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## The Population Genomics of Increased Virulence and Antibiotic Resistance in Human Commensal *Escherichia coli* over 30 Years in France

DOI: 10.1128/aem.00664-22  
, 2022, 88, .

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**Version:** 2024-04-27

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| 7 | Genomic Characterization of an Extensively Drug-Resistant Extra-Intestinal Pathogenic (ExPEC) <i>Escherichia coli</i> Clinical Isolate Co-Producing Two Carbapenemases and a 16S rRNA Methylase. <b>2022</b> , 11, 1479 |    | 0         |
| 6 | Urban Pigeons ( <i>Columba livia</i> ) as a Source of Broad-Spectrum $\beta$ -Lactamase-Producing <i>Escherichia coli</i> in Lisbon, Portugal. <b>2022</b> , 11, 1368                                                   |    | 1         |
| 5 | Community carriage of ESBL-producing <i>Escherichia coli</i> and <i>Klebsiella pneumoniae</i> : A cross-sectional study of risk factors and comparative genomics of carriage and clinical isolates.                     |    | 0         |
| 4 | Extended-spectrum $\beta$ -lactamase genes traverse the <i>Escherichia coli</i> populations of ICU patients, staff and environment.                                                                                     |    | 0         |
| 3 | Global Phylogeny and $\beta$ -Virulence Plasmid Carriage in Pandemic <i>Escherichia coli</i> ST1193. <b>2022</b> , 10,                                                                                                  |    | 0         |
| 2 | Extended-Spectrum $\beta$ -Lactamase Genes Traverse the <i>Escherichia coli</i> Populations of Intensive Care Unit Patients, Staff, and Environment. <b>2023</b> , 11,                                                  |    | 0         |
| 1 | Colonization with <i>Escherichia coli</i> ST131-H30R (H30R) Corresponds with Increased Serum Anti-O25 IgG Levels and Decreased TNF $\alpha$ and IL-10 Responsiveness to H30R. <b>2023</b> , 12, 603                     |    | 0         |