -lactam combined with β -lactamase inhibitors in <i>Escherichia coli</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 1991, 27, 569-575.	3.0	102
52	Mechanisms of iron acquisition and bacterial virulence. <i>FEMS Microbiology Letters</i> , 1990, 75, 45-56.	1.8	100
53	Overproduction of the multidrug efflux pump MexEF Δ OprN 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
54	<i>Stenotrophomonas maltophilia</i> drug resistance. <i>Future Microbiology</i> , 2009, 4, 655-660.	2.0	98

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55	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
56	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
57	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
58	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
59	Overexpression of the multidrug efflux pump SmeDEF impairs <i>Stenotrophomonas maltophilia</i> physiology. <i>Journal of Antimicrobial Chemotherapy</i> , 2004, 53, 432-434.	3.0	93
60	The intrinsic resistome of <i>Pseudomonas aeruginosa</i> to β -lactams. <i>Virulence</i> , 2011, 2, 144-146.	4.4	93
61	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
62	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
63	Biological Cost of AmpC Production for <i>Salmonella enterica</i> Serotype Typhimurium. <i>Antimicrobial Agents and Chemotherapy</i> , 2000, 44, 3137-3143.	3.2	90
64	Cloning and Characterization of SmeT, a Repressor of the <i>Stenotrophomonas maltophilia</i> Multidrug Efflux Pump SmeDEF. <i>Antimicrobial Agents and Chemotherapy</i> , 2002, 46, 3386-3393.	3.2	89
65	Structure of <i>Pseudomonas aeruginosa</i> Populations Analyzed by Single Nucleotide Polymorphism and Pulsed-Field Gel Electrophoresis Genotyping. <i>Journal of Bacteriology</i> , 2004, 186, 4228-4237.	2.2	84
66	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
67	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
68	Mechanisms of iron acquisition and bacterial virulence. <i>FEMS Microbiology Letters</i> , 1990, 75, 45-56.	1.8	81
69	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
70	Aerobactin production as a virulence factor: A reevaluation. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 1988, 7, 621-629.	2.9	78
71	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> , 1994, 238, 288-293.	4.2	77
72	RESISTANCE TO BETA-LACTAM/CLAVULANATE. <i>Lancet</i> , The, 1987, 330, 1473.	13.7	75

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73	SmQnr Contributes to Intrinsic Resistance to Quinolones in <i>Stenotrophomonas maltophilia</i> . Antimicrobial Agents and Chemotherapy, 2010, 54, 580-581.	3.2	75
74	A Function of SmeDEF, the Major Quinolone Resistance Determinant of <i>Stenotrophomonas maltophilia</i> , Is the Colonization of Plant Roots. Applied and Environmental Microbiology, 2014, 80, 4559-4565.	3.1	75
75	Effect of antibiotics on bacterial populations: a multi-hierarchical selection process. F1000Research, 2017, 6, 51.	1.6	75
76	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
77	Bottlenecks in the Transferability of Antibiotic Resistance from Natural Ecosystems to Human Bacterial Pathogens. Frontiers in Microbiology, 2011, 2, 265.	3.5	74
78	Mechanisms of antimicrobial resistance in <i>Stenotrophomonas maltophilia</i> : a review of current knowledge. Expert Review of Anti-Infective Therapy, 2020, 18, 335-347.	4.4	73
79	Evolutionary Pathways and Trajectories in Antibiotic Resistance. Clinical Microbiology Reviews, 2021, 34, e0005019.	13.6	71
80	Quinolone resistance by mutations in chromosomal gyrase genes. Just the tip of the iceberg?. Journal of Antimicrobial Chemotherapy, 1998, 42, 683-688.	3.0	68
81	Bacterial pathogens: from natural ecosystems to human hosts. Environmental Microbiology, 2013, 15, 325-333.	3.8	68
82	Double-Face Meets the Bacterial World: The Opportunistic Pathogen <i>Stenotrophomonas maltophilia</i> . Frontiers in Microbiology, 2017, 8, 2190.	3.5	66
83	Gene Transmission in the One Health Microbiosphere and the Channels of Antimicrobial Resistance. Frontiers in Microbiology, 2019, 10, 2892.	3.5	66
84	Antibiotic Resistance: Moving From Individual Health Norms to Social Norms in One Health and Global Health. Frontiers in Microbiology, 2020, 11, 1914.	3.5	64
85	Fitness costs associated with the acquisition of antibiotic resistance. Essays in Biochemistry, 2017, 61, 37-48.	4.7	62
86	Metabolic Compensation of Fitness Costs Is a General Outcome for Antibiotic-Resistant <i>Pseudomonas aeruginosa</i> Mutants Overexpressing Efflux Pumps. MBio, 2017, 8, .	4.1	61
87	Interplay between intrinsic and acquired resistance to quinolones in <i>Stenotrophomonas maltophilia</i> . Environmental Microbiology, 2014, 16, 1282-1296.	3.8	60
88	Clinical Impact of the Over-Expression of Efflux Pump in Nonfermentative Gram-Negative Bacilli, Development of Efflux Pump Inhibitors. Current Drug Targets, 2008, 9, 797-807.	2.1	60
89	Editorial: A Multidisciplinary Look at <i>Stenotrophomonas maltophilia</i> : An Emerging Multi-Drug-Resistant Global Opportunistic Pathogen. Frontiers in Microbiology, 2017, 8, 1511.	3.5	58
90	Metagenomic analysis of an urban resistome before and after wastewater treatment. Scientific Reports, 2020, 10, 8174.	3.3	58

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91	Contribution of a New Mutation in <i>parE</i> to Quinolone Resistance in Extended-Spectrum-β-Lactamase-Producing <i>Escherichia coli</i> Isolates. <i>Journal of Clinical Microbiology</i> , 2007, 45, 2740-2742.	3.9	57
92	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
93	The Origin of Niches and Species in the Bacterial World. <i>Frontiers in Microbiology</i> , 2021, 12, 657986.	3.5	56
94	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
95	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
96	Mutational Evolution of <i>Pseudomonas aeruginosa</i> Resistance to Ribosome-Targeting Antibiotics. <i>Frontiers in Genetics</i> , 2018, 9, 451.	2.3	52
97	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
98	Ecology and Evolution of Chromosomal Gene Transfer between Environmental Microorganisms and Pathogens. <i>Microbiology Spectrum</i> , 2018, 6, .	3.0	48
99	Small plasmids are involved in amoxicillin-clavulanate resistance in <i>Escherichia coli</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 1989, 33, 595.	3.2	46
100	<i>Dictyostelium</i> 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
101	Towards an ecological approach to antibiotics and antibiotic resistance genes. <i>Clinical Microbiology and Infection</i> , 2009, 15, 14-16.	6.0	46
102	Metagenomics and antibiotics. <i>Clinical Microbiology and Infection</i> , 2012, 18, 27-31.	6.0	45
103	Prioritizing risks of antibiotic resistance genes in all metagenomes. <i>Nature Reviews Microbiology</i> , 2015, 13, 396-396.	28.6	45
104	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
105	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
106	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
107	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
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

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109	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
110	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
111	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
112	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
113	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.	8.9	40
114	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
115	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
116	Multiple adaptive routes of <i>Salmonella enterica</i> Typhimurium to biocide and antibiotic exposure. <i>BMC Genomics</i> , 2016, 17, 491.	2.8	39
117	<i>Pseudomonas aeruginosa</i> : an antibiotic resilient pathogen with environmental origin. <i>Current Opinion in Microbiology</i> , 2021, 64, 125-132.	5.1	38
118	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> , 2004, 48, 2274-2276.	3.2	37
119	Increased Mutation Frequencies in <i>Escherichia coli</i> Isolates Harboring Extended-Spectrum β -Lactamases. <i>Antimicrobial Agents and Chemotherapy</i> , 2005, 49, 4754-4756.	3.2	37
120	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
121	A molecular biological protocol to distinguish potentially human pathogenic <i>Stenotrophomonas maltophilia</i> from plant-associated <i>Stenotrophomonas rhizophila</i> . <i>Environmental Microbiology</i> , 2005, 7, 1853-1858.	3.8	36
122	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
123	Transcriptional regulation of mexR, the repressor of <i>Pseudomonas aeruginosa</i> mexAB-oprM multidrug efflux pump. <i>FEMS Microbiology Letters</i> , 2002, 207, 63-68.	1.8	33
124	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
125	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
126	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

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127	Antimicrobial resistance: A multifaceted problem with multipronged solutions. <i>MicrobiologyOpen</i> , 2019, 8, e945.	3.0	32
128	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.	3.3	31
129	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
130	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
131	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
132	Incidence of aerobactin production in Gram-negative hospital isolates. <i>FEMS Microbiology Letters</i> , 1987, 43, 351-353.	1.8	29
133	Antibiotic resistance: Time of synthesis in a post-genomic age. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 3110-3124.	4.1	28
134	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.	3.8	27
135	Characterization of a novel Zn ²⁺ -dependent intrinsic imipenemase from <i>Pseudomonas aeruginosa</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 2972-2978.	3.0	26
136	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
137	Differential interactions within the <i>Caenorhabditis elegans</i> – <i>Pseudomonas aeruginosa</i> pathogenesis model. <i>Journal of Theoretical Biology</i> , 2003, 225, 469-476.	1.7	24
138	The antibiotic resistome: challenge and opportunity for therapeutic intervention. <i>Future Medicinal Chemistry</i> , 2012, 4, 347-359.	2.3	24
139	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
140	Antiviral effects of green tea (&#x201C; <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	24
141	Overexpression of the Efflux Pumps SmeVWX and SmeDEF Is a Major Cause of Resistance to Co-trimoxazole in <i>Stenotrophomonas maltophilia</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	3.2	24
142	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
143	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
144	Antibiotic inactivating enzymes from a clinical isolate of <i>Agrobacterium radiobacter</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 1989, 23, 283-284.	3.0	23

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145	Wildlife and Antibiotic Resistance. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, .	3.9	23
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