

## Species *Aquivivens invisus*<sup>Ts</sup>

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### Etymology

[in.vi'sus] L. masc. adj. *invisus*, unseen, referring to them being hidden or unseen as they occur in the subsurface

### Nomenclatural type

[NCBI Assembly: GCA\\_001804415.1](#)<sup>Ts</sup>

### Description

This species is the nomenclatural type for the genus *Aquivivens*. Genomes belonging to this species are predicted to range between 1.7 Mb and 2 Mb. %GC content for the species range between 62.83-63.50 %. Genomes of this species encode respiratory complexes I through V, with aerobic respiration being likely due to the presence of cytochrome c oxidase in the genomes. Nitrite is predicted as alternative terminal electron acceptor, while a metal-reducing cytochrome is also encoded by genomes belonging to this species. ADP/ATP translocase, components of the tight-adherence complex, genes for the production of a Type-4a pilus, and at least two very large ORFs are encoded by genomes of this species. Assemblies for this species originated from soil and groundwater samples from Rifle, Colorado, USA, with a pH of 7.28 and oxygen concentrations of 0.29 mM. The nomenclatural type for the species is the genome GCA\_001804415.1.

### Classification

*Bacteria* » *Omnitrophota* » *Aquiviventia* » *Aquiviventales* » *Aquiviventaceae* » *Aquivivens* » *Aquivivens invisus*<sup>Ts</sup>

### References

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

### Registry URL

<https://seqco.de/i:23665>

## References

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