

Erick Denamur

List of Publications by Year in descending order

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138
papers

14,328
citations

28274

55
h-index

21540

114
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155
all docs

155
docs citations

155
times ranked

10766
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome wide association study of Escherichia coli bloodstream infection isolates identifies genetic determinants for the portal of entry but not fatal outcome. PLoS Genetics, 2022, 18, e1010112.	3.5	22
2	Reduced Chlorhexidine Susceptibility Is Associated with Tetracycline Resistance <i>tet</i> Genes in Clinical Isolates of Escherichia coli. Antimicrobial Agents and Chemotherapy, 2022, 66, AAC0197221.	3.2	5
3	TisB Protein Protects Escherichia coli Cells Suffering Massive DNA Damage from Environmental Toxic Compounds. MBio, 2022, 13, e0038522.	4.1	4
4	A 16th century Escherichia coli draft genome associated with an opportunistic bile infection. Communications Biology, 2022, 5, .	4.4	2
5	The population genetics of pathogenic Escherichia coli. Nature Reviews Microbiology, 2021, 19, 37-54.	28.6	268
6	Escherichia coli Genomic Diversity within Extraintestinal Acute Infections Argues for Adaptive Evolution at Play. MSphere, 2021, 6, .	2.9	6
7	Phylogroup stability contrasts with high within sequence type complex dynamics of Escherichia coli bloodstream infection isolates over a 12-year period. Genome Medicine, 2021, 13, 77.	8.2	35
8	O-antigen targeted vaccines against E. coli may be useful in reducing morbidity, mortality and antimicrobial resistance. Clinical Infectious Diseases, 2021, , .	5.8	3
9	Dynamics of extended-spectrum beta-lactamase-producing Enterobacterales colonization in long-term carriers following travel abroad. Microbial Genomics, 2021, 7, .	2.0	11
10	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
11	Phylum barrier and Escherichia coli intra-species phylogeny drive the acquisition of antibiotic-resistance genes. Microbial Genomics, 2021, 7, .	2.0	9
12	The E phylogroup of Escherichia coli is highly diverse and mimics the whole E. coli species population structure. Environmental Microbiology, 2021, 23, 7139-7151.	3.8	16
13	The impact of genetic diversity on gene essentiality within the Escherichia coli species. Nature Microbiology, 2021, 6, 301-312.	13.3	76
14	Interplay between Bacterial Clones and Plasmids in the Spread of Antibiotic Resistance Genes in the Gut: Lessons from a Temporal Study in Veal Calves. Applied and Environmental Microbiology, 2021, 87, e0135821.	3.1	6
15	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
16	Prevalence, Risk Factors, and Genetic Characterization of Extended-Spectrum Beta-Lactamase Escherichia coli Isolated From Healthy Pregnant Women in Madagascar. Frontiers in Microbiology, 2021, 12, 786146.	3.5	9
17	Temporal dynamics of the fecal microbiota in veal calves in a 6-month field trial. Animal Microbiome, 2020, 2, 32.	3.8	7
18	Success of Escherichia coli O25b:H4 Sequence Type 131 Clade C Associated with a Decrease in Virulence. Infection and Immunity, 2020, 88, .	2.2	15

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19	Phylogenetic background and habitat drive the genetic diversification of <i>Escherichia coli</i> . <i>PLoS Genetics</i> , 2020, 16, e1008866.	3.5	131
20	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
21	Title is missing!. , 2020, 16, e1009065.		0
22	Title is missing!. , 2020, 16, e1009065.		0
23	Title is missing!. , 2020, 16, e1009065.		0
24	Title is missing!. , 2020, 16, e1009065.		0
25	Advantage of the F2:A1:B- IncF Pandemic Plasmid over IncC Plasmids in <i>In Vitro</i> Acquisition and Evolution of <i>bla</i> _{CTX-M} Gene-Bearing Plasmids in <i>Escherichia coli</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	26
26	<i>Escherichia coli</i> 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
27	The Arginine Deiminase Operon Is Responsible for a Fitness Trade-Off in Extended-Spectrum-β-Lactamase-Producing Strains of <i>Escherichia coli</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	11
28	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
29	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
30	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
31	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
32	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
33	Decreased susceptibility to chlorhexidine affects a quarter of <i>Escherichia coli</i> isolates responsible for pneumonia in ICU patients. <i>Intensive Care Medicine</i> , 2018, 44, 531-533.	8.2	16
34	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
35	Pathophysiology of <i>Escherichia coli</i> pneumonia: Respective contribution of pathogenicity islands to virulence. <i>International Journal of Medical Microbiology</i> , 2018, 308, 290-296.	3.6	17
36	ClermonTyping: an easy-to-use and accurate in silico method for <i>Escherichia</i> genus strain phylotyping. <i>Microbial Genomics</i> , 2018, 4, .	2.0	307

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37	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
38	Extended-spectrum β -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
39	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
40	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
41	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
42	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
43	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
44	Extra-corporeal membrane oxygenation-associated infections: implication of extra-intestinal pathogenic <i>Escherichia coli</i> clones. <i>Journal of Medical Microbiology</i> , 2017, 66, 1189-1195.	1.8	3
45	Diversity of the auxotrophic requirements in natural isolates of <i>Escherichia coli</i> . <i>Microbiology (United Kingdom)</i> , 2017, 163, 891-899.	1.8	16
46	Phenotype inference in an <i>Escherichia coli</i> strain panel. <i>ELife</i> , 2017, 6, .	6.0	38
47	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
48	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
49	Population Phylogenomics of Extraintestinal Pathogenic <i>Escherichia coli</i> . <i>Microbiology Spectrum</i> , 2016, 4, .	3.0	26
50	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
51	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
52	Diversit� des populations d'Escherichia coli et leurs variations au cours du temps au sein du microbiote intestinal. <i>Revue Francophone Des Laboratoires</i> , 2016, 2016, 35-43.	0.0	3
53	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
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	Escherichia coli Population Structure and Antibiotic Resistance at a Buffalo/Cattle Interface in Southern Africa. Applied and Environmental Microbiology, 2016, 82, 1459-1467.	3.1	42
56	Interactions between genotype and environment drive the metabolic phenotype within Escherichia coli isolates. Environmental Microbiology, 2016, 18, 100-117.	3.8	19
57	Phylogenetic, virulence and antibiotic resistance characteristics of commensal strain populations of Escherichia coli from community subjects in the Paris area in 2010 and evolution over 30 years. Microbiology (United Kingdom), 2016, 162, 642-650.	1.8	93
58	Quantitative analysis of commensal Escherichia coli populations reveals host-specific enterotypes at the intra-species level. MicrobiologyOpen, 2015, 4, 604-615.	3.0	51
59	Lack of dissemination of acquired resistance to β -lactams in small wild mammals around an isolated village in the Amazonian forest. Environmental Microbiology Reports, 2015, 7, 698-708.	2.4	13
60	Guide to the various phylogenetic classification schemes for Escherichia coli and the correspondence among schemes. Microbiology (United Kingdom), 2015, 161, 980-988.	1.8	139
61	High Recombinant Frequency in Extraintestinal Pathogenic Escherichia coli Strains. Molecular Biology and Evolution, 2015, 32, 1708-1716.	8.9	21
62	Virulence Patterns in a Murine Sepsis Model of ST131 Escherichia coli Clinical Isolates Belonging to Serotypes O25b:H4 and O16:H5 Are Associated to Specific Virotypes. PLoS ONE, 2014, 9, e87025.	2.5	44
63	Development of an allele-specific PCR for Escherichia coli B2 sub-typing, a rapid and easy to perform substitute of multilocus sequence typing. Journal of Microbiological Methods, 2014, 101, 24-27.	1.6	70
64	Rapid and Specific Detection, Molecular Epidemiology, and Experimental Virulence of the O16 Subgroup within Escherichia coli Sequence Type 131. Journal of Clinical Microbiology, 2014, 52, 1358-1365.	3.9	107
65	Molecular epidemiology and virulence of Escherichia coli O16:H5-ST131: Comparison with H30 and H30-Rx subclones of O25b:H4-ST131. International Journal of Medical Microbiology, 2014, 304, 1247-1257.	3.6	64
66	The rpoS Gene Is Predominantly Inactivated during Laboratory Storage and Undergoes Source-Sink Evolution in Escherichia coli Species. Journal of Bacteriology, 2014, 196, 4276-4284.	2.2	41
67	Extended-spectrum beta-lactamase-producing Escherichia coli infections in children: Are community-acquired strains different from nosocomial strains?. International Journal of Medical Microbiology, 2014, 304, 970-976.	3.6	15
68	Characterization of a P1-Like Bacteriophage Carrying an SHV-2 Extended-Spectrum β -Lactamase from an Escherichia coli Strain. Antimicrobial Agents and Chemotherapy, 2014, 58, 6550-6557.	3.2	80
69	Escherichia coli Bacteremia in Children. Pediatric Infectious Disease Journal, 2014, 33, 872-879.	2.0	28
70	Fitness, Stress Resistance, and Extraintestinal Virulence in Escherichia coli. Infection and Immunity, 2013, 81, 2733-2742.	2.2	33
71	Commensal Escherichia coli strains in Guiana reveal a high genetic diversity with host-dependant population structure. Environmental Microbiology Reports, 2013, 5, 49-57.	2.4	82
72	Complexity of Escherichia coli bacteremia pathophysiology evidenced by comparison of isolates from blood and portal of entry within single patients. International Journal of Medical Microbiology, 2013, 303, 529-532.	3.6	8

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73	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
74	Real-Time PCR for Quantitative Analysis of Human Commensal Escherichia coli Populations Reveals a High Frequency of Subdominant Phylogroups. Applied and Environmental Microbiology, 2013, 79, 5005-5012.	3.1	60
75	Characterization of Fecal Extended-Spectrum- β -Lactamase-Producing Escherichia coli in a Remote Community during a Long Time Period. Antimicrobial Agents and Chemotherapy, 2013, 57, 5060-5066.	3.2	29
76	Airway Fungal Colonization Compromises the Immune System Allowing Bacterial Pneumonia to Preval. Critical Care Medicine, 2013, 41, e191-e199.	0.9	54
77	Virulence of Escherichia coli Clinical Isolates in a Murine Sepsis Model in Relation to Sequence Type ST131 Status, Fluoroquinolone Resistance, and Virulence Genotype. Infection and Immunity, 2012, 80, 1554-1562.	2.2	101
78	Pathophysiology of Escherichia coli ventilator-associated pneumonia: implication of highly virulent extraintestinal pathogenic strains. Intensive Care Medicine, 2012, 38, 2007-2016.	8.2	26
79	Antibiotic resistance plasmids spread among natural isolates of Escherichia coli in spite of CRISPR elements. Microbiology (United Kingdom), 2012, 158, 2997-3004.	1.8	67
80	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
81	Variation in endogenous oxidative stress in Escherichia coli natural isolates during growth in urine. BMC Microbiology, 2012, 12, 120.	3.3	25
82	The CTX-M-15-Producing Escherichia coli Clone O25b: H4-ST131 Has High Intestine Colonization and Urinary Tract Infection Abilities. PLoS ONE, 2012, 7, e46547.	2.5	88
83	CRISPR Distribution within the Escherichia coli Species Is Not Suggestive of Immunity-Associated Diversifying Selection. Journal of Bacteriology, 2011, 193, 2460-2467.	2.2	139
84	Characterization of the cryptic <i>Escherichia</i> lineages: rapid identification and prevalence. Environmental Microbiology, 2011, 13, 2468-2477.	3.8	103
85	Animal and human pathogenic Escherichia coli strains share common genetic backgrounds. Infection, Genetics and Evolution, 2011, 11, 654-662.	2.3	169
86	Screening of Escherichia coli Species Biodiversity Reveals New Biofilm-Associated Antiadhesion Polysaccharides. MBio, 2011, 2, e00043-11.	4.1	81
87	Complete Nucleotide Sequence of Plasmid pTN48, Encoding the CTX-M-14 Extended-Spectrum β -Lactamase from an <i>Escherichia coli</i> O102-ST405 Strain. Antimicrobial Agents and Chemotherapy, 2011, 55, 1270-1273.	3.2	17
88	The interaction between a non-pathogenic and a pathogenic strain synergistically enhances extra-intestinal virulence in Escherichia coli. Microbiology (United Kingdom), 2011, 157, 774-785.	1.8	11
89	Core and Panmetabolism in <i>Escherichia coli</i> . Journal of Bacteriology, 2011, 193, 1461-1472.	2.2	51
90	Biofilm Formation by and Thermal Niche and Virulence Characteristics of Escherichia spp. Applied and Environmental Microbiology, 2011, 77, 2695-2700.	3.1	51

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91	Host Factors and Portal of Entry Outweigh Bacterial Determinants To Predict the Severity of Escherichia coli Bacteremia. <i>Journal of Clinical Microbiology</i> , 2011, 49, 777-783.	3.9	123
92	Influence of hydrological conditions on the Escherichia coli population structure in the water of a creek on a rural watershed. <i>BMC Microbiology</i> , 2010, 10, 222.	3.3	46
93	The population genetics of commensal Escherichia coli. <i>Nature Reviews Microbiology</i> , 2010, 8, 207-217.	28.6	1,104
94	From Grazing Resistance to Pathogenesis: The Coincidental Evolution of Virulence Factors. <i>PLoS ONE</i> , 2010, 5, e11882.	2.5	114
95	Probable intrafamily transmission of a highly virulent CTX-M-3-producing Escherichia coli belonging to the emerging phylogenetic subgroup D2 O102-ST405 clone. <i>Journal of Antimicrobial Chemotherapy</i> , 2010, 65, 1537-1539.	3.0	33
96	Emergence and Dissemination of Extended-Spectrum β -Lactamase-Producing Escherichia coli 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
97	Pathogenicity-Associated Islands in Extraintestinal Pathogenic Escherichia coli Are Fitness Elements Involved in Intestinal Colonization. <i>Journal of Bacteriology</i> , 2010, 192, 4885-4893.	2.2	105
98	Molecular and Evolutionary Bases of Within-Patient Genotypic and Phenotypic Diversity in Escherichia coli Extraintestinal Infections. <i>PLoS Pathogens</i> , 2010, 6, e1001125.	4.7	68
99	Real-time PCR for detection of the O25b-ST131 clone of Escherichia coli and its CTX-M-15-like extended-spectrum β -lactamases. <i>International Journal of Antimicrobial Agents</i> , 2010, 36, 355-358.	2.5	49
100	Meningitis Caused by Escherichia coli Producing TEM-52 Extended-Spectrum β -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
101	Prevalence and phylogenetic history of the TcpC virulence determinant in Escherichia coli. <i>International Journal of Medical Microbiology</i> , 2010, 300, 429-434.	3.6	21
102	Effects of single and multiple pathogenicity island deletions on uropathogenic Escherichia coli strain 536 intrinsic extra-intestinal virulence. <i>International Journal of Medical Microbiology</i> , 2010, 300, 435-439.	3.6	29
103	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
104	Rapid detection of the O25b-ST131 clone of Escherichia coli encompassing the CTX-M-15-producing strains. <i>Journal of Antimicrobial Chemotherapy</i> , 2009, 64, 274-277.	3.0	328
105	A Module Located at a Chromosomal Integration Hot Spot Is Responsible for the Multidrug Resistance of a Reference Strain from Escherichia coli Clonal Group A. <i>Antimicrobial Agents and Chemotherapy</i> , 2009, 53, 2283-2288.	3.2	33
106	The Plasmid of Escherichia coli Strain S88 (O45:K1:H7) That Causes Neonatal Meningitis Is Closely Related to Avian Pathogenic E. coli 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
107	Multiple acquisitions of CTX-M plasmids in the rare D2 genotype of Escherichia coli provide evidence for convergent evolution. <i>Microbiology (United Kingdom)</i> , 2009, 155, 1656-1668.	1.8	37
108	Organised Genome Dynamics in the Escherichia coli Species Results in Highly Diverse Adaptive Paths. <i>PLoS Genetics</i> , 2009, 5, e1000344.	3.5	1,005

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109	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
110	oes, 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
111	Evidence for a human-specific <i>Escherichia coli</i> clone. <i>Environmental Microbiology</i> , 2008, 10, 1000-1006.	3.8	86
112	Characteristics of human intestinal <i>Escherichia coli</i> with changing environments. <i>Environmental Microbiology</i> , 2008, 10, 2132-2137.	3.8	43
113	Assigning <i>Escherichia coli</i> strains to phylogenetic groups: multi-locus sequence typing versus the PCR triplex method. <i>Environmental Microbiology</i> , 2008, 10, 2484-2496.	3.8	253
114	Phylogenetic and genomic diversity of human bacteremic <i>Escherichia coli</i> strains. <i>BMC Genomics</i> , 2008, 9, 560.	2.8	297
115	The CTX-M-15-producing <i>Escherichia coli</i> diffusing clone belongs to a highly virulent B2 phylogenetic subgroup. <i>Journal of Antimicrobial Chemotherapy</i> , 2008, 61, 1024-1028.	3.0	261
116	Extraintestinal Virulence Is a Coincidental By-Product of Commensalism in B2 Phylogenetic Group <i>Escherichia coli</i> Strains. <i>Molecular Biology and Evolution</i> , 2007, 24, 2373-2384.	8.9	225
117	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
118	<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
119	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
120	Evolution of mutation rates in bacteria. <i>Molecular Microbiology</i> , 2006, 60, 820-827.	2.5	319
121	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
122	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
123	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
124	Genetic Background of <i>Escherichia coli</i> and Extended-spectrum β -Lactamase Type. <i>Emerging Infectious Diseases</i> , 2005, 11, 54-61.	4.3	155
125	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
126	Large-Scale Population Structure of Human Commensal <i>Escherichia coli</i> Isolates. <i>Applied and Environmental Microbiology</i> , 2004, 70, 5698-5700.	3.1	204

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127	A Specific Genetic Background Is Required for Acquisition and Expression of Virulence Factors in <i>Escherichia coli</i> . <i>Molecular Biology and Evolution</i> , 2004, 21, 1085-1094.	8.9	304
128	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
129	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
130	Stress-Induced Mutagenesis in Bacteria. <i>Science</i> , 2003, 300, 1404-1409.	12.6	508
131	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
132	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
133	<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
134	Commensal <i>Escherichia coli</i> isolates are phylogenetically distributed among geographically distinct human populations. <i>Microbiology (United Kingdom)</i> , 2001, 147, 1671-1676.	1.8	267
135	Evolutionary Implications of the Frequent Horizontal Transfer of Mismatch Repair Genes. <i>Cell</i> , 2000, 103, 711-721.	28.9	246
136	The Link between Phylogeny and Virulence in <i>Escherichia coli</i> Extraintestinal Infection. <i>Infection and Immunity</i> , 1999, 67, 546-553.	2.2	690
137	<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
138	Population Phylogenomics of Extraintestinal Pathogenic <i>Escherichia coli</i> . , 0, , 207-233.		1