Teresa M Coque

List of Publications by Year in descending order

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21540 19657 114 14,663 181 61 citations h-index g-index papers 197 197 197 11039 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	PLASmid TAXonomic PCR (PlasTax-PCR), a Multiplex Relaxase MOB Typing to Assort Plasmids into Taxonomic Units. Methods in Molecular Biology, 2022, 2392, 127-142.	0.9	2
2	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
3	Evolution of Chlorhexidine Susceptibility and of the EfrEF Operon among Enterococcus faecalis from Diverse Environments, Clones, and Time Spans. Microbiology Spectrum, 2022, 10, .	3.0	O
4	Apparent nosocomial adaptation of Enterococcus faecalis predates the modern hospital era. Nature Communications, 2021, 12, 1523.	12.8	69
5	The Origin of Niches and Species in the Bacterial World. Frontiers in Microbiology, 2021, 12, 657986.	3.5	56
6	Fitness cost of vancomycin-resistant <i>Enterococcus faecium</i> plasmids associated with hospital infection outbreaks. Journal of Antimicrobial Chemotherapy, 2021, 76, 2757-2764.	3.0	6
7	Diversity of metal and antibiotic resistance genes in Enterococcus spp. from the last century reflects multiple pollution and genetic exchange among phyla from overlapping ecosystems. Science of the Total Environment, 2021, 787, 147548.	8.0	13
8	Allogenous Selection of Mutational Collateral Resistance: Old Drugs Select for New Resistance Within Antibiotic Families. Frontiers in Microbiology, 2021, 12, 757833.	3.5	15
9	PATO: Pangenome Analysis Toolkit. Bioinformatics, 2021, 37, 4564-4566.	4.1	9
10	Altered Ecology of the Respiratory Tract Microbiome and Nosocomial Pneumonia. Frontiers in Microbiology, 2021, 12, 709421.	3.5	9
11	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
12	Comment on: Emergence of plasmid-mediated oxazolidinone resistance gene poxtA from CC17 Enterococcus faecium of pig origin. Journal of Antimicrobial Chemotherapy, 2020, 75, 1358-1359.	3.0	1
13	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
14	Simulating the Influence of Conjugative-Plasmid Kinetic Values on the Multilevel Dynamics of Antimicrobial Resistance in a Membrane Computing Model. Antimicrobial Agents and Chemotherapy, 2020, 64, .	3.2	11
15	Ecogenetics of antibiotic resistance in <i>Listeria monocytogenes</i> . Molecular Microbiology, 2020, 113, 570-579.	2.5	50
16	Detection of \hat{l}^2 -Lactamase-Producing Enterococcus faecalis and Vancomycin-Resistant Enterococcus faecium Isolates in Human Invasive Infections in the Public Hospital of Tandil, Argentina. Pathogens, 2020, 9, 142.	2.8	9
17	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
18	Statistical Analysis of Accessory Genome. Methods in Molecular Biology, 2020, 2075, 341-353.	0.9	6

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19	Isolation and Visualization of Plasmids from Gram-Positive Bacteria of Interest in Public Health. Methods in Molecular Biology, 2020, 2075, 21-38.	0.9	3
20	Methods to Quantify DNA Transfer in Enterococcus. Methods in Molecular Biology, 2020, 2075, 111-122.	0.9	0
21	Defining and combating antibiotic resistance from One Health and Global Health perspectives. Nature Microbiology, 2019, 4, 1432-1442.	13.3	614
22	2CS-CHX ^T Operon Signature of Chlorhexidine Tolerance among Enterococcus faecium Isolates. Applied and Environmental Microbiology, 2019, 85, .	3.1	10
23	Transfer dynamics of Tn6648, a composite integrative conjugative element generated by tandem accretion of Tn5801 and Tn6647 in Enterococcus faecalis. Journal of Antimicrobial Chemotherapy, 2019, 74, 2517-2523.	3.0	8
24	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
25	Transmission in the Origins of Bacterial Diversity, From Ecotypes to Phyla. , 2019, , 311-343.		4
26	Causality in Biological Transmission: Forces and Energies. , 2019, , 15-31.		2
27	Selection and Transmission of Antibiotic-Resistant Bacteria. , 2019, , 117-137.		2
28	Ecology and Evolution of Chromosomal Gene Transfer between Environmental Microorganisms and Pathogens., 2019,, 139-160.		1
29	Food-to-Humans Bacterial Transmission. , 2019, , 161-193.		3
30	Natural and Artificial Strategies to Control the Conjugative Transmission of Plasmids. , 2019, , 33-64.		0
31	Gene Transmission in the One Health Microbiosphere and the Channels of Antimicrobial Resistance. Frontiers in Microbiology, 2019, 10, 2892.	3.5	66
32	Prediction of the intestinal resistome by a three-dimensional structure-based method. Nature Microbiology, 2019, 4, 112-123.	13.3	129
33	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
34	Distribution of putative virulence markers in Enterococcus faecium: towards a safety profile review. Journal of Antimicrobial Chemotherapy, 2018, 73, 306-319.	3.0	40
35	High rates of colonisation by ampicillin-resistant enterococci in residents of long-term care facilities in Porto, Portugal. International Journal of Antimicrobial Agents, 2018, 51, 503-507.	2.5	11
36	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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37	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
38	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
39	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
40	Antimicrobial Resistance in <i>Enterococcus</i> spp. of animal origin. Microbiology Spectrum, 2018, 6, .	3.0	147
41	In-depth resistome analysis by targeted metagenomics. Microbiome, 2018, 6, 11.	11.1	115
42	Wild corvid birds colonized with vancomycin-resistant Enterococcus faecium of human origin harbor epidemic vanA plasmids. Environment International, 2018, 118, 125-133.	10.0	13
43	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
44	Complete Genome Sequences of Isolates of Enterococcus faecium Sequence Type 117, a Globally Disseminated Multidrug-Resistant Clone. Genome Announcements, 2017, 5, .	0.8	12
45	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
46	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
47	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
48	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
49	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
50	Global Emergence and Dissemination of Enterococci as Nosocomial Pathogens: Attack of the Clones?. Frontiers in Microbiology, 2016, 7, 788.	3 . 5	248
51	Dissemination of Novel Antimicrobial Resistance Mechanisms through the Insertion Sequence Mediated Spread of Metabolic Genes. Frontiers in Microbiology, 2016, 7, 1008.	3 . 5	40
52	Co-diversification of Enterococcus faecium Core Genomes and PBP5: Evidences of pbp5 Horizontal Transfer. Frontiers in Microbiology, 2016, 7, 1581.	3.5	34
53	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
54	Multiple adaptive routes of Salmonella enterica Typhimurium to biocide and antibiotic exposure. BMC Genomics, 2016, 17, 491.	2.8	39

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55	The impact of host metapopulation structure on the population genetics of colonizing bacteria. Journal of Theoretical Biology, 2016, 396, 53-62.	1.7	13
56	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
57	Relevance of <i>tcrYAZB </i> operon acquisition for <i>Enterococcus </i> survival at high copper concentrations under anaerobic conditions: TableÂ1 Journal of Antimicrobial Chemotherapy, 2016, 71, 560-563.	3.0	10
58	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
59	A membrane computing simulator of trans-hierarchical antibiotic resistance evolution dynamics in nested ecological compartments (ARES). Biology Direct, 2015, 10, 41.	4.6	21
60	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
61	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
62	Antibiotic-Resistant Klebsiella pneumoniae and Escherichia coli High-Risk Clones and an IncFII $\langle \text{sub} \rangle \text{k} \langle \text{sub} \rangle$ Mosaic Plasmid Hosting Tn $\langle \text{i} \rangle \text{l} \langle \text{i} \rangle \text{la} \langle \text{i} \rangle \langle \text{sub} \rangle \text{TEM-4} \langle \text{sub} \rangle$) in Isolates from 1990 to 2004. Antimicrobial Agents and Chemotherapy, 2015, 59, 2904-2908.	3.2	9
63	Sequencing of plasmids pAMBL1 and pAMBL2 from (i>Pseudomonas aeruginosa $<$ i>reveals a $<$ i>bla $<$ ii> $<$ sub $>$ VIM-1 $<$ sub $>$ amplification causing high-level carbapenem resistance. Journal of Antimicrobial Chemotherapy, 2015, 70, 3000-3003.	3.0	35
64	Prioritizing risks of antibiotic resistance genes in all metagenomes. Nature Reviews Microbiology, 2015, 13, 396-396.	28.6	45
65	A hospital sewage ST17 Enterococcus faecium with a transferable Inc18-like plasmid carrying genes coding for resistance to antibiotics and quaternary ammonium compounds (qacZ). Journal of Global Antimicrobial Resistance, 2015, 3, 49-51.	2.2	9
66	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
67	Investigating the mobilome in clinically important lineages of Enterococcus faecium and Enterococcus faecalis. BMC Genomics, 2015, 16, 282.	2.8	82
68	Public health evolutionary biology of antimicrobial resistance: priorities for intervention. Evolutionary Applications, 2015, 8, 223-239.	3.1	47
69	What is a resistance gene? Ranking risk in resistomes. Nature Reviews Microbiology, 2015, 13, 116-123.	28.6	698
70	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
71	Widening the Spaces of Selection: Evolution along Sublethal Antimicrobial Gradients. MBio, 2014, 5, e02270.	4.1	27
72	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

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73	Counteracting antibiotic resistance: breaking barriers among antibacterial strategies. Expert Opinion on Therapeutic Targets, 2014, 18, 851-861.	3.4	22
74	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
75	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
76	Antibiotic resistant enterococciâ€"Tales of a drug resistance gene trafficker. International Journal of Medical Microbiology, 2013, 303, 360-379.	3.6	139
77	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
78	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
79	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
80	Antibiotic resistance shaping multi-level population biology of bacteria. Frontiers in Microbiology, 2013, 4, 15.	3.5	153
81	Microevolutionary Events Involving Narrow Host Plasmids Influences Local Fixation of Vancomycin-Resistance in Enterococcus Populations. PLoS ONE, 2013, 8, e60589.	2.5	56
82	Commensal Enterobacteriaceae as reservoirs of extended-spectrum beta-lactamases, integrons, and sul genes in Portugal. Frontiers in Microbiology, 2013, 4, 80.	3.5	29
83	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
84	Reply to "Expansion of Clonal Complex 258 KPC-2-Producing Klebsiella pneumoniae in Latin American Hospitals: Report of the SENTRY Antimicrobial Surveillance Program― Antimicrobial Agents and Chemotherapy, 2012, 56, 1670-1671.	3.2	5
85	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
86	Characterization of Globally Spread Escherichia coli ST131 Isolates (1991 to 2010). Antimicrobial Agents and Chemotherapy, 2012, 56, 3973-3976.	3.2	49
87	Reply to "Clonal Complex 258, the Most Frequently Found Multilocus Sequence Type Complex in KPC-2-Producing Klebsiella pneumoniae Isolated in Brazilian Hospitals― Antimicrobial Agents and Chemotherapy, 2012, 56, 4565-4565.	3.2	1
88	Different Genetic Supports for the <i>tet</i> (S) Gene in Enterococci. Antimicrobial Agents and Chemotherapy, 2012, 56, 6014-6018.	3.2	15
89	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
90	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

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91	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
92	A tet(S/M) hybrid from CTn6000 and CTn916 recombination. Microbiology (United Kingdom), 2012, 158, 2710-2711.	1.8	8
93	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
94	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
95	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
96	Multilevel population genetics in antibiotic resistance. FEMS Microbiology Reviews, 2011, 35, 705-706.	8.6	37
97	Human and Swine Hosts Share Vancomycin-Resistant Enterococcus faecium CC17 and CC5 and Enterococcus faecalis CC2 Clonal Clusters Harboring Tn $\langle i \rangle 1546 \langle j \rangle$ on Indistinguishable Plasmids. Journal of Clinical Microbiology, 2011, 49, 925-931.	3.9	126
98	Host range of enterococcal vanA plasmids among Gram-positive intestinal bacteria. Journal of Antimicrobial Chemotherapy, 2011, 66, 273-282.	3.0	55
99	Association of Composite IS <i>26-sul3</i> Elements with Highly Transmissible Incl1 Plasmids in Extended-Spectrum-β-Lactamase-Producing Escherichia coli Clones from Humans. Antimicrobial Agents and Chemotherapy, 2011, 55, 2451-2457.	3.2	47
100	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
101	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
102	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
103	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
104	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
105	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
106	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
107	Evolutionary Trajectories of Beta-Lactamase CTX-M-1 Cluster Enzymes: Predicting Antibiotic Resistance. PLoS Pathogens, 2010, 6, e1000735.	4.7	100
108	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

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109	Assessment of prevalence and changing epidemiology of extended-spectrum \hat{l}^2 -lactamase \hat{a} producing Enterobacteriaceae fecal carriers using a chromogenic medium. Diagnostic Microbiology and Infectious Disease, 2010, 67, 376-379.	1.8	32
110	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
111	Leakage into Portuguese aquatic environments of extended-spectrum-Â-lactamase-producing Enterobacteriaceae. Journal of Antimicrobial Chemotherapy, 2009, 63, 616-618.	3.0	26
112	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
113	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
114	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
115	Longer Intestinal Persistence of Enterococcus faecalis Compared to Enterococcus faecium Clones in Intensive-Care-Unit Patients. Journal of Clinical Microbiology, 2009, 47, 345-351.	3.9	13
116	Extended-spectrum \hat{I}^2 -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
117	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
118	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
119	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
120	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
121	High Rate of Intestinal Colonization with Extended-Spectrum-Î ² -Lactamase-Producing Organisms in Household Contacts of Infected Community Patients. Journal of Clinical Microbiology, 2008, 46, 2796-2799.	3.9	157
122	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
123	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
124	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
125	Preservation of Integron Types among <i>Enterobacteriaceae</i> Producing Extended-Spectrum \hat{l}^2 -Lactamases in a Spanish Hospital over a 15-Year Period (1988 to 2003). Antimicrobial Agents and Chemotherapy, 2007, 51, 2201-2204.	3.2	42
126	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

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127	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
128	Clinical variables associated with the isolation of Klebsiella pneumoniae expressing different extended-spectrum \hat{I}^2 -lactamases. Clinical Microbiology and Infection, 2007, 13, 532-538.	6.0	11
129	CTX-M: changing the face of ESBLs in Europe. Journal of Antimicrobial Chemotherapy, 2006, 59, 165-174.	3.0	756
130	The CTX-M β-lactamase pandemic. Current Opinion in Microbiology, 2006, 9, 466-475.	5.1	982
131	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
132	Antimicrobial resistance among faecal enterococci from healthy individuals in Portugal. Clinical Microbiology and Infection, 2006, 12, 1131-1134.	6.0	34
133	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
134	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
135	Antibiotic Coresistance in Extended-Spectrum-β-Lactamase-Producing <i>Enterobacteriaceae</i> Vitro Activity of Tigecycline. Antimicrobial Agents and Chemotherapy, 2006, 50, 2695-2699.	3.2	145
136	Dissemination in Portugal of CTX-M-15-, OXA-1-, and TEM-1-Producing Enterobacteriaceae Strains Containing the aac(6 $\hat{a} \in 2$)-lb-cr Gene, Which Encodes an Aminoglycoside- and Fluoroquinolone-Modifying Enzyme. Antimicrobial Agents and Chemotherapy, 2006, 50, 3220-3221.	3.2	95
137	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
138	Vancomycin-resistant <i>Enterococcus faecium</i> Clone in Swine, Europe. Emerging Infectious Diseases, 2005, 11, 1985-1987.	4.3	15
139	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
140	Environmental Contamination with Vancomycin-Resistant Enterococci from Hospital Sewage in Portugal. Applied and Environmental Microbiology, 2005, 71, 3364-3368.	3.1	85
141	Increased Mutation Frequencies in Escherichia coli Isolates Harboring Extended-Spectrum β-Lactamases. Antimicrobial Agents and Chemotherapy, 2005, 49, 4754-4756.	3.2	37
142	Molecular Characterization of Glycopeptide-Resistant Enterococcus faecium Isolates from Portuguese Hospitals. Antimicrobial Agents and Chemotherapy, 2005, 49, 3073-3079.	3.2	24
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