

# Genome Sequence of OXA-48 Carbapenemase-Producing *Klebsiella pneumoniae* KpO3210

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***Klebsiella pneumoniae* KpO3210 is a OXA-48 carbapenemase-producing isolate obtained from a blood culture in the context of an outbreak in Hospital Universitario La Paz (Madrid, Spain) in 2010. It belongs to the major clone detected during the outbreak and is resistant to all beta-lactams and to several other antibiotics.**

*Klebsiella pneumoniae* is a Gram-negative bacterium of the family *Enterobacteriaceae* and a close relative of familiar genera such as *Escherichia* and *Salmonella*. *K. pneumoniae* is of increasing medical importance due to its role as an opportunistic pathogen and frequent cause of nosocomial and urinary tract infections (2). As *K. pneumoniae* strains are frequently associated with both extended-spectrum  $\beta$ -lactamases and carbapenemases, infection with *K. pneumoniae* often leads to severely limited treatment options (3).

*K. pneumoniae* KpO3210 was obtained from a blood culture in the context of a carbapenemase-producing *Klebsiella* outbreak (5). It is resistant to all beta-lactams, belongs to ST405, and was found to carry *bla*<sub>TEM-1</sub>, *bla*<sub>SHV-76</sub>, *bla*<sub>CTX-M-15</sub>, *bla*<sub>OXA-1</sub>, and *bla*<sub>OXA-48</sub> genes.

DNA samples were fragmented using a Bioruptor (Diagenode). DNA fragments sized around 400 bp were excised from agarose gels and purified, and TruSeq libraries (Illumina) were prepared according to the manufacturer's instructions. DNA libraries were checked for size, concentration, and integrity using a Bioanalyzer (Agilent) and quantified by quantitative PCR (qPCR) in order to accurately estimate the quantity of DNA. Whole-genome shotgun sequencing was performed using an Illumina GAIIx sequencer. Paired-end reads (2 × 100) were generated according to the manufacturer's instructions (Illumina, Inc.). After quality filtering (removal of adapters, artifacts, low-quality reads, and duplicates), a total of 14 million reads were used for *de novo* assembly using Velvet (6) and oriented into scaffolds using Nucmer of the Mummer package (4) against *K. pneumoniae* MGH 78578, the chosen reference strain. The genome sequence of *K. pneumoniae* KpO3210 was annotated using the RAST server (1).

The draft genome sequence of strain KpO3210 contains 214 contigs with an  $N_{50}$  of 198,533 nucleotides (nt) and a total length of 6,419,209 nt that were arranged into 64 scaffolds. The length of the longest scaffold was 5,662,754 nt, thus representing the major

part of the chromosome; 3 scaffolds represent major parts of three plasmids of *K. pneumoniae* KpO3210; and 4 contigs represent the OXA-48 carbapenemase-producing plasmid pOXA-48.

**Nucleotide sequence accession number.** The whole-genome shotgun sequence of *Klebsiella pneumoniae* KpO3210 is available in GenBank under accession number [AMRH00000000](http://www.ncbi.nlm.nih.gov/GenBank/AMRH00000000).

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