Genome Sequence of *Galbibacter marinum* Type Strain ck-I2-15

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*Galbibacter marinum* strain ck-I2-15\(^T\) was isolated from an arsenite-resistant consortium enriched from the deep sea sediment of a hydrothermal vent field on the Southwest Indian Ocean Ridge. Here, we present the draft genome of strain ck-I2-15\(^T\), which contains 3,572,447 bp with a G+C content of 37.04% and contains 3,099 protein-coding genes and 38 tRNA genes.

*Galbibacter marinum* strain ck-I2-15\(^T\) (CCTCC AB 209062\(^T\), LMG 25228\(^T\), MCCC 1A03044\(^T\)) was isolated from an arsenite-resistant consortium enriched from the deep sea sediment of the Southwest Indian Ocean Ridge (1, 3). Until now, only one strain of this species was isolated from marine environments by our lab, and there are no other strains (with >97% 16S rRNA gene sequence similarity) that can be retrieved in NCBI. The genus *Galbibacter* was first proposed by Khan (2) and contains two species at the time of writing, including *G. marinum* ck-I2-15 (3).

The genome sequence of *G. marinum* ck-I2-15\(^T\) was determined by Shanghai Majorbio Bio-pharm Technology Co., Ltd. (Shanghai, China), using Solexa paired-end sequencing technology. A total of 8,270,066 paired-end reads (500-bp library) were generated to reach a 375-fold depth of coverage with Illumina/Solexa Genome Analyzer IIx (Illumina, SanDiego, CA), and the gaps among scaffolds were closed by specific PCR and Sanger sequencing using an ABI3730 system (Applied Biosystems). The genome of *G. marinum* ck-I2-15\(^T\) consists of 80 contigs (\(N\_90\)) of 3,572,447 bp and had an average G+C content of 37.04%. Automatic gene annotation was carried out by the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP) (http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html), followed by manual editing. The genome contains 3,099 candidate protein-encoding genes (with an average size of 1,019 bp), giving a coding intensity of 88.5%. A total of 2,157 proteins were assigned to cluster of orthologous groups (COG) families (4). Thirty-eight tRNA genes for 19 amino acids (lack of Lys) were identified.

There are an arsenate reductase and an arsenical resistance protein present in the genome of strain CK-I2-15\(^T\). The genome sequence of CK-I2-15\(^T\) and its curated annotation are important assets to better understand the physiology and metabolic potential of *Galbibacter marinum* and will open up new opportunities in the functional genomics of this species.

**Nucleotide sequence accession number.** The draft genome sequence of *Galbibacter marinum* ck-I2-15\(^T\) has been deposited at GenBank under accession number AM8500000000 (chromosome).

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**REFERENCES**


