

## Species *Aquitaenariimonas noxiae*<sup>Ts</sup>

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### Etymology

[nox.i'ae] N.L. fem. gen. n. *noxiae*, of Nox, named for the Roman primordial goddess and personification of the night

### Nomenclatural type

[NCBI Assembly: GCA\\_002780005.1](#)<sup>Ts</sup>

### Description

This species is the type for the genus *Aquitaenariimonas*. The estimated genome size for members of this species is approximately 2 Mb. Two unique assemblies are available for this species, and range in % GC content from 42.05-42.75 %. The highest quality genome available for the species encodes a very large ORF, and genes associated with acetogenesis and the Wood-Ljungdahl pathway, but an Rnf complex is absent. A respiratory F-type ATPase, membrane-bound Group 4g [NiFe] hydrogenase and all components for a Type-4a pilus investigated are encoded in the genomes. This species has been recovered from metagenomic samples of groundwater from Crystal Geyser, near Green River, Utah, USA, with temperature measurements at sampling recorded at 17 °C. The nomenclatural type for the species is the genome GCA\_002780005.1.

### Classification

*Bacteria* » *Omnitrophota* » “Gorgyraia” » *Aquitaenariimonadales* » *Aquitaenariimonadaceae* » *Aquitaenariimonas* » *Aquitaenariimonas noxiae*<sup>Ts</sup>

### References

Effective publication: Seymour et al., 2023 [1]

### Registry URL

<https://seqco.de/i:23724>

## References

1. Seymour et al. (2023). Hyperactive nanobacteria with host-dependent traits pervade Omnitrophota. *Nature Microbiology*. DOI:10.1038/s41564-022-01319-1