



## Genome announcement

# Complete genome sequence of *Fron dih abitans* sp. strain PAMC28766, a novel carotenoid-producing and radiation-resistant strain isolated from an Antarctic lichen



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## ABSTRACT

Here, we report the first complete genome sequence of *Fron dih abitans* sp. strain PAMC28766, which was found to consist of three plasmids, one chromosome (4,345,897 bp), and a series of genes involved in carotenoid biosynthesis and nucleotide excision repair. An analysis of the *Fron dih abitans* sp. PAMC28766 genome will improve our understanding of the carotenoid biosynthesis pathway. Furthermore, the sequence data will provide novel insight into UV radiation-resistance in extremely cold environments.

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*Fron dih abitans* sp. strain PAMC28766 (deposited as PAMC28766 in the Polar and Alpine Microbial Collection, Korea Polar Research Institute, Incheon, Korea) was isolated from *Himantormia* sp., an Antarctic lichen species collected on Barton Peninsula, King George Island, Antarctica (62°13'S, 58°47'W), an extreme environment with high UV radiation levels, low temperatures, and low oxygen levels. Greene et al. (2009) recently established the genus *Fron dih abitans* as a member of the family *Microbacteriaceae*. *Fron dih abitans* replaced the illegitimate genus name *Fron dicolar* (Zhang et al., 2007), as described by Lee (2010) and Cardinale et al. (2011). Until now, little has been known about this species, and there have been no reports of the complete genome sequence of bacteria from this genus. In this paper, we report the first complete genome sequence of *Fron dih abitans* sp. PAMC28766.

Genomic DNA was extracted from *Fron dih abitans* sp. PAMC28766 using a QIAamp DNA Mini Kit (Qiagen, Valencia, CA), and the quantity and purity were determined using an Agilent 2100 Bioanalyzer (Agilent Technologies, Santa Clara, CA). Genome

sequencing was performed using PacBio RS II single-molecule real-time (SMRT) sequencing technology (Pacific Biosciences, Menlo Park, CA). Ten-kilobase SMRTbell library inserts were sequenced using SMRT cells. Raw sequence data were generated from 100,791 reads and 1,483,767,986 bp that were de novo assembled using the hierarchical genome-assembly process (HGAP) protocol (Chin et al., 2013) and RS HGAP Assembly 2 in SMRT analysis version 2.3 software (Pacific Biosciences; <https://github.com/PacificBiosciences/SMRT-Analysis>).

The complete circular chromosome was 4,345,897 bp with a G+C content of 68.9%. Coding DNA sequences (CDSs) were predicted and annotated using the Rapid Annotation using Subsystem Technology (RAST) server (Aziz et al., 2008). Predicted gene sequences were translated and searched against the National Center for Biotechnology Information (NCBI) non-redundant database, Clusters of Orthologous Groups (COG), and Kyoto Encyclopedia of Genes and Genomes (KEGG). A total of 4,260 CDSs were predicted; the coding region accounted for 87.75% of the *Fron dih abitans* sp. PAMC28766 genome. In addition, 47 tRNA and 6 rRNA were predicted in the complete chromosome 1 (Table 1).

Preliminary annotations of the CDSs from the *Fron dih abitans* sp. PAMC28766 genome revealed carotenoid biosynthesis genes, including those encoding lycopene elongase (AX769.02545), C<sub>50</sub> carotenoid epsilon cyclases (AX769.02550 and AX769.02555), phytoene dehydrogenases (AX769.02560 and AX769.09510),

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**Table 1**  
Genome features of *Fronidhabitans* sp. PAMC28766.

Features	Chromosome 1	Plasmid 1	Plasmid 2	Plasmid 3
Genome size (bp)	4,345,897	212,902	135,614	72,450
Contig numbers	1	1	1	1
G + C content (%)	68.90	64.35	63.65	64.08
Protein coding genes	4260	253	158	82
rRNA genes	6	–	–	–
tRNA genes	47	–	–	–

phytoene synthase (AX769\_02565), geranylgeranyl diphosphate synthases (AX769\_02570 and AX769\_11910), geranylgeranyl pyrophosphate synthetase (AX769\_19160), and 4-hydroxy-3-methylbut-2-enyl diphosphate reductase (AX769\_08815). Furthermore, the sequence data revealed the presence of nucleotide excision repair (NER) genes encoding subunits that comprise the excinuclease UvrABC protein complex. Specifically, genes encoding three copies of subunit A (AX769\_01295, AX769\_03450 and AX769\_12800), one copy of subunit B (AX769\_12810), and one copy of subunit C (AX769\_12795) were identified.

These whole genome data will allow us to better understand the molecular basis of carotenoid biosynthesis and resistance to UV radiation in extremely environments such as those found in Antarctica.

#### Nucleotide sequence accession numbers

The complete genome information of *Fronidhabitans* sp. PAMC28766 was deposited in GenBank under the accession numbers CP014513–CP014516.

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