

## Species *Phelpsiimicrobium noxiivivens*<sup>Ts</sup>

---

### Etymology

[nox.i.i.vi'vens] N.L. fem. n. *Nox*, from the Roman primordial goddess and personification of the night, Nox; L. pres. part. *vivens*, living; N.L. part. adj. *noxiivivens*, living in darkness

### Nomenclatural type

[NCBI Assembly: GCA\\_001873995.1](#)<sup>Ts</sup>

### Description

This species is the type for the genus *Phelpsiimicrobium*. The estimated genome size for the species is between 1.5 to 1.8 Mb, with %GC for genomes ranging between 43.80-44.08 %. Genes for acetogenic pathways, and an Rnf complex is present in the genomes of this species. Genes for respiratory complexes I and V (respiratory F-type ATPase) are also present in the genomes, and are likely involved in redox balancing and ATP synthesis. All genes associated with the tight-adherence (Tad) complex, and the production of a Type-4a pilus is present in the genomes. A "symbiotic" F-type ATPase and very large ORFs are encoded by the genomes. All assemblies assigned to this species originate from Crystal Geysir, near Green River, Utah, USA. The nomenclatural type for the species is the genome GCA\_001873995.1.

### Classification

*Bacteria* » *Omnitrophota* » "Velamenicoccia" » "Velamenicoccales" » "Velamenicoccaceae" » *Phelpsiimicrobium* » *Phelpsiimicrobium noxiivivens*<sup>Ts</sup>

### References

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

### Registry URL

<https://seqco.de/i:23740>

## 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)