Williamsia profundi sp. nov.

Submitted by Pu, Shuwei

Species *Williamsia profundi*

Etymology
[pro.fun'di] **L. gen. n.** *profundi*, of the depths, living within the depths of the oceans

Nomenclatural type
Genome sc|0005466 [Ts]

Reference Strain
Strain sc|0043580: = MCCC 1K09832 = JCM 37991

Description
Cells are aerobic, Gram-stain-positive, non-motile, and exhibit a coccoid to rod-shaped morphology (0.8–3.3 × 0.4–0.6 µm). Growth occurs at 1–40°C (optimum: 32°C) on 2216E agar. The major fatty acids are C16:0, C18:1ω9c, 10-methyl C18:0, C16:1ω6c, and C18:0. The genomic DNA G+C content of the type strain is 70.1 mol%.

The reference strain, SKLECPSW1T, was isolated from a deep-sea water sample collected from the Eastern Indian Ocean (89°59.938′ E, 9°59.938′ S). It has been deposited in the Marine Culture Collection of China (MCCC) under accession number MCCC 1K09832T and in the Japan Collection of Microorganisms (JCM) as JCM 37991T. The 16S rRNA gene sequence is available in GenBank under accession number PQ858246.2. Raw genome sequencing data have been submitted to the Sequence Read Archive under accession number SRR31976005.

Classification
Bacteria » *Actinomycetota* » *Actinomycetes* » *Mycobacteriales* » *Gordoniaceae* » *Williamsia* » *Williamsia profundi*

References
Effective publication: Pu et al., 2026 [1]

Registry URL
https://seqco.de/i:52933

References

1. Pu et al. (2026). Williamsia profundi sp. nov., a novel deep-sea Actinomycetota isolate with versatile metabolic potential and specialized ecological adaptability. *Systematic and Applied Microbiology*. DOI: 10.1016/j.syapm.2026.126775

Register List Certificate of Validation

On behalf of the *Committee on the Systematics of Prokaryotes Described from Sequence Data* (SeqCode Committee), we hereby certify that the Register List **seqco.de/r:hg8tm-ca** submitted by **Pu, Shuwei** and including 1 new name has been successfully validated.

Date of Priority: 2026-11-09 02:14 UTC
DOI: 10.57973/seqcode.r:hg8tm-ca