

**Complete genome sequence data of an Antarctic bacterium *Arthrobacter* sp. EM1  
from the freshwater lake of the King George Island**

**ABSTRACT**

*Arthrobacter* sp. EM1 is a cold-adapted bacterium isolated from the Antarctic region, which was known to exhibit mannan-degrading activity. Accordingly, this strain not only promises a cell factory for mannan-degrading enzymes, widely used in industry but also serves as a model organism to decipher its cold adaptation mechanism. Accordingly, whole genome sequencing of the EM1 strain was performed via Single Molecule Real Time sequencing under the PacBio platform, followed by genome HGAP de novo assembly and genome annotation through Rapid Annotation System Technology (RAST) server. The chromosome of this strain is 3,885,750 bp in size with a GC content of 65.8. The annotation predicted a total of 3607 protein-coding genes and 65 RNA genes, which were classified under 398 subsystems. The subsystem with the highest number of genes is carbohydrate metabolism (397 genes), which includes two genes encoding mannan-degrading enzymes (endoglucanase and  $\alpha$ -mannosidase). This confirmed that the EM1 strain is able to produce cold-adapted mannan degrading enzymes. The complete genome sequence data have been submitted to the National Center for Biotechnology Information (NCBI) and have been deposited at GenBank (Bioproject ID Accession Number: PRJNA963062; Biosample ID Accession Number: SAMN34434776; GenBank: CP124836.1; <https://www.ncbi.nlm.nih.gov/nucleotide/CP124836>).