

# Draft Whole-Genome Sequence of *Bacillus altitudinis* Strain B-388, a Producer of Extracellular RNase

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Here, we present a draft genome sequence of *Bacillus altitudinis* strain B-388, including a putative plasmid. The strain was isolated from the intestine of Indian meal moth, a common pest of stored grains, and it is characterized by the production of extracellular RNase, similar to binase, which is of interest for comparative studies and biotechnology.

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The species *Bacillus altitudinis* was described for the first time in 2006 as a microorganism found in air samples collected at an altitude of 41 km (1). Later, it was isolated from slaughterhouse soil (2), the digestive tract of a fish (3), silt (4), and plant rhizosphere (5). *B. altitudinis* strain B-388 was initially secured as *Bacillus entomocidus* from the intestinal tract of *Plodia interpunctella* (Indian meal moth), a common pest of stored grains, in the 1950s; it was recently reidentified using molecular methods. It produces an extracellular guanyl-preferring RNase similar to binase (6), an RNase secreted by a lately sequenced strain of *Bacillus pumilus* (7) and possessing antitumor and antiviral properties (8, 9). It also can be used as an RNA-degrading tool. The whole-genome shotgun sequencing project reported here is the second one for the species, following that of its type strain, *B. altitudinis* 41KF2b (DDBJ/EMBL/GenBank accession no. ASJC00000000.1).

The sequencing of *B. altitudinis* B-388 genomic DNA was performed on a 454-GS Junior system (Roche, USA), with approximately 20-fold overall genome coverage. The obtained 157,508 reads were assembled with the GS *de novo* Assembler (Newbler software suite, version May 2014), resulting in 59 contigs (>200 bp) with an  $N_{50}$  size of 127,734 bp. The calculated genome size was 3,706,590 bp, with a G+C content of 41.2 mol%. Contig 45 represents a putative plasmid of 4,528 bp. The genome was annotated using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) version 2.6 (<http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html>). A total of 3,730 genes and 3,555 coding sequences (CDSs) were predicted, and 77 RNAs were identified, including 71 tRNAs, 5 rRNAs, and 1 noncoding RNA (ncRNA). The total size of the assembly, G+C content, and the numbers of coding sequences and RNAs are in agreement with the respective figures for the type strain of *B. altitudinis* 41KF2b (3,678,935 bp, 41.3 mol%, 3,800 CDSs, and 55 RNAs).

A subsequent analysis of the genome content of *B. altitudinis* B-388 will help to determine the key aspects of its interaction with the environment and conduct thorough comparative studies with the closest phylogenetic neighbor *B. pumilus*, which produces extracellular RNase bearing only 1 amino acid substitution compared with the *B. altitudinis* RNase.

**Nucleotide sequence accession number.** This whole-genome shotgun project has been deposited in DDBJ/EMBL/GenBank under the accession no. JOVS00000000. The version described in this paper is the first version.

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