

Draft Genome Sequence of *Pseudoalteromonas* sp. Strain A2, an Isolate with High Antioxidative Activity from Arctic Seawater

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Here we report the draft genome sequence of *Pseudoalteromonas* strain A2, isolated from Arctic seawater in the pack-ice zone, which has high antioxidative activity against H₂O₂. The genomics information of this strain will facilitate the study of antioxidative mechanisms, cold adaptation properties, and evolution of this genus.

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The genus *Pseudoalteromonas* is one of the largest genera within the class *Gammaproteobacteria* and currently comprises more than 30 species. It was described to accommodate nonpigmented, Gram-negative, heterotrophic, aerobic, polar-flagellated species of marine bacteria that have DNA G+C contents ranging from 38 to 50 mol% (1). In recent years, novel species belonging to *Pseudoalteromonas* have been isolated from a wide range of habitats, including seawater (2, 3), marine sediment (4), tidal flat (5), and sponge (6). *Pseudoalteromonas* sp. strain A2 was isolated from Arctic seawater in the pack-ice zone (120°21.017' E, 86°48.196' N), collected during the 5th Chinese National Arctic Expedition, and it has high antioxidative activity against H₂O₂.

The genome of *Pseudoalteromonas* sp. strain A2 was sequenced with Illumina HiSeq 2000 platforms by Shanghai Majorbio Biopharm Technology Co., Ltd. (Shanghai, China). A paired-end library with a fragment length of 300–500 bp and a mate-pair library with a fragment length of approximately 3 kb were constructed, generating a total of 3,563,169 and 2,851,727 high-quality paired reads and representing 159-fold and 127-fold coverage, respectively. SOAPdenovo version 1.05 (<http://soap.genomics.org.cn>) was used to assemble the genome with multiple k-mer parameters. GapCloser software (from the SOAPdenovo website) was subsequently applied to fill the remaining local inner gaps and correct the single-base polymorphism for the final assembly result. Glimmer version 3.0 (7), tRNAscan-SE (8), and RNAmmer (9) were used to predict protein-encoding genes (CDSs), tRNAs, and rRNAs, respectively. Then all gene models were blasted against the NCBI nonredundant (NR), Swiss-Prot (<http://uniprot.org>), KEGG (<http://www.genome.jp/kegg>), and Clusters of Orthologous Groups (COG; <http://www.ncbi.nlm.nih.gov/COG>) databases for functional annotation.

The draft genome of *Pseudoalteromonas* sp. strain A2 comprises 4,170,731 bp, with an average G+C content of 40.13%, consisting of 59 contigs (contig N₅₀, 214,730 bp). The genome sequence contains 3,703 candidate CDSs, and the average gene length is 984 bp. In addition, 161 tRNA genes for 20 amino acids and a 16S rRNA operon were identified in the genome. The genome sequence enables the further study of the antioxidative mechanisms, cold adaptation properties, and evolution of this genus.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number **JPMC00000000**. The version described in this paper is version JPMC01000000.

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