Acinetobacter baumannii is a widespread serious pathogen (1) causing nosocomial infections (2). Also, community-acquired infections initiated by this pathogen feature high mortality rates (3). In this study, we present the complete genome sequence of the strain R2090, representing a community-acquired A. baumannii sequence type.

The strain R2090 was recovered from a rectal swab from a patient hospitalized in an Egyptian hospital. It was classified as belonging to the species A. baumannii, since its 16S rRNA gene sequence is identical to the corresponding sequence of the A. baumannii type strain ATCC 19606 (4).

For the establishment of the A. baumannii R2090 genome sequence, purified chromosomal DNA was used to construct an 8-kb mate pair sequencing library (Nextera mate pair preparation kit, Illumina, Inc.). The sequencing approach on an Illumina MiSeq system yielded 3,108,361 sequence reads accounting for 699,271,346 bases sequence information. Thus, a 183-fold coverage was achieved for the 3.8-Mb genome sequence of the strain R2090. An in silico gap closure approach followed by a PCR-based finishing strategy (7–9) was applied to complete the circular chromosome. Annotations for 3,601 coding sequences, 73 tRNA genes, and 6 rrn operons were deposited in the EMBL/GenBank database (EBI, NCBI) under the accession number LN868200.

ACKNOWLEDGMENTS

The bioinformatics support of the BMBF-funded project "Bielefeld-Gießen Center for Microbial Bioinformatics"—BiGi (grant 031A533) within the German Network for Bioinformatics Infrastructure (de.NBI) is gratefully acknowledged. I.M. and D.W. acknowledge the receipt of a scholarship from the CLIB Graduate Cluster "Industrial Biotechnology,” cofinanced by the Ministry of Innovation of North Rhine-Westphalia.

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