

# Erick Denamur

## List of Publications by Year in descending order

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138  
papers

14,328  
citations

28274

55  
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21540

114  
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155  
all docs

155  
docs citations

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times ranked

10766  
citing authors

#	ARTICLE	IF	CITATIONS
1	The <i>C</i> ermont <i>E</i> scherichia coli phylo-typing method revisited: improvement of specificity and detection of new phylo-groups. Environmental Microbiology Reports, 2013, 5, 58-65.	2.4	1,360
2	The population genetics of commensal Escherichia coli. Nature Reviews Microbiology, 2010, 8, 207-217.	28.6	1,104
3	Organised Genome Dynamics in the Escherichia coli Species Results in Highly Diverse Adaptive Paths. PLoS Genetics, 2009, 5, e1000344.	3.5	1,005
4	The Link between Phylogeny and Virulence in <i>Escherichia coli</i> Extraintestinal Infection. Infection and Immunity, 1999, 67, 546-553.	2.2	690
5	Stress-Induced Mutagenesis in Bacteria. Science, 2003, 300, 1404-1409.	12.6	508
6	Rapid detection of the O25b-ST131 clone of Escherichia coli encompassing the CTX-M-15-producing strains. Journal of Antimicrobial Chemotherapy, 2009, 64, 274-277.	3.0	328
7	Evolution of mutation rates in bacteria. Molecular Microbiology, 2006, 60, 820-827.	2.5	319
8	ClermonTyping: an easy-to-use and accurate in silico method for Escherichia genus strain phylotyping. Microbial Genomics, 2018, 4, .	2.0	307
9	A Specific Genetic Background Is Required for Acquisition and Expression of Virulence Factors in Escherichia coli. Molecular Biology and Evolution, 2004, 21, 1085-1094.	8.9	304
10	Phylogenetic and genomic diversity of human bacteremic Escherichia coli strains. BMC Genomics, 2008, 9, 560.	2.8	297
11	The population genetics of pathogenic Escherichia coli. Nature Reviews Microbiology, 2021, 19, 37-54.	28.6	268
12	Commensal Escherichia coli isolates are phylogenetically distributed among geographically distinct human populations. Microbiology (United Kingdom), 2001, 147, 1671-1676.	1.8	267
13	The CTX-M-15-producing Escherichia coli diffusing clone belongs to a highly virulent B2 phylogenetic subgroup. Journal of Antimicrobial Chemotherapy, 2008, 61, 1024-1028.	3.0	261
14	Assigning <i>Escherichia coli</i> strains to phylogenetic groups: multi-locus sequence typing versus the PCR triplex method. Environmental Microbiology, 2008, 10, 2484-2496.	3.8	253
15	Evolutionary Implications of the Frequent Horizontal Transfer of Mismatch Repair Genes. Cell, 2000, 103, 711-721.	28.9	246
16	Extraintestinal Virulence Is a Coincidental By-Product of Commensalism in B2 Phylogenetic Group Escherichia coli Strains. Molecular Biology and Evolution, 2007, 24, 2373-2384.	8.9	225
17	The enemy within us: lessons from the 2011 European <i>Escherichia coli</i> O104:H4 outbreak. EMBO Molecular Medicine, 2012, 4, 841-848.	6.9	215
18	Large-Scale Population Structure of Human Commensal Escherichia coli Isolates. Applied and Environmental Microbiology, 2004, 70, 5698-5700.	3.1	204

#	ARTICLE	IF	CITATIONS
19	Identification of forces shaping the commensal <i>Escherichia coli</i> genetic structure by comparing animal and human isolates. <i>Environmental Microbiology</i> , 2006, 8, 1975-1984.	3.8	201
20	Effect of human vicinity on antimicrobial resistance and integrons in animal faecal <i>Escherichia coli</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2006, 57, 1215-1219.	3.0	189
21	Animal and human pathogenic <i>Escherichia coli</i> strains share common genetic backgrounds. <i>Infection, Genetics and Evolution</i> , 2011, 11, 654-662.	2.3	169
22	High Frequency of Mutator Strains among Human Uropathogenic <i>Escherichia coli</i> Isolates. <i>Journal of Bacteriology</i> , 2002, 184, 605-609.	2.2	157
23	Genetic Background of <i>Escherichia coli</i> and Extended-spectrum $\beta$ -Lactamase Type. <i>Emerging Infectious Diseases</i> , 2005, 11, 54-61.	4.3	155
24	Characterization and rapid identification of phylogroup G in <i>Escherichia coli</i> , a lineage with high virulence and antibiotic resistance potential. <i>Environmental Microbiology</i> , 2019, 21, 3107-3117.	3.8	152
25	Experimental Mouse Lethality of <i>Escherichia coli</i> isolates, in Relation to Accessory Traits, Phylogenetic Group, and Ecological Source. <i>Journal of Infectious Diseases</i> , 2006, 194, 1141-1150.	4.0	146
26	CRISPR Distribution within the <i>Escherichia coli</i> Species Is Not Suggestive of Immunity-Associated Diversifying Selection. <i>Journal of Bacteriology</i> , 2011, 193, 2460-2467.	2.2	139
27	Guide to the various phylogenetic classification schemes for <i>Escherichia coli</i> and the correspondence among schemes. <i>Microbiology (United Kingdom)</i> , 2015, 161, 980-988.	1.8	139
28	Phylogenetic background and habitat drive the genetic diversification of <i>Escherichia coli</i> . <i>PLoS Genetics</i> , 2020, 16, e1008866.	3.5	131
29	<i>Yersinia</i> High-Pathogenicity Island Contributes to Virulence in <i>Escherichia coli</i> Causing Extraintestinal Infections. <i>Infection and Immunity</i> , 2002, 70, 5335-5337.	2.2	128
30	Host Factors and Portal of Entry Outweigh Bacterial Determinants To Predict the Severity of <i>Escherichia coli</i> Bacteremia. <i>Journal of Clinical Microbiology</i> , 2011, 49, 777-783.	3.9	123
31	The Plasmid of <i>Escherichia coli</i> Strain S88 (O45:K1:H7) That Causes Neonatal Meningitis Is Closely Related to Avian Pathogenic <i>E. coli</i> Plasmids and Is Associated with High-Level Bacteremia in a Neonatal Rat Meningitis Model. <i>Infection and Immunity</i> , 2009, 77, 2272-2284.	2.2	119
32	Integron-Associated Antibiotic Resistance and Phylogenetic Grouping of <i>Escherichia coli</i> Isolates from Healthy Subjects Free of Recent Antibiotic Exposure. <i>Antimicrobial Agents and Chemotherapy</i> , 2005, 49, 3062-3065.	3.2	115
33	Determination of <i>Escherichia coli</i> O types by allele-specific polymerase chain reaction: application to the O types involved in human septicemia. <i>Diagnostic Microbiology and Infectious Disease</i> , 2007, 57, 129-136.	1.8	115
34	From Grazing Resistance to Pathogenesis: The Coincidental Evolution of Virulence Factors. <i>PLoS ONE</i> , 2010, 5, e11882.	2.5	114
35	Rapid and Specific Detection, Molecular Epidemiology, and Experimental Virulence of the O16 Subgroup within <i>Escherichia coli</i> Sequence Type 131. <i>Journal of Clinical Microbiology</i> , 2014, 52, 1358-1365.	3.9	107
36	Pathogenicity-Associated Islands in Extraintestinal Pathogenic <i>Escherichia coli</i> Are Fitness Elements Involved in Intestinal Colonization. <i>Journal of Bacteriology</i> , 2010, 192, 4885-4893.	2.2	105

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37	Characterization of the cryptic <i>Escherichia</i> lineages: rapid identification and prevalence. <i>Environmental Microbiology</i> , 2011, 13, 2468-2477.	3.8	103
38	Meningitis Caused by <i>Escherichia coli</i> Producing TEM-52 Extended-Spectrum $\beta$ -Lactamase within an Extensive Outbreak in a Neonatal Ward: Epidemiological Investigation and Characterization of the Strain. <i>Journal of Clinical Microbiology</i> , 2010, 48, 2459-2463.	3.9	102
39	Virulence of <i>Escherichia coli</i> Clinical Isolates in a Murine Sepsis Model in Relation to Sequence Type ST131 Status, Fluoroquinolone Resistance, and Virulence Genotype. <i>Infection and Immunity</i> , 2012, 80, 1554-1562.	2.2	101
40	Role of Intraspecies Recombination in the Spread of Pathogenicity Islands within the <i>Escherichia coli</i> Species. <i>PLoS Pathogens</i> , 2009, 5, e1000257.	4.7	93
41	Phylogenetic, virulence and antibiotic resistance characteristics of commensal strain populations of <i>Escherichia coli</i> from community subjects in the Paris area in 2010 and evolution over 30 years. <i>Microbiology (United Kingdom)</i> , 2016, 162, 642-650.	1.8	93
42	The Evolutionary History of <i>Shigella</i> and Enteroinvasive <i>Escherichia coli</i> Revised. <i>Journal of Molecular Evolution</i> , 2003, 57, 140-148.	1.8	89
43	The CTX-M-15-Producing <i>Escherichia coli</i> Clone O25b: H4-ST131 Has High Intestine Colonization and Urinary Tract Infection Abilities. <i>PLoS ONE</i> , 2012, 7, e46547.	2.5	88
44	Evidence for a human-specific <i>Escherichia coli</i> clone. <i>Environmental Microbiology</i> , 2008, 10, 1000-1006.	3.8	86
45	Commensal <i>Escherichia coli</i> strains in Guiana reveal a high genetic diversity with host-dependant population structure. <i>Environmental Microbiology Reports</i> , 2013, 5, 49-57.	2.4	82
46	Screening of <i>Escherichia coli</i> Species Biodiversity Reveals New Biofilm-Associated Antiadhesion Polysaccharides. <i>MBio</i> , 2011, 2, e00043-11.	4.1	81
47	Characterization of a P1-Like Bacteriophage Carrying an SHV-2 Extended-Spectrum $\beta$ -Lactamase from an <i>Escherichia coli</i> Strain. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 6550-6557.	3.2	80
48	The impact of genetic diversity on gene essentiality within the <i>Escherichia coli</i> species. <i>Nature Microbiology</i> , 2021, 6, 301-312.	13.3	76
49	<i>Shigella</i> and enteroinvasive <i>Escherichia coli</i> strains are derived from distinct ancestral strains of <i>E. coli</i> . <i>Microbiology (United Kingdom)</i> , 1998, 144, 2667-2672.	1.8	73
50	Mutator phenotype confers advantage in <i>Escherichia coli</i> chronic urinary tract infection pathogenesis. <i>FEMS Immunology and Medical Microbiology</i> , 2005, 44, 317-321.	2.7	71
51	Development of an allele-specific PCR for <i>Escherichia coli</i> B2 sub-typing, a rapid and easy to perform substitute of multilocus sequence typing. <i>Journal of Microbiological Methods</i> , 2014, 101, 24-27.	1.6	70
52	Molecular and Evolutionary Bases of Within-Patient Genotypic and Phenotypic Diversity in <i>Escherichia coli</i> Extraintestinal Infections. <i>PLoS Pathogens</i> , 2010, 6, e1001125.	4.7	68
53	Antibiotic resistance plasmids spread among natural isolates of <i>Escherichia coli</i> in spite of CRISPR elements. <i>Microbiology (United Kingdom)</i> , 2012, 158, 2997-3004.	1.8	67
54	Emergence of Antimicrobial-Resistant <i>Escherichia coli</i> of Animal Origin Spreading in Humans. <i>Molecular Biology and Evolution</i> , 2016, 33, 898-914.	8.9	65

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55	Colistin resistance in Parisian inpatient faecal <i>Escherichia coli</i> as the result of two distinct evolutionary pathways. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 1521-1530.	3.0	65
56	Molecular epidemiology and virulence of <i>Escherichia coli</i> O16:H5-ST131: Comparison with H30 and H30-Rx subclones of O25b:H4-ST131. <i>International Journal of Medical Microbiology</i> , 2014, 304, 1247-1257.	3.6	64
57	Using long-term experimental evolution to uncover the patterns and determinants of molecular evolution of an <i>Escherichia coli</i> natural isolate in the streptomycin-treated mouse gut. <i>Molecular Ecology</i> , 2017, 26, 1802-1817.	3.9	63
58	Emergence and Dissemination of Extended-Spectrum $\beta$ -Lactamase-Producing <i>Escherichia coli</i> in the Community: Lessons from the Study of a Remote and Controlled Population. <i>Journal of Infectious Diseases</i> , 2010, 202, 515-523.	4.0	60
59	Real-Time PCR for Quantitative Analysis of Human Commensal <i>Escherichia coli</i> Populations Reveals a High Frequency of Subdominant Phylogroups. <i>Applied and Environmental Microbiology</i> , 2013, 79, 5005-5012.	3.1	60
60	<i>Caenorhabditis elegans</i> as a simple model to study phenotypic and genetic virulence determinants of extraintestinal pathogenic <i>Escherichia coli</i> . <i>Microbes and Infection</i> , 2007, 9, 214-223.	1.9	59
61	Evolution of a Dominant Natural Isolate of <i>Escherichia coli</i> in the Human Gut over the Course of a Year Suggests a Neutral Evolution with Reduced Effective Population Size. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	58
62	Major role of iron uptake systems in the intrinsic extra-intestinal virulence of the genus <i>Escherichia</i> revealed by a genome-wide association study. <i>PLoS Genetics</i> , 2020, 16, e1009065.	3.5	56
63	Airway Fungal Colonization Compromises the Immune System Allowing Bacterial Pneumonia to Prevail. <i>Critical Care Medicine</i> , 2013, 41, e191-e199.	0.9	54
64	Bacteriophage LM33_P1, a fast-acting weapon against the pandemic ST131-O25b:H4 <i>Escherichia coli</i> clonal complex. <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 3072-3080.	3.0	53
65	The FimH A27V Mutation Is Pathoadaptive for Urovirulence in <i>Escherichia coli</i> B2 Phylogenetic Group Isolates. <i>Infection and Immunity</i> , 2003, 71, 3619-3622.	2.2	51
66	Core and Panmetabolism in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2011, 193, 1461-1472.	2.2	51
67	Biofilm Formation by and Thermal Niche and Virulence Characteristics of <i>Escherichia</i> spp. <i>Applied and Environmental Microbiology</i> , 2011, 77, 2695-2700.	3.1	51
68	Quantitative analysis of commensal <i>Escherichia coli</i> populations reveals host-specific enterotypes at the intra-species level. <i>MicrobiologyOpen</i> , 2015, 4, 604-615.	3.0	51
69	Decreasing the effects of horizontal gene transfer on bacterial phylogeny: the <i>Escherichia coli</i> case study. <i>Molecular Phylogenetics and Evolution</i> , 2004, 30, 243-250.	2.7	50
70	Real-time PCR for detection of the O25b-ST131 clone of <i>Escherichia coli</i> and its CTX-M-15-like extended-spectrum $\beta$ -lactamases. <i>International Journal of Antimicrobial Agents</i> , 2010, 36, 355-358.	2.5	49
71	Influence of hydrological conditions on the <i>Escherichia coli</i> population structure in the water of a creek on a rural watershed. <i>BMC Microbiology</i> , 2010, 10, 222.	3.3	46
72	Virulence Patterns in a Murine Sepsis Model of ST131 <i>Escherichia coli</i> Clinical Isolates Belonging to Serotypes O25b:H4 and O16:H5 Are Associated to Specific Virotypes. <i>PLoS ONE</i> , 2014, 9, e87025.	2.5	44

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73	Characteristics of human intestinal <i>Escherichia coli</i> with changing environments. <i>Environmental Microbiology</i> , 2008, 10, 2132-2137.	3.8	43
74	Pneumonia-Specific <i>Escherichia coli</i> with Distinct Phylogenetic and Virulence Profiles, France, 2012–2014. <i>Emerging Infectious Diseases</i> , 2019, 25, 710-718.	4.3	43
75	<i>Escherichia coli</i> Population Structure and Antibiotic Resistance at a Buffalo/Cattle Interface in Southern Africa. <i>Applied and Environmental Microbiology</i> , 2016, 82, 1459-1467.	3.1	42
76	The <i>rpoS</i> Gene Is Predominantly Inactivated during Laboratory Storage and Undergoes Source-Sink Evolution in <i>Escherichia coli</i> Species. <i>Journal of Bacteriology</i> , 2014, 196, 4276-4284.	2.2	41
77	Ceftriaxone and Cefotaxime Have Similar Effects on the Intestinal Microbiota in Human Volunteers Treated by Standard-Dose Regimens. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	41
78	Phenotype inference in an <i>Escherichia coli</i> strain panel. <i>ELife</i> , 2017, 6, .	6.0	38
79	Multiple acquisitions of CTX-M plasmids in the rare D2 genotype of <i>Escherichia coli</i> provide evidence for convergent evolution. <i>Microbiology (United Kingdom)</i> , 2009, 155, 1656-1668.	1.8	37
80	Phylogroup stability contrasts with high within sequence type complex dynamics of <i>Escherichia coli</i> bloodstream infection isolates over a 12-year period. <i>Genome Medicine</i> , 2021, 13, 77.	8.2	35
81	A Module Located at a Chromosomal Integration Hot Spot Is Responsible for the Multidrug Resistance of a Reference Strain from <i>Escherichia coli</i> Clonal Group A. <i>Antimicrobial Agents and Chemotherapy</i> , 2009, 53, 2283-2288.	3.2	33
82	Probable intrafamily transmission of a highly virulent CTX-M-3-producing <i>Escherichia coli</i> belonging to the emerging phylogenetic subgroup D2 O102-ST405 clone. <i>Journal of Antimicrobial Chemotherapy</i> , 2010, 65, 1537-1539.	3.0	33
83	Fitness, Stress Resistance, and Extraintestinal Virulence in <i>Escherichia coli</i> . <i>Infection and Immunity</i> , 2013, 81, 2733-2742.	2.2	33
84	Extended-spectrum $\beta$ -lactamase-encoding genes are spreading on a wide range of <i>Escherichia coli</i> plasmids existing prior to the use of third-generation cephalosporins. <i>Microbial Genomics</i> , 2018, 4, .	2.0	33
85	Fine-Scale Structure Analysis Shows Epidemic Patterns of Clonal Complex 95, a Cosmopolitan <i>Escherichia coli</i> Lineage Responsible for Extraintestinal Infection. <i>MSphere</i> , 2017, 2, .	2.9	32
86	Links between Transcription, Environmental Adaptation and Gene Variability in <i>Escherichia coli</i> : Correlations between Gene Expression and Gene Variability Reflect Growth Efficiencies. <i>Molecular Biology and Evolution</i> , 2016, 33, 2515-2529.	8.9	31
87	Strain-specific impact of the high-pathogenicity island on virulence in extra-intestinal pathogenic <i>Escherichia coli</i> . <i>International Journal of Medical Microbiology</i> , 2017, 307, 44-56.	3.6	31
88	Effects of single and multiple pathogenicity island deletions on uropathogenic <i>Escherichia coli</i> strain 536 intrinsic extra-intestinal virulence. <i>International Journal of Medical Microbiology</i> , 2010, 300, 435-439.	3.6	29
89	Characterization of Fecal Extended-Spectrum- $\beta$ -Lactamase-Producing <i>Escherichia coli</i> in a Remote Community during a Long Time Period. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 5060-5066.	3.2	29
90	Change in the Structure of <i>Escherichia coli</i> Population and the Pattern of Virulence Genes along a Rural Aquatic Continuum. <i>Frontiers in Microbiology</i> , 2017, 8, 609.	3.5	29

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91	Escherichia coli Bacteremia in Children. <i>Pediatric Infectious Disease Journal</i> , 2014, 33, 872-879.	2.0	28
92	Pathophysiology of Escherichia coli ventilator-associated pneumonia: implication of highly virulent extraintestinal pathogenic strains. <i>Intensive Care Medicine</i> , 2012, 38, 2007-2016.	8.2	26
93	Population Phylogenomics of Extraintestinal Pathogenic <i>Escherichia coli</i> . <i>Microbiology Spectrum</i> , 2016, 4, .	3.0	26
94	Advantage of the F2:A1:B- IncF Pandemic Plasmid over IncC Plasmids in <i>In Vitro</i> Acquisition and Evolution of <i>bla</i> <sub>CTX-M</sub> Gene-Bearing Plasmids in Escherichia coli. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	26
95	Variation in endogenous oxidative stress in Escherichia coli natural isolates during growth in urine. <i>BMC Microbiology</i> , 2012, 12, 120.	3.3	25
96	Genome wide association study of Escherichia coli bloodstream infection isolates identifies genetic determinants for the portal of entry but not fatal outcome. <i>PLoS Genetics</i> , 2022, 18, e1010112.	3.5	22
97	Prevalence and phylogenetic history of the T <sub>cpC</sub> virulence determinant in Escherichia coli. <i>International Journal of Medical Microbiology</i> , 2010, 300, 429-434.	3.6	21
98	High Recombinant Frequency in Extraintestinal Pathogenic Escherichia coli Strains. <i>Molecular Biology and Evolution</i> , 2015, 32, 1708-1716.	8.9	21
99	Interactions between genotype and environment drive the metabolic phenotype within <i>Escherichia coli</i> isolates. <i>Environmental Microbiology</i> , 2016, 18, 100-117.	3.8	19
100	Small variable segments constitute a major type of diversity of bacterial genomes at the species level. <i>Genome Biology</i> , 2010, 11, R45.	9.6	17
101	Complete Nucleotide Sequence of Plasmid pTN48, Encoding the CTX-M-14 Extended-Spectrum $\hat{I}^2$ -Lactamase from an <i>Escherichia coli</i> O102-ST405 Strain. <i>Antimicrobial Agents and Chemotherapy</i> , 2011, 55, 1270-1273.	3.2	17
102	Pathophysiology of Escherichia coli pneumonia: Respective contribution of pathogenicity islands to virulence. <i>International Journal of Medical Microbiology</i> , 2018, 308, 290-296.	3.6	17
103	Decreased susceptibility to chlorhexidine affects a quarter of Escherichia coli isolates responsible for pneumonia in ICU patients. <i>Intensive Care Medicine</i> , 2018, 44, 531-533.	8.2	16
104	The E phylogroup of <i>Escherichia coli</i> is highly diverse and mimics the whole <i>E. coli</i> species population structure. <i>Environmental Microbiology</i> , 2021, 23, 7139-7151.	3.8	16
105	Diversity of the auxotrophic requirements in natural isolates of Escherichia coli. <i>Microbiology (United Kingdom)</i> , 2017, 163, 891-899.	1.8	16
106	Extended-spectrum beta-lactamase-producing Escherichia coli infections in children: Are community-acquired strains different from nosocomial strains?. <i>International Journal of Medical Microbiology</i> , 2014, 304, 970-976.	3.6	15
107	Escherichia coli B2 Phylogenetic Subgroups in the Infant Gut Microbiota: Predominance of Uropathogenic Lineages in Swedish Infants and Enteropathogenic Lineages in Pakistani Infants. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	15
108	Success of Escherichia coli O25b:H4 Sequence Type 131 Clade C Associated with a Decrease in Virulence. <i>Infection and Immunity</i> , 2020, 88, .	2.2	15

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109	Lack of dissemination of acquired resistance to $\beta$ -lactams in small wild mammals around an isolated village in the Amazonian forest. <i>Environmental Microbiology Reports</i> , 2015, 7, 698-708.	2.4	13
110	The interaction between a non-pathogenic and a pathogenic strain synergistically enhances extra-intestinal virulence in <i>Escherichia coli</i> . <i>Microbiology (United Kingdom)</i> , 2011, 157, 774-785.	1.8	11
111	The Arginine Deiminase Operon Is Responsible for a Fitness Trade-Off in Extended-Spectrum- $\beta$ -Lactamase-Producing Strains of <i>Escherichia coli</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	11
112	Dynamics of extended-spectrum beta-lactamase-producing Enterobacterales colonization in long-term carriers following travel abroad. <i>Microbial Genomics</i> , 2021, 7, .	2.0	11
113	esrB, the gene encoding the esterase B in <i>Escherichia coli</i> , is a powerful phylogenetic marker of the species. <i>BMC Microbiology</i> , 2009, 9, 273.	3.3	9
114	Phylum barrier and <i>Escherichia coli</i> intra-species phylogeny drive the acquisition of antibiotic-resistance genes. <i>Microbial Genomics</i> , 2021, 7, .	2.0	9
115	Prevalence, Risk Factors, and Genetic Characterization of Extended-Spectrum Beta-Lactamase <i>Escherichia coli</i> Isolated From Healthy Pregnant Women in Madagascar. <i>Frontiers in Microbiology</i> , 2021, 12, 786146.	3.5	9
116	Complexity of <i>Escherichia coli</i> bacteremia pathophysiology evidenced by comparison of isolates from blood and portal of entry within single patients. <i>International Journal of Medical Microbiology</i> , 2013, 303, 529-532.	3.6	8
117	Small Intestine Early Innate Immunity Response during Intestinal Colonization by <i>Escherichia coli</i> Depends on Its Extra-Intestinal Virulence Status. <i>PLoS ONE</i> , 2016, 11, e0153034.	2.5	8
118	Prospective Cohort Study of the Relative Abundance of Extended-Spectrum-Beta-Lactamase-Producing <i>Escherichia coli</i> in the Gut of Patients Admitted to Hospitals. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 6941-6944.	3.2	8
119	Rare Spontaneous Loss of Multiresistance Gene Carrying IncI/ST12 Plasmid in <i>Escherichia coli</i> in Pig Microbiota. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 6046-6049.	3.2	8
120	Day-to-Day Dynamics of Commensal <i>Escherichia coli</i> in Zimbabwean Cows Evidence Temporal Fluctuations within a Host-Specific Population Structure. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	8
121	Temporal dynamics of the fecal microbiota in veal calves in a 6-month field trial. <i>Animal Microbiome</i> , 2020, 2, 32.	3.8	7
122	<i>Escherichia coli</i> Genomic Diversity within Extraintestinal Acute Infections Argues for Adaptive Evolution at Play. <i>MSphere</i> , 2021, 6, .	2.9	6
123	Interplay between Bacterial Clones and Plasmids in the Spread of Antibiotic Resistance Genes in the Gut: Lessons from a Temporal Study in Veal Calves. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0135821.	3.1	6
124	Specialization of small non-conjugative plasmids in <i>Escherichia coli</i> according to their family types. <i>Microbial Genomics</i> , 2019, 5, .	2.0	5
125	Reduced Chlorhexidine Susceptibility Is Associated with Tetracycline Resistance <i>tetA</i> Genes in Clinical Isolates of <i>Escherichia coli</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2022, 66, AAC0197221.	3.2	5
126	Genotypic and phenotypic characteristics of <i>Escherichia coli</i> involved in transfusion-transmitted bacterial infections: implications for preventive strategies. <i>Transfusion</i> , 2018, 58, 1940-1950.	1.6	4



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127	TisB Protein Protects Escherichia coli Cells Suffering Massive DNA Damage from Environmental Toxic Compounds. MBio, 2022, 13, e0038522.	4.1	4
128	Diversité des populations d'Escherichia coli et leurs variations au cours du temps au sein du microbiote intestinal. Revue Francophone Des Laboratoires, 2016, 2016, 35-43.	0.0	3
129	O-antigen targeted vaccines against E. coli may be useful in reducing morbidity, mortality and antimicrobial resistance. Clinical Infectious Diseases, 2021, , .	5.8	3
130	Lack of association between colistin resistance and chlorhexidine reduced susceptibility in clinical isolates of Escherichia coli. Journal of Antimicrobial Chemotherapy, 2021, 76, 2736-2737.	3.0	3
131	Extra-corporeal membrane oxygenation-associated infections: implication of extra-intestinal pathogenic Escherichia coli clones. Journal of Medical Microbiology, 2017, 66, 1189-1195.	1.8	3
132	A 16th century Escherichia coli draft genome associated with an opportunistic bile infection. Communications Biology, 2022, 5, .	4.4	2
133	Population Phylogenomics of Extraintestinal Pathogenic Escherichia coli. , 0, , 207-233.		1
134	Impact of Escherichia coli probiotic strains ED1a and Nissle 1917 on the excretion and gut carriage of extended-spectrum beta-lactamase-producing E. coli in pigs. Veterinary and Animal Science, 2021, 14, 100217.	1.5	1
135	Title is missing!. , 2020, 16, e1009065.		0
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