

The population genetics of commensal *Escherichia coli*

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Citation Report

#	ARTICLE	IF	CITATIONS
2	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.	1.3	46
3	LEEways: tales of EPEC, ATEC and EHEC. <i>Cellular Microbiology</i> , 2010, 12, 1544-1552.	1.1	131
4	From Grazing Resistance to Pathogenesis: The Coincidental Evolution of Virulence Factors. <i>PLoS ONE</i> , 2010, 5, e11882.	1.1	114
5	ICE <i>Ec2</i> , a New Integrative and Conjugative Element Belonging to the pKLC102/PAGI-2 Family, Identified in <i>Escherichia coli</i> Strain BEN374. <i>Journal of Bacteriology</i> , 2010, 192, 5026-5036.	1.0	21
6	Distribution of Human Commensal <i>Escherichia coli</i> Phylogenetic Groups. <i>Journal of Clinical Microbiology</i> , 2010, 48, 3455-3456.	1.8	48
7	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.	2.1	68
8	Silent Mischief: Bacteriophage Mu Insertions Contaminate Products of <i>Escherichia coli</i> Random Mutagenesis Performed Using Suicidal Transposon Delivery Plasmids Mobilized by Broad-Host-Range RP4 Conjugative Machinery. <i>Journal of Bacteriology</i> , 2010, 192, 6418-6427.	1.0	276
9	Bacteriophage PhiX174's Ecological Niche and the Flexibility of Its <i>Escherichia coli</i> Lipopolysaccharide Receptor. <i>Applied and Environmental Microbiology</i> , 2010, 76, 7310-7313.	1.4	51
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13	A Theory-Based Pragmatism for Discovering and Classifying Newly Divergent Bacterial Species. , 2011, , 21-41.		14
14	Evolution of Lipopolysaccharide Biosynthesis Genes. , 2011, , 339-370.		10
15	CTX-M-15-Producing <i>Escherichia coli</i> Clinical Isolates in Cairo (Egypt), Including Isolates of Clonal Complex ST10 and Clones ST131, ST73, and ST405 in Both Community and Hospital Settings. <i>Microbial Drug Resistance</i> , 2011, 17, 67-73.	0.9	84
16	<i>E. coli</i> Lipopolysaccharide: Acute oral toxicity study in mice. <i>Food and Chemical Toxicology</i> , 2011, 49, 1770-1772.	1.8	10
17	What defines extraintestinal pathogenic <i>Escherichia coli</i> ?. <i>International Journal of Medical Microbiology</i> , 2011, 301, 642-647.	1.5	236
18	A high-throughput open-array qPCR gene panel to identify, virulotype, and subtype O157 and non-O157 enterohemorrhagic <i>Escherichia coli</i> . <i>Molecular and Cellular Probes</i> , 2011, 25, 222-230.	0.9	25
19	Host-microbial symbiosis in the vertebrate gastrointestinal tract and the <i>Lactobacillus reuteri</i> paradigm. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4645-4652.	3.3	283

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22	Urgent advice on the public health risk of Shiga-toxin producing <i>Escherichia coli</i> in fresh vegetables. <i>EFSA Journal</i> , 2011, 9, 2274.	0.9	44
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27	Epidemic population structure of extraintestinal pathogenic <i>Escherichia coli</i> determined by single nucleotide polymorphism pyrosequencing. <i>Infection, Genetics and Evolution</i> , 2011, 11, 1655-1663.	1.0	3
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35	Role of microbiota in postnatal maturation of intestinal T-cell responses. <i>Current Opinion in Gastroenterology</i> , 2011, 27, 502-508.	1.0	26
36	Effect of diet and gut dynamics on the establishment and persistence of <i>Escherichia coli</i> . <i>Microbiology (United Kingdom)</i> , 2011, 157, 1375-1384.	0.7	18
37	The Evolution of Host Specialization in the Vertebrate Gut Symbiont <i>Lactobacillus reuteri</i> . <i>PLoS Genetics</i> , 2011, 7, e1001314.	1.5	270
38	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.	0.7	11

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55	Phylogenetic Grouping and Virulence Potential of Extended-Spectrum β -Lactamase-Producing <i>Escherichia coli</i> Strains in Cattle. <i>Applied and Environmental Microbiology</i> , 2012, 78, 4677-4682.	1.4	58
56	Quantifying Homologous Replacement of Loci between Haloarchaeal Species. <i>Genome Biology and Evolution</i> , 2012, 4, 1223-1244.	1.1	55

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109	Adhesion of Human and Animal <i>Escherichia coli</i> Strains in Association with Their Virulence-Associated Genes and Phylogenetic Origins. <i>Applied and Environmental Microbiology</i> , 2013, 79, 5814-5829.	1.4	55
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117	Phenotypic and Genotypic Characterization of <i>Escherichia coli</i> Isolated from Untreated Surface Waters. <i>Open Microbiology Journal</i> , 2013, 7, 9-19.	0.2	28
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134	Commercial Lysogeny Broth culture media and oxidative stress: A cautious tale. <i>Free Radical Biology and Medicine</i> , 2014, 74, 245-251.	1.3	28
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#	ARTICLE	IF	CITATIONS
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280	Comparison between virulence characteristics of dominant and non-dominant <i>Escherichia coli</i> strains of the gut and their interaction with Caco-2 cells. <i>Microbial Pathogenesis</i> , 2017, 105, 171-176.	1.3	10
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292	Mechanisms and consequences of intestinal dysbiosis. <i>Cellular and Molecular Life Sciences</i> , 2017, 74, 2959-2977.	2.4	401
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295	Antibiotic resistance is linked to carriage of <i>papC</i> and <i>iutA</i> virulence genes and phylogenetic group D background in commensal and uropathogenic <i>Escherichia coli</i> from infants and young children. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2017, 36, 721-729.	1.3	25

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