



# Draft Genome Sequence of a *Bacteroides fragilis* Strain Isolated from Peritoneal Fluid of a Patient from Kazakhstan

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**ABSTRACT** Here, we report the draft genome sequence of *Bacteroides fragilis* strain KZ02, isolated from a patient with peritonitis hospitalized in a health facility in Nur-Sultan, Kazakhstan. The genome of the strain contains 4,103 protein-coding genes, including the *cepA* gene, which causes resistance to beta-lactam antibiotics.

The *Bacteroides* genus, including the *Bacteroides fragilis* group, dominates in intra-abdominal anaerobic infections (1). The *B. fragilis* group consists of 24 species, including *B. fragilis*, *B. vulgatus*, *B. ovatus*, *B. thetaiotaomicron*, *B. uniformis*, *B. caccae*, and *Parabacteroides distasonis* (2). *B. fragilis* has a capsular polysaccharide complex and a virulence factor, which enhance the pathogenic properties of the bacterium (3). Differences in rates of resistance to some antibiotics were detected among the *Bacteroides* species and between isolates from different clinical sources (4).

Here, we sequenced the genome of *B. fragilis* strain KZ02 using an Ion Torrent Personal Genome Machine (PGM) sequencing platform (Thermo Fisher). The *B. fragilis* strain KZ02 was isolated from a patient with peritonitis hospitalized in Nur-Sultan, Kazakhstan. Informed consent and questionnaires were approved by the Local Ethics Committee of the RSE National Center for Biotechnology of the Ministry of Education and Science of the Republic of Kazakhstan (extract from protocol no. 4 of 29 August 2017). Organisms were collected using swabs from wounds from the drainage and subsequent immersion of probes in a tube containing Amies medium. Bacterial cultures were cultivated on bile esculin agar (BEA) in an anaerobic medium (in anaerobic jars using the Gas-pak method) at 37°C for 72 h. *B. fragilis* strain KZ02 was identified using 16S rRNA gene sequence analysis and the MALDI Biotyper microbial identification system (Bruker). The stocks of the strain were stored at –70°C in a cryoprotective medium. DNA was extracted using the traditional cetyltrimethylammonium bromide (CTAB) procedure (5). The whole-genome shotgun (WGS) sequence data were retrieved with the Ion Torrent sequencing platform as described previously (6). DNA libraries were prepared using an Ion Xpress Plus fragment library kit (Thermo Fisher). An Ion PGM HiQ sequencing kit and an Ion 318 Chip v.2 BC (both Thermo Fisher) were used for sequencing. The complete genome of *B. fragilis* strain KZ02 has a length of 5,148,042 bp. The genome of *B. fragilis* was sequenced with 33-fold coverage, a mean read length of 252 bp, and a G+C content of 43.09%. A total of 844,759 reads were produced. The quality check of the reads was done using FastQC v.0.11.9 (7). A total of 89 contigs, with an  $N_{50}$  value of 254,934 bp, were *de novo* assembled using SPAdes v.3.1.0 (8). The final assemblies were annotated with the NCBI Prokaryotic Genome Annotation Pipeline v.4.10 (9). Default parameters were used for all software. Annotation of the KZ02 genome with the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) identified a total of 4,503 genes, 4,103 of which predicted coding sequences, including the *cepA* gene, which causes resistance to beta-lactam antibiotics. In addition, 61 tRNAs and 1 complete 16S rRNA were detected and predicted to be responsible for the bacterium's pathogenicity and transmission patterns.

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**Data availability.** This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession no. [SSKK01000000](https://doi.org/10.1128/CMR.00008-07). The raw data from BioProject no. [PRJNA531645](https://doi.org/10.1128/genomeA.01101-13) were submitted to the NCBI SRA under experiment accession no. [SRX5656190](https://doi.org/10.1128/genomeA.01101-13).

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