Idiomarina abyssalis KMM 227T is an aerobic flagellar gammaproteobacterium found at a depth of 4,000 to 5,000 m below sea level in the Pacific Ocean. This paper presents a draft genome sequence for *I. abyssalis* KMM 227T, with a predicted composition of 2,684,812 bp (47.15% G+C content) and 2,611 genes, of which 2,508 were predicted coding sequences.

The contigs were analyzed using QUAST version 2.3 and were found to have a total length of 2,684,812 bp and an average coverage of 13.2 (11). The largest contig was 983,913 bp, with an N50 value of 170,438 bp and a G+C content of 47.15%, just under the figure of 50% reported by Ivanova et al. (1). The National Center for Bioinformatics (NCBI) automatic annotation pipeline was used for genome annotation (12). A total of 2,611 genes, 2,508 coding sequences (CDSs), 40 pseudogenes, seven rRNAs, 55 tRNAs, and one noncoding RNA (ncRNA) were discovered using the NCBI pipeline. Comparisons of this genome with the *Idiomarina zobellii* genome and others will enable a more comprehensive metabolic and genetic study of adaptations to different saline environments.

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. LGOW00000000. The version described in this paper is version LGOW01000000.

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