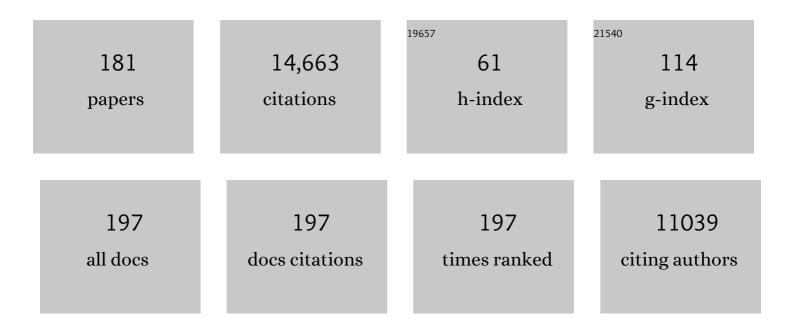
List of Publications by Year in descending order

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TERESA M COOLE

#	Article	IF	CITATIONS
1	The CTX-M β-lactamase pandemic. Current Opinion in Microbiology, 2006, 9, 466-475.	5.1	982
2	CTX-M: changing the face of ESBLs in Europe. Journal of Antimicrobial Chemotherapy, 2006, 59, 165-174.	3.0	756
3	What is a resistance gene? Ranking risk in resistomes. Nature Reviews Microbiology, 2015, 13, 116-123.	28.6	698
4	Dissemination of Clonally Related <i>Escherichia coli</i> Strains Expressing Extended-Spectrum β-Lactamase CTX-M-15. Emerging Infectious Diseases, 2008, 14, 195-200.	4.3	672
5	Defining and combating antibiotic resistance from One Health and Global Health perspectives. Nature Microbiology, 2019, 4, 1432-1442.	13.3	614
6	Global Spread of Vancomycin-resistant <i>Enterococcus faecium</i> from Distinct Nosocomial Genetic Complex. Emerging Infectious Diseases, 2005, 11, 821-828.	4.3	491
7	Multilocus Sequence Typing Scheme for Enterococcus faecalis Reveals Hospital-Adapted Genetic Complexes in a Background of High Rates of Recombination. Journal of Clinical Microbiology, 2006, 44, 2220-2228.	3.9	321
8	Dramatic Increase in Prevalence of Fecal Carriage of Extended-Spectrum β-Lactamase-Producing <i>Enterobacteriaceae</i> during Nonoutbreak Situations in Spain. Journal of Clinical Microbiology, 2004, 42, 4769-4775.	3.9	290
9	Mobile genetic elements and their contribution to the emergence of antimicrobial resistant Enterococcus faecalis and Enterococcus faecium. Clinical Microbiology and Infection, 2010, 16, 541-554.	6.0	285
10	Vancomycin-resistant enterococci from nosocomial, community, and animal sources in the United States. Antimicrobial Agents and Chemotherapy, 1996, 40, 2605-2609.	3.2	270
11	Global Emergence and Dissemination of Enterococci as Nosocomial Pathogens: Attack of the Clones?. Frontiers in Microbiology, 2016, 7, 788.	3.5	248
12	Incidence of Hemolysin, Gelatinase, and Aggregation Substance among Enterococci Isolated from Patients with Endocarditis and Other Infections and from Feces of Hospitalized and Community-Based Persons. Journal of Infectious Diseases, 1995, 171, 1223-1229.	4.0	229
13	Public Health Risks of Enterobacterial Isolates Producing Extended-Spectrum Â-Lactamases or AmpC Â-Lactamases in Food and Food-Producing Animals: An EU Perspective of Epidemiology, Analytical Methods, Risk Factors, and Control Options. Clinical Infectious Diseases, 2013, 56, 1030-1037.	5.8	225
14	Plasmid Flux in Escherichia coli ST131 Sublineages, Analyzed by Plasmid Constellation Network (PLACNET), a New Method for Plasmid Reconstruction from Whole Genome Sequences. PLoS Genetics, 2014, 10, e1004766.	3.5	179
15	Genes Encoding TEM-4, SHV-2, and CTX-M-10 Extended-Spectrum β-Lactamases Are Carried by Multiple <i>Klebsiella pneumoniae</i> Clones in a Single Hospital (Madrid, 1989 to 2000). Antimicrobial Agents and Chemotherapy, 2002, 46, 500-510.	3.2	178
16	Integron Content of Extended-Spectrum-β-Lactamase-Producing Escherichia coli Strains over 12 Years in a Single Hospital in Madrid, Spain. Antimicrobial Agents and Chemotherapy, 2005, 49, 1823-1829.	3.2	174
17	Ecology and Evolution as Targets: the Need for Novel Eco-Evo Drugs and Strategies To Fight Antibiotic Resistance. Antimicrobial Agents and Chemotherapy, 2011, 55, 3649-3660.	3.2	171
18	Dissemination of <i>bla</i> _{KPC-2} by the Spread of Klebsiella pneumoniae Clonal Complex 258 Clones (ST258, ST11, ST437) and Plasmids (IncFII, IncN, IncL/M) among Enterobacteriaceae Species in Brazil. Antimicrobial Agents and Chemotherapy, 2011, 55, 3579-3583.	3.2	168

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19	Update on prevalence and mechanisms of resistance to linezolid, tigecycline and daptomycin in enterococci in Europe: Towards a common nomenclature. Drug Resistance Updates, 2018, 40, 25-39.	14.4	165
20	Extended-spectrum β-lactamase-producing Escherichia coli in Spain belong to a large variety of multilocus sequence typing types, including ST10 complex/A, ST23 complex/A and ST131/B2. International Journal of Antimicrobial Agents, 2009, 34, 173-176.	2.5	164
21	High Rate of Intestinal Colonization with Extended-Spectrum-β-Lactamase-Producing Organisms in Household Contacts of Infected Community Patients. Journal of Clinical Microbiology, 2008, 46, 2796-2799.	3.9	157
22	Antibiotic resistance shaping multi-level population biology of bacteria. Frontiers in Microbiology, 2013, 4, 15.	3.5	153
23	Antibiotic resistance integrons and extended-spectrum Â-lactamases among Enterobacteriaceae isolates recovered from chickens and swine in Portugal. Journal of Antimicrobial Chemotherapy, 2008, 62, 296-302.	3.0	147
24	Antimicrobial Resistance in <i>Enterococcus</i> spp. of animal origin. Microbiology Spectrum, 2018, 6, .	3.0	147
25	In vivo testing of anEnterococcus faecalis efaAmutant and use ofefaAhomologs for species identification. FEMS Immunology and Medical Microbiology, 1998, 21, 323-331.	2.7	145
26	Antibiotic Coresistance in Extended-Spectrum-β-Lactamase-Producing <i>Enterobacteriaceae</i> and In Vitro Activity of Tigecycline. Antimicrobial Agents and Chemotherapy, 2006, 50, 2695-2699.	3.2	145
27	Nationwide Study of Escherichia coli and Klebsiella pneumoniae Producing Extended-Spectrum β-Lactamases in Spain. Antimicrobial Agents and Chemotherapy, 2005, 49, 2122-2125.	3.2	139
28	Antibiotic resistant enterococci—Tales of a drug resistance gene trafficker. International Journal of Medical Microbiology, 2013, 303, 360-379.	3.6	139
29	Evaluation of Epidemiological Cut-Off Values Indicates that Biocide Resistant Subpopulations Are Uncommon in Natural Isolates of Clinically-Relevant Microorganisms. PLoS ONE, 2014, 9, e86669.	2.5	135
30	Multilevel population genetic analysis of <i>vanA</i> and <i>vanB Enterococcus faecium</i> causing nosocomial outbreaks in 27 countries (1986–2012). Journal of Antimicrobial Chemotherapy, 2016, 71, 3351-3366.	3.0	129
31	Prediction of the intestinal resistome by a three-dimensional structure-based method. Nature Microbiology, 2019, 4, 112-123.	13.3	129
32	Human and Swine Hosts Share Vancomycin-Resistant Enterococcus faecium CC17 and CC5 and Enterococcus faecalis CC2 Clonal Clusters Harboring Tn <i>1546</i> on Indistinguishable Plasmids. Journal of Clinical Microbiology, 2011, 49, 925-931.	3.9	126
33	Epidemiology of Extended-Spectrum Â-Lactamase-Producing Enterobacter Isolates in a Spanish Hospital during a 12-Year Period. Journal of Clinical Microbiology, 2002, 40, 1237-1243.	3.9	119
34	In-depth resistome analysis by targeted metagenomics. Microbiome, 2018, 6, 11.	11.1	115
35	Spread of <i>bla</i> _{CTX-M-14} Is Driven Mainly by IncK Plasmids Disseminated among <i>Escherichia coli</i> Phylogroups A, B1, and D in Spain. Antimicrobial Agents and Chemotherapy, 2009, 53, 5204-5212.	3.2	112
36	Emergence and Dissemination of Enterobacteriaceae Isolates Producing CTX-M-1-Like Enzymes in Spain Are Associated with IncFII (CTX-M-15) and Broad-Host-Range (CTX-M-1, -3, and -32) Plasmids. Antimicrobial Agents and Chemotherapy, 2007, 51, 796-799.	3.2	110

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37	Complex Clonal and Plasmid Epidemiology in the First Outbreak of Enterobacteriaceae Infection Involving VIM-1 Metallo-Â-Lactamase in Spain: Toward Endemicity?. Clinical Infectious Diseases, 2007, 45, 1171-1178.	5.8	109
38	Dissemination and Persistence of bla CTX-M-9 Are Linked to Class 1 Integrons Containing CR1 Associated with Defective Transposon Derivatives from Tn 402 Located in Early Antibiotic Resistance Plasmids of IncHI2, IncP1-α, and IncFI Groups. Antimicrobial Agents and Chemotherapy, 2006, 50, 2741-2750.	3.2	108
39	Nucleotide Sequence and Characterization of a Novel Cefotaxime-Hydrolyzing β-Lactamase (CTX-M-10) Isolated in Spain. Antimicrobial Agents and Chemotherapy, 2001, 45, 616-620.	3.2	106
40	Multi-resistant Gram-negative bacilli: from epidemics to endemics. Current Opinion in Infectious Diseases, 2003, 16, 315-325.	3.1	106
41	Insight into antimicrobial susceptibility and population structure of contemporary human Enterococcus faecalis isolates from Europe. Journal of Antimicrobial Chemotherapy, 2012, 67, 551-558.	3.0	102
42	Evolutionary Trajectories of Beta-Lactamase CTX-M-1 Cluster Enzymes: Predicting Antibiotic Resistance. PLoS Pathogens, 2010, 6, e1000735.	4.7	100
43	Dissemination in Portugal of CTX-M-15-, OXA-1-, and TEM-1-Producing Enterobacteriaceae Strains Containing the aac(6 ′)-Ib-cr Gene, Which Encodes an Aminoglycoside- and Fluoroquinolone-Modifying Enzyme. Antimicrobial Agents and Chemotherapy, 2006, 50, 3220-3221.	3.2	95
44	High occurrence and persistence of antibiotic-resistant enterococci in poultry food samples in Portugal. Journal of Antimicrobial Chemotherapy, 2005, 56, 1139-1143.	3.0	86
45	Environmental Contamination with Vancomycin-Resistant Enterococci from Hospital Sewage in Portugal. Applied and Environmental Microbiology, 2005, 71, 3364-3368.	3.1	85
46	Dispersal of Carbapenemase <i>bla</i> _{VIM-1} Gene Associated with Different Tn <i>402</i> Variants, Mercury Transposons, and Conjugative Plasmids in <i>Enterobacteriaceae</i> and <i>Pseudomonas aeruginosa</i> . Antimicrobial Agents and Chemotherapy, 2010, 54, 320-327.	3.2	84
47	The Plasmidome of Firmicutes: Impact on the Emergence and the Spread of Resistance to Antimicrobials. Microbiology Spectrum, 2015, 3, PLAS-0039-2014.	3.0	83
48	Investigating the mobilome in clinically important lineages of Enterococcus faecium and Enterococcus faecalis. BMC Genomics, 2015, 16, 282.	2.8	82
49	Population Structure of Enterococcus faecium Causing Bacteremia in a Spanish University Hospital: Setting the Scene for a Future Increase in Vancomycin Resistance?. Antimicrobial Agents and Chemotherapy, 2005, 49, 2693-2700.	3.2	79
50	Antimicrobial Resistance in Recent Fecal Enterococci from Healthy Volunteers and Food Handlers in Spain: Genes and Phenotypes. Microbial Drug Resistance, 2003, 9, 47-60.	2.0	76
51	Clonal expansion within clonal complex 2 and spread of vancomycin-resistant plasmids among different genetic lineages of Enterococcus faecalis from Portugal. Journal of Antimicrobial Chemotherapy, 2009, 63, 1104-1111.	3.0	76
52	Population Biology of Intestinal Enterococcus Isolates from Hospitalized and Nonhospitalized Individuals in Different Age Groups. Applied and Environmental Microbiology, 2015, 81, 1820-1831.	3.1	75
53	Emergence of blaKPC-3-Tn4401a associated with a pKPN3/4-like plasmid within ST384 and ST388 Klebsiella pneumoniae clones in Spain. Journal of Antimicrobial Chemotherapy, 2010, 65, 1608-1614.	3.0	74
54	Spread of multidrug-resistant Enterococcus to animals and humans: an underestimated role for the pig farm environment. Journal of Antimicrobial Chemotherapy, 2013, 68, 2746-2754.	3.0	74

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55	CTX-M-10 Linked to a Phage-Related Element Is Widely Disseminated among Enterobacteriaceae in a Spanish Hospital. Antimicrobial Agents and Chemotherapy, 2005, 49, 1567-1571.	3.2	70
56	Apparent nosocomial adaptation of Enterococcus faecalis predates the modern hospital era. Nature Communications, 2021, 12, 1523.	12.8	69
57	Fecal Carriage of Carbapenemase-Producing Enterobacteriaceae: a Hidden Reservoir in Hospitalized and Nonhospitalized Patients. Journal of Clinical Microbiology, 2012, 50, 1558-1563.	3.9	68
58	Co-transfer of resistance to high concentrations of copper and first-line antibiotics among Enterococcus from different origins (humans, animals, the environment and foods) and clonal lineages. Journal of Antimicrobial Chemotherapy, 2014, 69, 899-906.	3.0	68
59	Global Spread of the <i>hyl</i> _{Efm} Colonization-Virulence Gene in Megaplasmids of the <i>Enterococcus faecium</i> CC17 Polyclonal Subcluster. Antimicrobial Agents and Chemotherapy, 2010, 54, 2660-2665.	3.2	67
60	Characterization of plasmids encoding blaESBL and surrounding genes in Spanish clinical isolates of Escherichia coli and Klebsiella pneumoniae. Journal of Antimicrobial Chemotherapy, 2008, 63, 60-66.	3.0	66
61	A multiresistance megaplasmid pLG1 bearing a hylEfm genomic island in hospital Enterococcus faecium isolates. International Journal of Medical Microbiology, 2011, 301, 165-175.	3.6	66
62	Gene Transmission in the One Health Microbiosphere and the Channels of Antimicrobial Resistance. Frontiers in Microbiology, 2019, 10, 2892.	3.5	66
63	Diversity of Tn <i>1546</i> and Its Role in the Dissemination of Vancomycin-Resistant Enterococci in Portugal. Antimicrobial Agents and Chemotherapy, 2008, 52, 1001-1008.	3.2	64
64	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
65	Detection of optrA in the African continent (Tunisia) within a mosaic Enterococcus faecalis plasmid from urban wastewaters. Journal of Antimicrobial Chemotherapy, 2017, 72, 3245-3251.	3.0	61
66	Characterization of Dihydrofolate Reductase Genes from Trimethoprim-Susceptible and Trimethoprim-Resistant Strains of <i>Enterococcus faecalis</i> . Antimicrobial Agents and Chemotherapy, 1999, 43, 141-147.	3.2	58
67	High occurrence of esp among ampicillin-resistant and vancomycin-susceptible Enterococcus faecium clones from hospitalized patients. Journal of Antimicrobial Chemotherapy, 2002, 50, 1035-1038.	3.0	56
68	Microevolutionary Events Involving Narrow Host Plasmids Influences Local Fixation of Vancomycin-Resistance in Enterococcus Populations. PLoS ONE, 2013, 8, e60589.	2.5	56
69	The Origin of Niches and Species in the Bacterial World. Frontiers in Microbiology, 2021, 12, 657986.	3.5	56
70	Host range of enterococcal vanA plasmids among Gram-positive intestinal bacteria. Journal of Antimicrobial Chemotherapy, 2011, 66, 273-282.	3.0	55
71	Large clonal outbreak of multidrug-resistant CC17 ST17 Enterococcus faecium containing Tn5382 in a Spanish hospital. Journal of Antimicrobial Chemotherapy, 2009, 63, 17-20.	3.0	54
72	High diversity of extended-spectrum Â-lactamases among clinical isolates of Enterobacteriaceae from Portugal. Journal of Antimicrobial Chemotherapy, 2007, 60, 1370-1374.	3.0	53

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73	In Vitro Activities of Two Ketolides, HMR 3647 and HMR 3004, against Gram-Positive Bacteria. Antimicrobial Agents and Chemotherapy, 1999, 43, 930-936.	3.2	52
74	Dispersion of Multidrug-Resistant <i>Enterococcus faecium</i> Isolates Belonging to Major Clonal Complexes in Different Portuguese Settings. Applied and Environmental Microbiology, 2009, 75, 4904-4908.	3.1	52
75	Diversity and Evolution of the Tn <i>5801-tet</i> (M)-Like Integrative and Conjugative Elements among Enterococcus, Streptococcus, and Staphylococcus. Antimicrobial Agents and Chemotherapy, 2016, 60, 1736-1746.	3.2	51
76	Long-term clonal dynamics of <i>Enterococcus faecium</i> strains causing bloodstream infections (1995–2015) in Spain. Journal of Antimicrobial Chemotherapy, 2017, 72, 48-55.	3.0	51
77	Complex molecular epidemiology of extended-spectrum -lactamases in Klebsiella pneumoniae: a long-term perspective from a single institution in Madrid. Journal of Antimicrobial Chemotherapy, 2007, 61, 64-72.	3.0	50
78	Ecogenetics of antibiotic resistance in <i>Listeria monocytogenes</i> . Molecular Microbiology, 2020, 113, 570-579.	2.5	50
79	High-Level Resistance to Aminoglycosides: Comparison of Community and Nosocomial Fecal Isolates of Enterococci. Clinical Infectious Diseases, 1995, 20, 1048-1051.	5.8	49
80	Characterization of Globally Spread Escherichia coli ST131 Isolates (1991 to 2010). Antimicrobial Agents and Chemotherapy, 2012, 56, 3973-3976.	3.2	49
81	Multiclonal dispersal of KPC genes following the emergence of non-ST258 KPC-producing Klebsiella pneumoniae clones in Madrid, Spain. Journal of Antimicrobial Chemotherapy, 2013, 68, 2487-2492.	3.0	48
82	AcCNET (<u>Ac</u> cessory Genome <u>C</u> onstellation <u>Net</u> work): comparative genomics software for accessory genome analysis using bipartite networks. Bioinformatics, 2017, 33, 283-285.	4.1	48
83	Association of Composite IS <i>26-sul3</i> Elements with Highly Transmissible Incl1 Plasmids in Extended-Spectrum-Î2-Lactamase-Producing Escherichia coli Clones from Humans. Antimicrobial Agents and Chemotherapy, 2011, 55, 2451-2457.	3.2	47
84	Public health evolutionary biology of antimicrobial resistance: priorities for intervention. Evolutionary Applications, 2015, 8, 223-239.	3.1	47
85	Group B Streptococcus: A Cause of Urinary Tract Infection in Nonpregnant Adults. Clinical Infectious Diseases, 1992, 14, 492-496.	5.8	45
86	Prioritizing risks of antibiotic resistance genes in all metagenomes. Nature Reviews Microbiology, 2015, 13, 396-396.	28.6	45
87	Genomic and metagenomic technologies to explore the antibiotic resistance mobilome. Annals of the New York Academy of Sciences, 2017, 1388, 26-41.	3.8	43
88	Preservation of Integron Types among <i>Enterobacteriaceae</i> Producing Extended-Spectrum β-Lactamases in a Spanish Hospital over a 15-Year Period (1988 to 2003). Antimicrobial Agents and Chemotherapy, 2007, 51, 2201-2204.	3.2	42
89	International Spread and Persistence of TEM-24 Is Caused by the Confluence of Highly Penetrating <i>Enterobacteriaceae</i> Clones and an IncA/C ₂ Plasmid Containing Tn <i>1696</i> ::Tn <i>1</i> and IS <i>5075</i> -Tn <i>21</i> . Antimicrobial Agents and Chemotherapy, 2010, 54, 825-834.	3.2	41
90	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. Antimicrobial Agents and Chemotherapy, 2015, 59, 3413-3423.	3.2	41

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91	Mutational Events in Cefotaximase Extended-Spectrum β-Lactamases of the CTX-M-1 Cluster Involved in Ceftazidime Resistance. Antimicrobial Agents and Chemotherapy, 2008, 52, 2377-2382.	3.2	40
92	Dissemination of Novel Antimicrobial Resistance Mechanisms through the Insertion Sequence Mediated Spread of Metabolic Genes. Frontiers in Microbiology, 2016, 7, 1008.	3.5	40
93	Distribution of putative virulence markers in Enterococcus faecium: towards a safety profile review. Journal of Antimicrobial Chemotherapy, 2018, 73, 306-319.	3.0	40
94	Multiple adaptive routes of Salmonella enterica Typhimurium to biocide and antibiotic exposure. BMC Genomics, 2016, 17, 491.	2.8	39
95	Comparative in-vitro activity of the new fluoroquinolone trovafloxacin (CP-99,219) against Gram-positive cocci. Journal of Antimicrobial Chemotherapy, 1996, 37, 1011-1016.	3.0	37
96	Increased Mutation Frequencies in Escherichia coli Isolates Harboring Extended-Spectrum β-Lactamases. Antimicrobial Agents and Chemotherapy, 2005, 49, 4754-4756.	3.2	37
97	Multilevel population genetics in antibiotic resistance. FEMS Microbiology Reviews, 2011, 35, 705-706.	8.6	37
98	Allodemics. Lancet Infectious Diseases, The, 2002, 2, 591-592.	9.1	36
99	Local Genetic Patterns within a Vancomycin-Resistant Enterococcus faecalis Clone Isolated in Three Hospitals in Portugal. Antimicrobial Agents and Chemotherapy, 2004, 48, 3613-3617.	3.2	35
100	Diversity and biofilm-production ability among isolates of Escherichia coli phylogroup D belonging to ST69, ST393 and ST405 clonal groups. BMC Microbiology, 2013, 13, 144.	3.3	35
101	Significant Differences Characterise the Correlation Coefficients between Biocide and Antibiotic Susceptibility Profiles in Staphylococcus aureus. Current Pharmaceutical Design, 2015, 21, 2054-2057.	1.9	35
102	Sequencing of plasmids pAMBL1 and pAMBL2 from <i>Pseudomonas aeruginosa</i> reveals a <i>bla</i> _{VIM-1} amplification causing high-level carbapenem resistance. Journal of Antimicrobial Chemotherapy, 2015, 70, 3000-3003.	3.0	35
103	Antimicrobial resistance among faecal enterococci from healthy individuals in Portugal. Clinical Microbiology and Infection, 2006, 12, 1131-1134.	6.0	34
104	In117, an Unusual In0-Like Class 1 Integron Containing CR1 and bla CTX-M-2 and Associated with a Tn 21 -Like Element. Antimicrobial Agents and Chemotherapy, 2006, 50, 799-802.	3.2	34
105	Co-diversification of Enterococcus faecium Core Genomes and PBP5: Evidences of pbp5 Horizontal Transfer. Frontiers in Microbiology, 2016, 7, 1581.	3.5	34
106	Assessment of prevalence and changing epidemiology of extended-spectrum β-lactamase–producing Enterobacteriaceae fecal carriers using a chromogenic medium. Diagnostic Microbiology and Infectious Disease, 2010, 67, 376-379.	1.8	32
107	Clonal outbreak of ST17 multidrug-resistant Enterococcus faecium harbouring an Inc18-like::Tn1546 plasmid in a haemo-oncology ward of a Spanish hospital. Journal of Antimicrobial Chemotherapy, 2012, 67, 832-836.	3.0	32
108	The challenges of designing a benchmark strategy for bioinformatics pipelines in the identification of antimicrobial resistance determinants using next generation sequencing technologies. F1000Research, 2018, 7, 459.	1.6	31

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109	Identification of Enterococcus faecalis strains by DNA hybridization and pulsed-field gel electrophoresis. Journal of Clinical Microbiology, 1995, 33, 3368-3369.	3.9	30
110	Commensal Enterobacteriaceae as reservoirs of extended-spectrum beta-lactamases, integrons, and sul genes in Portugal. Frontiers in Microbiology, 2013, 4, 80.	3.5	29
111	Water supply and feed as sources of antimicrobial-resistant Enterococcus spp. in aquacultures of rainbow trout (Oncorhyncus mykiss), Portugal. Science of the Total Environment, 2018, 625, 1102-1112.	8.0	29
112	Recurrent group B streptococcal disease in infants: Who should receive rifampin?. Journal of Pediatrics, 1998, 132, 537-539.	1.8	28
113	Risk factors associated with ampicillin resistance in patients with bacteraemia caused by Enterococcus faecium. Journal of Antimicrobial Chemotherapy, 2002, 50, 1003-1009.	3.0	28
114	First Report of Vancomycinâ€Resistant Enterococcus faecium Isolated in Argentina. Clinical Infectious Diseases, 1998, 26, 235-236.	5.8	27
115	Contribution of IncFII and Broad-Host IncA/C and IncN Plasmids to the Local Expansion and Diversification of Phylogroup B2 Escherichia coli ST131 Clones Carrying <i>bla</i> _{CTX-M-15} and <i>qnrS1</i> Genes. Antimicrobial Agents and Chemotherapy, 2012, 56, 2763-2766.	3.2	27
116	Widening the Spaces of Selection: Evolution along Sublethal Antimicrobial Gradients. MBio, 2014, 5, e02270.	4.1	27
117	Enterococcus spp. in Ragusano PDO and Pecorino Siciliano cheese types: A snapshot of their antibiotic resistance distribution. Food and Chemical Toxicology, 2018, 120, 277-286.	3.6	27
118	Leakage into Portuguese aquatic environments of extended-spectrum-Â-lactamase-producing Enterobacteriaceae. Journal of Antimicrobial Chemotherapy, 2009, 63, 616-618.	3.0	26
119	In vitro activity of the trinem sanfetrinem (GV104326) against gram-positive organisms. Antimicrobial Agents and Chemotherapy, 1996, 40, 2142-2146.	3.2	24
120	Molecular Characterization of Glycopeptide-Resistant Enterococcus faecium Isolates from Portuguese Hospitals. Antimicrobial Agents and Chemotherapy, 2005, 49, 3073-3079.	3.2	24
121	Genetic and phenotypic differences among Enterococcus faecalis clones from intestinal colonisation and invasive disease. Clinical Microbiology and Infection, 2006, 12, 1193-1198.	6.0	24
122	The challenges of designing a benchmark strategy for bioinformatics pipelines in the identification of antimicrobial resistance determinants using next generation sequencing technologies. F1000Research, 2018, 7, 459.	1.6	24
123	Non-susceptibility to tigecycline in enterococci from hospitalised patients, food products and community sources. International Journal of Antimicrobial Agents, 2011, 38, 174-176.	2.5	23
124	A 21-Year Survey of Escherichia coli from Bloodstream Infections (BSI) in a Tertiary Hospital Reveals How Community-Hospital Dynamics of B2 Phylogroup Clones Influence Local BSI Rates. MSphere, 2021, 6, e0086821.	2.9	23
125	Emergence of an Incl plasmid encoding CMY-2 Â-lactamase associated with the international ST19 OXA-30-producing Â-lactamase Salmonella Typhimurium multidrug-resistant clone. Journal of Antimicrobial Chemotherapy, 2010, 65, 2097-2100.	3.0	22
126	High-density fecal Enterococcus faecium colonization in hospitalized patients is associated with the presence of the polyclonal subcluster CC17. European Journal of Clinical Microbiology and Infectious Diseases, 2012, 31, 519-522.	2.9	22

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127	Counteracting antibiotic resistance: breaking barriers among antibacterial strategies. Expert Opinion on Therapeutic Targets, 2014, 18, 851-861.	3.4	22
128	Population Analysis and Epidemiological Features of Inhibitor-Resistant-TEM-β-Lactamase-Producing <i>Escherichia coli</i> Isolates from both Community and Hospital Settings in Madrid, Spain. Journal of Clinical Microbiology, 2010, 48, 2368-2372.	3.9	21
129	A membrane computing simulator of trans-hierarchical antibiotic resistance evolution dynamics in nested ecological compartments (ARES). Biology Direct, 2015, 10, 41.	4.6	21
130	Fitness Costs of Plasmids: A Limit to Plasmid Transmission. , 0, , 65-79.		18
131	Validation of the VITEK2 and the advance expert system with a collection of enterobacteriaceae harboring extended spectrum or inhibitor resistant β-lactamases. Diagnostic Microbiology and Infectious Disease, 2001, 41, 65-70.	1.8	17
132	Emergence of CTX-M β-lactamase-producing Enterobacteriaceae in Portugal: report of an Escherichia coli isolate harbouring blaCTX-M-14. Clinical Microbiology and Infection, 2004, 10, 755-757.	6.0	17
133	The interplay between community and hospital Enterococcus faecium clones within health-care settings: a genomic analysis. Lancet Microbe, The, 2022, 3, e133-e141.	7.3	17
134	First Report of an OXA-48- and CTX-M-213-Producing Kluyvera Species Clone Recovered from Patients Admitted in a University Hospital in Madrid, Spain. Antimicrobial Agents and Chemotherapy, 2018, 62, .	3.2	16
135	Vancomycin-resistant <i>Enterococcus faecium</i> Clone in Swine, Europe. Emerging Infectious Diseases, 2005, 11, 1985-1987.	4.3	15
136	Different Genetic Supports for the <i>tet</i> (S) Gene in Enterococci. Antimicrobial Agents and Chemotherapy, 2012, 56, 6014-6018.	3.2	15
137	Early OXA-48-Producing <i>Enterobacterales</i> Isolates Recovered in a Spanish Hospital Reveal a Complex Introduction Dominated by Sequence Type 11 (ST11) and ST405 Klebsiella pneumoniae Clones. MSphere, 2020, 5, .	2.9	15
138	Allogenous Selection of Mutational Collateral Resistance: Old Drugs Select for New Resistance Within Antibiotic Families. Frontiers in Microbiology, 2021, 12, 757833.	3.5	15
139	Rapid detection of high-risk Enterococcus faecium clones by matrix-assisted laser desorption ionization time-of-flight mass spectrometry. Diagnostic Microbiology and Infectious Disease, 2017, 87, 299-307.	1.8	14
140	Phylogenomics of <i>Enterococcus faecalis</i> from wild birds: new insights into hostâ€associated differences in core and accessory genomes of the species. Environmental Microbiology, 2019, 21, 3046-3062.	3.8	14
141	Application of Molecular Techniques to the Study of Nosocomial Infections Caused by Enterococci. , 1998, 15, 469-494.		13
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