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. LGOW0000000. The version described in this paper is version LGOW01000000.

ACKNOWLEDGMENTS

This work was supported by a Manchester Undergraduate Project Support grant and Richard Freed Enrichment Award from UNH Manchester to Bruce A. Rheaume, and an Undergraduate Research Award and Research Presentation Grant from the Hamel Center for Undergraduate Research at UNH to Bruce A. Rheaume. The Biological Sciences program at UNH Manchester also provided funds for sequencing. The funders had no role in the study design, data collection and interpretation, or the decision to submit the work for publication.

Sequencing was undertaken at the Hubbard Center for Genome Studies at UNH with the kind assistance of Kelley Thomas, Jordan Ramsdell, and Stephen Simpson. This work was the inaugural project of the Microbiology Education through Genome Annotation-New Hampshire (MEGA-NH) program.

REFERENCES


