

# Complete Genome Sequences for Three Chromosomes of the *Burkholderia stabilis* Strain (ATCC BAA-67)

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**We report here the complete annotated genome sequence of the *Burkholderia stabilis* type strain ATCC BAA-67. There were three circular chromosomes with a combined size of 8,527,947 bp and G+C composition of 66.4%. These characteristics closely resemble the genomes of other sequenced members of the *Burkholderia cepacia* complex.**

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The *Burkholderia stabilis* strain ATCC BAA-67, which is referred to in other culture collections as LMG 14294, CCUG 34168, CIP 106845, or NCTC 13011, was originally isolated in 1993 from the sputum from a cystic fibrosis patient in Leuven, Belgium (1). The *B. stabilis* species belongs to the *Burkholderia cepacia* complex (Bcc) and can be distinguished from other members of this complex by its biochemical and physiological properties (1). ATCC BAA-67 is the type strain for the *B. stabilis* species.

Genomic DNA for sequence analysis was extracted using the MasterPure complete DNA and RNA purification kit (Epicentre), according to the manufacturer's DNA purification protocol for cell samples. The 20-kb libraries were generated with the Pacific Biosciences SMRTbell DNA template preparation kit. Sequence analysis was performed with the DNA/polymerase binding kit P6 version 2 and a PacBio RSII sequencer with two single-molecule real-time cells using C4 version 2 chemistry and 360-min movies.

Sequence reads were assembled *de novo* using RS\_HGAP Assembly.3 in the SMRT Analysis 2.3.0 portal, resulting in three complete circularized contigs that correspond to three chromosomes for this strain. The average depth of coverage was >105× for all three chromosomes. This assembly was verified using whole-genome mapping (Argus; OpGen) with the BamHI restriction enzyme (New England BioLabs).

The BAA-67 chromosome sizes were 3,886,092 bp, 3,318,880 bp, and 1,322,975 bp. G+C composition values were 66.3%, 66.9%, and 65.5% for each chromosome, respectively. The number of chromosomes, their lengths, and the high G+C content are similar to previously sequenced Bcc strains (see references 2 and 3 or Bcc taxid: 87882 on <http://www.ncbi.nlm.nih.gov/genome/browse/>).

The genome of BAA-67 was annotated with the Prokaryotic Genomes Annotation Pipeline at NCBI (NCBI\_PGAP). It was predicted to contain 7,425 coding genes, 6 rRNA operons, and 68 tRNAs. Chromosome 1, the largest, contained three intact rRNA operons and one operon, with the 23S rRNA gene broken by the

insertion of a transposase gene. Chromosomes 2 and 3 each contained one rRNA operon with a complete set of 16S, 23S, and 5S rRNA genes. Although the third and smallest chromosome carries rRNA genes and multiple unique enzymes, it may be nonessential for growth *in vitro*, since Bcc bacteria, including *B. stabilis* species, could be cured of this replicon (4, 5). The third chromosome has been described as a virulence plasmid, because its loss is associated with loss of virulence in several infection models (4, 5).

Previously reported pulsed-field gel electrophoresis typing experiments indicate that the genomes of different strains within *B. stabilis* species are conserved (1), suggesting that the genome of the strain ATCC BAA-67, which is the first completely sequenced genome for *B. stabilis*, is a good reference model for studies of other strains of this species.

**Accession number(s).** The finished annotated sequences of the three chromosomes of *Burkholderia stabilis* ATCC BAA-67 have been deposited in NCBI GenBank under the accession numbers CP016442, CP016443, and CP016444. The sequence reads were uploaded to the NCBI SRA under the accession number SRP079204.

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